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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:47:40 ; Search time 32.57 Seconds
(without alignments)
19,831 Million cell updates/sec

Title: US-08-981-824-1

Perfect score: 110
Sequence: 1 DVNATFLHATDLPACDGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1436

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	23.6	19	1	P31066 desulfobact
2	22.7	23	1	P30254 manduca sex
3	24	12	1	P14405 streptomyc
4	21.8	18	1	P01360 escherichia
5	21.8	23	1	P30253 manduca sex
6	23	10	1	P38553 locusta mtg
7	20.9	10	1	P21144 leucophaea
8	23	10	1	P41494 drosophila
9	20.9	19	1	P80704 comonomas t
10	22	19	1	P36503 streptomyc
11	22	19	1	P38655 streptomyc
12	20.0	24	1	P26317 heliothis v
13	22	25	1	P80376 thermus aqu
14	21	19	1	P36504 streptomyc
15	21	19	1	P36502 streptomyc
16	21	19	1	P31061 bos laurus
17	20.5	13	1	P15987 glycine max
18	20.5	17	1	P21983 treponema p
19	20.5	25	1	P18523 manduca sex
20	20	10	1	P15471 conus stria
21	20	13	1	P01520 conus geogr
22	20	13	1	P28878 conus stria
23	20	14	1	P01521 conus magus
24	20	14	1	P01519 conus geogr
25	20	15	1	P01519 conus geogr
26	20	15	1	P01519 conus geogr
27	20	16	1	P01519 conus geogr
28	20	16	1	P01519 conus geogr
29	20	16	1	P01519 conus geogr
30	20	16	1	P01519 conus geogr
31	20	16	1	P01519 conus geogr
32	20	16	1	P01519 conus geogr
33	20	16	1	P01519 conus geogr

34	20	18.2	21	1	P14475 muntiacus m
35	20	18.2	21	1	P33036 actinobact
36	20	18.2	25	1	P22028 bochrops ja
37	20	18.2	25	1	P80891 vibrio fusc
38	19.5	17.7	22	1	P80530 fasciola he
39	19	17.3	13	1	P82036 uperoleta 1
40	19	17.3	14	1	P23039 alteromonas
41	19	17.3	14	1	P11760 ardiaea pun
42	19	17.3	15	1	P80636 zea mayis (m
43	19	17.3	16	1	P32371 eubacterium
44	19	17.3	16	1	P50984 conus penne
45	19	17.3	16	1	P50985 conus penne

ALIGNMENTS

RESULT 1	ID	PHSL_DESBN	STANDARD	PRT	19 AA.
AC	P13066				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	01-JAN-1990 (Rel. 13, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	PERIPLASMIC [NIFESE] HYDROGENASE LARGE SUBUNIT (EC 1.18.99.1) (NIFESE DE HYDROGENYLASE LARGE CHAIN) (FRAGMENT).				
OS	Desulfobactrio baculatus (strain Norway 4).				
OC	Bacteria; Proteobacteria; delta subdivision; Desulfomicrobium.				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE-88106446; PubMed-3322275;				
RA	Decker B.C., He S.H., Li C., Menon N., Choi E.S., Przybyla A.E.,				
RA	Devartanian D.V., Peck H.D. Jr., Faugue G., le Gall J., Teixeira M.,				
RA	Moura I., Moura J.J.G., Patil D., Huynh B.H.;				
RT	Identification of three classes of hydrogenase in the genus,				
RT	Desulfobactrio.				
RT	Biochem. Biophys. Res. Commun. 149:369-377(1987).				
CC	-1- CATALYTIC ACTIVITY: 2 REDUCED FERREDOXIN + 2 H(+) -> 2 OXIDIZED				
CC	-1- FERREDOXIN + H(2).				
CC	-1- COFACTOR: ONE NICKEL ION, TWO 4FE-4S CLUSTERS AND ONE				
CC	SELENOCYSTEINE.				
CC	-1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.				
CC	-1- SUBCELLULAR LOCATION: PERIPLASMIC.				
CC	-1- SIMILARITY: BELONGS TO THE [NIFE]/[NIFESE] HYDROGENASE LARGE				
DR	P1R; H27480; H27480.				
DR	INTERPRO: IPR001501; .				
DR	PROSITE: PS00507; NI_HGNASE_L.1; PARTIAL.				
KW	PROSITE: PS00508; NI_HGNASE_L.2; PARTIAL.				
DR	Oxidoreductase; Periplasmic; Nickel; Selenium; Selenocysteine.				
FT	NON_TER 19				
SQ	SEQUENCE 19 AA; 1942 MW; 2BFCDD2360F00367 CRC64;				

Query Match Score 26; DB 1; Length 19;
Best Local Similarity 57.1%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 14 PACDGER 20
DB 6 PADGK 12

RESULT 2
ID PAP2_MANSE STANDARD; PRT; 23 AA.
AC P30254;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARALYTIC PEPTIDE II (PP II).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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OC Pepterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Spilargidae; Spilargidae; Spilargidae; Manduca.
RN [1]
RP SEQUENCE.
RC TISSUE=HEMOLYMPH;
RX MEDLINE=91302298; PubMed=2071576;
RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
RA Quistad G.B.,
RT "Isolation and identification of paralytic peptides from hemolymph of
RT the lepidopteran insects Manduca sexta, Spodoptera exigua, and
RT Heliothis virescens."
RL J. Biol. Chem. 266:12873-12877(1991).
CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
DR PIR: B39855; B39855.
KW Hemolymph.
FT DISULFID
SQ SEQUENCE 23 AA: 2420 MW: 0B26CB5C31265FE4 CRC64;

Query Match 22.7%; Score 25; DB 1; Length 23;
Best Local Similarity 43.8%; Pred. No. 5.9e+02;
Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 NYAFHATDLPACDG 18
|:| | | | | |
Db 2 NFAGCATGFLRTADG 17

RESULT 3
XYLA_STRVN
ID XYLA_STRVN STANDARD; PRT; 12 AA.
AC P14405;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE XYLOSE ISOMERASE (EC 5.3.1.5) (FRAGMENT).
OS Streptomyces violaceoruber.
OC Bacteria; Firmicutes; Actinobacteriae; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE.
RC STRAIN=IMG 7183;
RX MEDLINE=90104230; PubMed=2604694;
RA Vangyispetre W., Ampe C., Kersters-Hilderson H., Tempst P.;
RT "Single active-site histidine in D-xylose isomerase from Streptomyces
RT violaceoruber. Identification by chemical derivatization and peptide
RT mapping."
RL Biochem. J. 263:195-199(1989).
CC -1- CATALYTIC ACTIVITY: D-XYLOSE -> D-XYLULOSE.
CC -1- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
DR HSPSP: P37031; I0XI.
DR INTERPRO: IPR001998;
DR PROSITE: PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
DR PROSITE: PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
KW Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
FT ACT_SITE 1 5
FT NON_TER 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA: 1375 MW: E749268EBA1AAAA1 CRC64;

Query Match 21.8%; Score 24; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 HATDLP 14
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Db 5 HDDDLIP 11

RESULT 4
HSTB_ECOLI
ID HSTB_ECOLI STANDARD; PRT; 18 AA.
AC P01560;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HEAT-STABLE ENTEROTOXIN ST-2 (ST-B).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE.
RC STRAIN=18D / SEROTYPE 0.42:K86:H37;
RX MEDLINE=81264141; PubMed=7021541;
RA Chan S.-K., Giannelis R.A.;
RT "Amino acid sequence of heat-stable enterotoxin produced by
RT Escherichia coli pathogenic for man."
RL J. Biol. Chem. 256:7744-7746(1981).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=87191003; PubMed=3552731;
RA Shimomishi Y., Hidaka Y., Kozizumi M., Hane M.,imoto S., Takeda T.,
RA Miyatani T., Takeda Y.,
RT "Mode of disulfide bond formation of a heat-stable enterotoxin (StH)
RT produced by a human strain of enterotoxigenic Escherichia coli."
RL FEBS Lett. 215:165-170(1987).
CC -1- FUNCTION: TOXIN WHICH ACTIVATES THE PARTICULATE FORM OF GUANYLATE
CC CYCLASE AND INCREASES CYCLIC GMP LEVELS WITHIN THE HOST
CC INTERNAL EPITHELIAL CELLS.
CC -1- DISEASE: BOTH HEAT-STABLE AND HEAT-LABILE ENTEROTOXINS ARE
CC PRODUCED BY PATHOGENIC STRAINS OF E. COLI AND AFFECT THE DIGESTIVE
CC TRACT OF MAMMALS.
CC -1- SIMILARITY: BELONGS TO THE HEAT-STABLE ENTEROTOXIN FAMILY.
DR PIR: A01823; OHCC2.
DR HSPSP: P01559; 1ETN.
DR INTERPRO: IPR001489;
DR PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
KW Toxin; Enterotoxin.
FT DISULFID 5 10
FT DISULFID 6 14
FT DISULFID 9 17
FT DISULFID 9 17
SQ SEQUENCE 18 AA: 1978 MW: D0C975F49D600650 CRC64;

Query Match 21.8%; Score 24; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 14 PACDG 18
| | | |
Db 12 PACAG 16

RESULT 5
PAP1_MANSE
ID PAP1_MANSE STANDARD; PRT; 23 AA.
AC P30253;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARALYTIC PEPTIDE I (PP I).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pepterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Spilargidae; Spilargidae; Spilargidae; Manduca.
RN [1]
RP SEQUENCE.
RC TISSUE=HEMOLYMPH;
RX MEDLINE=91302298; PubMed=2071576;

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RA Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L.,
 RA Quistad G.B.:
 RT "Isolation and identification of paralytic peptides from hemolymph of
 RT the lepidopteran insects *Manduca sexta*, *Spodoptera exigua*, and
 RT *Heliothis virescens*.";
 RL J. Biol. Chem. 266:12873-12877(1991).
 CC -1- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO
 CC LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE
 CC HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.
 CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
 CC PIR: A39855; A39855.
 DR Hemolymph.
 FT DISULFID 7 19 BY SIMILARITY.
 SQ SEQUENCE 23 AA: 2436 MW: 0B26CB5C29855FE4 CRC64;

Query Match 21.8%; Score 24; DB 1; Length 23;
 Best Local Similarity 43.8%; Pred. No. 8.6e+02;
 Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 NYAFHATDLPACDG 18
 DB 2 NFAGCATGYLRTADG 17

RESULT 6
 FARP.LOCMI STANDARD; PRT; 10 AA.
 AC P38553;
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SCHISTOFLERAMIDE (PDVDFLRF-AMIDE) (CARDIOEXCITATORY NEUROPEPTIDE).
 OS Locusta migratoria (Migratory locust), and
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.
 RN [1]
 RP SEQUENCE.
 RC SPECIES-S.GREGARIA; TISSUE-THORACIC NERVOUS SYSTEM;
 RX MEDLINE-93324430; PubMed-7687352;
 RA Schoofs L., Holman G.M., Paemen L., Veeleert D., Amelknck M.,
 RA de Loof A.:
 RT "Isolation, identification, and synthesis of PDVDFLRFamide
 RT (Schistoflrfamide) in *Locusta migratoria* and its association with the
 RT male accessory glands, the salivary glands, the heart, and the
 RT oviduct.";
 RL Peptides 14:409-421(1993).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-S.GREGARIA; TISSUE-THORACIC NERVOUS SYSTEM;
 RX MEDLINE-89246543; PubMed-2719702;
 RA Robb S., Packman L.C., Evans P.D.:
 RT "Isolation, primary structure and bioactivity of schistoflrfamide, a
 RT FMRF-amide-like neuropeptide from the locust, *Schistocerca*
 RT gregaria.";
 RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
 CC -1- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
 CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
 CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
 CC -1- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
 CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC PIR: A32543; A32543.
 DR Neuropeptide; Amidation.
 FT MOD.RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA: 1244 MW: D3C51729D2C1EAB2 CRC64;

Query Match 20.9%; Score 23; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 5.5e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DVNYAF 7
 DB 2 DVDHVF 8

RESULT 7
 LCMS.LEUMA STANDARD; PRT; 10 AA.
 AC P21144; P41497;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE LEUCOMYOSUPPRESSIN (LMS) (LEM-MS).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberidae; Blaberidae; Leucophaea.
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-HEAD;
 RA Holman G.M., Cook B.J., Nachman R.J.:
 RT "Isolation, primary structure and synthesis of leucomyosuppressin,
 RT an insect neuropeptide that inhibits spontaneous contractions of the
 RT cockroach hindgut.";
 RL Comp. Biochem. Physiol. 85C:329-333(1986).
 CC -1- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH
 CC PROTEODEUM (HINDGUT).
 CC Neuropeptide; Amidation.
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA: 1275 MW: D3C45229D2C1EAB2 CRC64;

Query Match 20.9%; Score 23; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 5.5e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVNYAF 7
 DB 2 DVDHVF 8

RESULT 8
 NEMS.DROME STANDARD; PRT; 10 AA.
 AC P41494;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE NEOMYOSUPPRESSIN (NEB-MS).
 GN NEMS.
 OS Drosophila melanogaster (Fruit fly), and
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydrioidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE.
 RC SPECIES-D.MELANOGASTER;
 RX MEDLINE-93002195; PubMed-1390001;
 RA Nichols R.:
 RT "Isolation and structural characterization of Drosophila
 RT TDVDFLRFamide and FMRFamide-containing neural peptides.";
 RL J. Mol. Neurosci. 3:213-218(1992).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-S.BULLATA; TISSUE-HEAD;
 RX MEDLINE-93047886; PubMed-1358537;
 RA Fonagy A., Schoofs L., Proost P., Van Damme J., Bueds H., De Loof A.:
 RT "Isolation, primary structure and synthesis of neomyosuppressin, a
 RT myoinhibiting neuropeptide from the grey fleshfly, *Neobellieria*

RT bullata.";
 RL Comp. Biochem. Physiol. 102C:239-245(1992).
 CC -1- FUNCTION: MYOINHIBITING NEUROPEPTIDE.
 DR FLVASE; FBgn0013996; Nems.
 KM Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1248 MW; D3C00329D2C1EAB2 CRC64;

 Query Match 20.9%; Score 23; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 5.5e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 DVNTAF 7
 Db 2 DVNTAF 8

 RESULT 9
 DHAB_COMTE STANDARD; PRT; 19 AA.
 AC P80704;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ALDEHYDE DEHYDROGENASE, BETA CHAIN (EC 1.2.99.3) (ALDH) (FRAGMENT).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 CC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-ATCC 15667;
 RA Lytkx D.M.A.M., Kim S.W., de Vries S., Duine J.A.;
 RL Submitted (JUL-1996) to the SWISS-PROT data bank.
 CC -1- CATALYTIC ACTIVITY: AN ALDEHYDE + ACCEPTOR + H(2)O = AN ACID +
 CC REDUCED ACCEPTOR.
 CC -1- COFACTOR: MOLYBDENUM.
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA AND A GAMMA
 CC CHAIN.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2096 MW; 89BD67D4D05A212E CRC64;

 Query Match 20.9%; Score 23; DB 1; Length 19;
 Best Local Similarity 57.1%; Pred. No. 1e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 4 YAFUAT 10
 Db 2 YAFYST 8

 RESULT 10
 DURC_STRGP STANDARD; PRT; 19 AA.
 AC P36503;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE LANTIBIOTIC DURAMYCIN C.
 OS Streptomyces griseolutes.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-R2107;
 RX MEDLINE-91107436; Pubmed-2125590;
 RA Fredericq A., Fendrich G., Marki F., Marki W., Gruner J.,
 RA Raschdorf F., Peter H.H.;
 RT "Duramycin B and C, two new lanthionine containing antibiotics as
 RT inhibitors of phospholipase A2. Structural revision of duramycin and
 RT cinnamycin."
 RL J. Antibiot. 43:1403-1412(1990).

RN [2]
 RP STRUCTURE BY NMR.
 RA Zimmermann N., Freund S., Fredericq A., Jung G.;
 RT "Solution structure of the lantibiotics duramycin B and C.";
 RL (in) Schneider C.H., Eberle A.N. (eds.);
 RL Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1992).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE-93387292; Pubmed-8375380;
 RA Zimmermann N., Freund S., Fredericq A., Jung G.;
 RT "Solution structures of the lantibiotics duramycin B and C.";
 RL Eur. J. Biochem. 216:419-428(1993).
 CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
 CC -1- FTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF
 CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE
 CC BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND
 CC CLEAVAGE OF THE MODIFIED PRECURSOR.
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 KW Antibiotic; Lantibiotic.
 FT MOD_RES 4 4
 FT MOD_RES 6 6
 FT MOD_RES 11 11
 FT MOD_RES 18 18
 FT MOD_RES 19 19
 FT THIOETH 1 1
 FT THIOETH 4 4
 FT THIOETH 14 14
 FT THIOETH 11 11
 SQ SEQUENCE 19 AA; 2007 MW; E2404E3E3F5286A CRC64;

 Query Match 20.0%; Score 22; DB 1; Length 19;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 15 ACDE 18
 Db 13 SCDE 16

 RESULT 11
 LANC_STRSQ STANDARD; PRT; 19 AA.
 ID LANC_STRSQ
 AC P38655;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE LANTIBIOTIC ANCOVENIN.
 OS Streptomyces sp. (strain A647P-2).
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE.
 RA Wakamaya T., Ueki Y., Shiba T., Kido Y., Motoki Y.;
 RT "The structure of ancovenin, a new peptide inhibitor of angiotensin I
 RT converting enzyme.";
 RL retrahedron Lett. 26:665-668(1985).
 CC -1- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.
 CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 DR PIR; A61284; EWSMAN.
 KW Antibiotic; Lantibiotic.
 FT MOD_RES 4 4
 FT MOD_RES 6 6
 FT MOD_RES 11 11
 FT MOD_RES 18 18
 FT MOD_RES 19 19
 FT THIOETH 1 1
 FT THIOETH 4 4
 FT THIOETH 14 14
 FT THIOETH 11 11
 SQ SEQUENCE 19 AA; 2033 MW; FA34299E2736286A CRC64;

 Query Match 20.0%; Score 22; DB 1; Length 19;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 ACDB 18
:111
Db 13 SCDB 16

RESULT 12
CH60_HELVI
ID CH60_HELVI STANDARD; PRT; 24 AA.
AC P26317;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 60 KDA CHAPERONIN, MITOCHONDRIAL (P60) (FRAGMENT).
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Plekoyota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
RN [1]
RP SEQUENCE.
RC TISSUE-TESTIS;
RX MEDLINE-90339485; PubMed-1974308;
RA Miller S.G., Leclerc R.F., Erdos G.W.;
RT "Identification and characterization of a testis-specific isoform of a chaperonin in a moth, *Heliothis virescens*.";
RL J. Mol. Biol. 214:407-422(1990).
CC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A SINGLE SEVEN-MEMBER RING COMPLEX, IN TIGHT ASSOCIATION WITH THE P63 PROTEIN.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- DEVELOPMENTAL STAGE: FROM THE SECOND HALF OF THE LARVAL FINAL-INSTAR, THROUGH THE FIRST TWO DAYS OF PUPAL DEVELOPMENT.
CC -1- MISCELLANEOUS: SHOWS ATPASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR HSP: P06139; IAOB.
DR INTERPRO: IPR001844;
DR PROSITE: PS00296; CHAPERONINS_CPN60; PARTIAL.
KM Chaperone: ATP-binding; Testis; Mitochondrion.
FT NON_TER 24
SQ SEQUENCE 24 AA; 2531 MW; 2B34508F8CA981CF CRC64;

Query Match 20.0%; Score 22; DB 1; Length 24;
Best Local Similarity 38.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 DVNYAFLATDIL 13
:111111
Db 9 DVRAIMLOQVDVL 21

RESULT 13
RS11_THERH
ID RS11_THERH STANDARD; PRT; 25 AA.
AC P80376;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S RIBOSOMAL PROTEIN S11 (FRAGMENT).
GN RPSK OR RPS11.
OS *Thermus aquaticus* (subsp. *therophilus*).
OC Bacteria; *Thermus*/Deinococcus group; *Thermus* group; *Thermus*.
RN [1]
RP SEQUENCE.
RX MEDLINE-95045586; PubMed-7957245;
RA Tsiiboli P., Herfurth E., Choll T.;

RT "Purification and characterization of the 30S ribosomal proteins from *the bacterium Thermus thermophilus*.";
RL Eur. J. Biochem. 226:169-177(1994).
CC -1- FUNCTION: S11 PLAYS AN ESSENTIAL ROLE FOR THE SELECTION OF THE CORRECT TRNA IN PROTEIN BIOSYNTHESIS. IT IS LOCATED ON THE LARGE LOBE OF THE SMALL SUBUNIT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S11P FAMILY OF RIBOSOMAL PROTEINS.
DR INTERPRO: IPR001971;
DR PROSITE: PS00054; RIBOSOMAL_S11; PARTIAL.
KM Ribosomal protein.
FT NON_TER 25
SQ SEQUENCE 25 AA; 2816 MW; 59A3F932857D88F CRC64;

Query Match 20.0%; Score 22; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 5 AFLHAT 10
:11111
Db 18 AYTHAS 23

RESULT 14
DURA_STRGV
ID DURA_STRGV STANDARD; PRT; 19 AA.
AC P36504;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE LANTIBIOTIC DURAMYCIN (LEUCOPEPTIN) (ANTIBIOTIC PA48009).
OS Streptococcus *griseoviridicillium*.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae;
OC Streptoviridicillium.
RN [1]
RP SEQUENCE AND STRUCTURE BY NMR.
RC STRAIN-PA-48009;
RX MEDLINE-91107438; PubMed-2272918;
RA Hayashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K., Itazaki H.;
RT "The structure of PA48009: the revised structure of duramycin.";
RL J. Antibiot. 43:1421-1430(1990).
RN [2]
RP SEQUENCE.
RX MEDLINE-91107436; PubMed-2125590;
RA Fiedenhagen A., Fendrich G., Markl F., Markl W., Gruner J., Raschdorf F., Peter H.H.;
RT "Duramycin B and C, two new lantibiotics containing antibiotics as inhibitors of phospholipase A2. Structural revision of duramycin and cinnamycin.";
RL J. Antibiot. 43:1403-1412(1990).
CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
CC -1- PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF THR, SER, AND CYS INTO DEHYDROXY AA AND THE FORMATION OF SULFIDE BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND CLEAVAGE OF THE MODIFIED PRECURSOR.
CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
KM Antidiotic; Lantibiotic.
FT MOD_RES 4 4
FT MOD_RES 6 6
FT MOD_RES 11 11
FT MOD_RES 18 18
FT MOD_RES 19 19
FT THIOETH 1 18
FT THIOETH 4 14
FT THIOETH 5 11
SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;

Query Match 19.1%; Score 21; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CDG 18
DB 14 CDG 16

RESULT 15

DURB_STRGM STANDARD: PRT: 19 AA.

AC P36502: 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE LANTIBIOTIC DURAMYCIN B.
OS Streptovorticillium sp. (strain R2075).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae;
OC Streptovorticillium.
CC [1]
RN SEQUENCE.
RP MEDLINE-91107436; PubMed-2125590;
RA Friedenham A., Fendrich G., Markl F., Gruner J.,
RA Raschdorf F., Peter H.H.;
RT "Duramycin B and C, two new lantibiotics containing antibiotics as
RT inhibitors of phospholipase A2. Structural revision of duramycin and
RT cinnamycin."
RL J. Antibiot. 43:1403-1412(1990).
RN [2]
RN STRUCTURE BY NMR.
RA Zimmermann N., Freund S., Friedenham A., Jung G.;
RT "Solution structure of the lantibiotics duramycin B and C."
RL (In) Schneider C.H., Eberles A.N. (eds.);
RL Peptides 1992, pp.519-520, ESCOM Science Publishers, Leiden (1993).
RN [3]
RN STRUCTURE BY NMR.
RP MEDLINE-93387292; PubMed-8375380;
RA Zimmermann N., Freund S., Friedenham A., Jung G.;
RT "Solution structures of the lantibiotics duramycin B and C."
RL Eur. J. Biochem. 216:419-428(1993).

CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
CC -1- PTM: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF
CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE
CC BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND
CC CLEAVAGE OF THE MODIFIED PRECURSOR.

CC -1- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
CC Antibiotic; Lantibiotic.

FT MOD_RES 4 4 D-ALANINE.
FT MOD_RES 6 6 D-ABU (BONDED TO 19).
FT MOD_RES 11 11 D-ABU (AMINOBTYRIC ACID).
FT MOD_RES 18 18 D-ABU (AMINOBTYRIC ACID).
FT MOD_RES 19 19 LYSINOLANINE (BONDED TO 6).
FT THIOETH 1 18 ABU-S-CYS (METHYLLANTHIONINE).
FT THIOETH 4 14 ALA-S-CYS (LANTHIONINE).
FT THIOETH 5 11 ABU-S-CYS (METHYLLANTHIONINE).
SQ SEQUENCE 19 AA; 2063 MW; 0133445E27362F00 CRC64;

Query Match 19.1%; Score 21; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 CDG 18
DB 14 CDG 16

RESULT 16

CH60_BOVIN STANDARD: PRT: 22 AA.

AC P31081: 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP60) (60 KDA CHAPERONIN)
DE (CPN60) (HEAT SHOCK PROTEIN 60) (HSP-60) (MITOCHONDRIAL MATRIX PROTEIN
DE P1) (FRAGMENT).
GN HSPD1 OR HSP60.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

RN [1]
RN SEQUENCE.
RP TISSUE-ADRENAL GLAND;
RC MEDLINE-93208180; PubMed-8096152;
RA Dai Z., Lackland H., Stein S., Li Q., Radziewicz R., Williams R.,
RA Sigal L.H.;
RT "Molecular mimicry in Lyme disease: monoclonal antibody H9724 to B.
RT burgdorferi flagellin specifically detects chaperonin-HSP60."
RL Biochim. Biophys. Acta 1181:97-100(1993).

CC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND
CC MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF
CC IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE
CC REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED
CC UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX.

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR HSSP: P06139; IAO.
DR INTERPRO: IPR001844;
DR PROSITE: PS00296; CHAPERONINS CPN60; PARTIAL.
KM Chaperone; ATP-binding; Mitochondrion.
FT NON_TER 22
SQ SEQUENCE 22 AA; 2303 MW; E09D2EB934475F5 CRC64;

Query Match 19.1%; Score 21; DB 1; Length 22;
Best Local Similarity 38.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 DYNALFHTDLDL 13
DB 9 DARNLMQGVLL 21

RESULT 17

ACT7_SOYBN STANDARD: PRT: 13 AA.

AC P15987: 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN 7 (FRAGMENT).
GN SACT.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I;
OC Fabales; Fabaceae; Papilionoideae; Glycine.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-CV, WAYNE;
RA MEDLINE-91346640; PubMed-2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes."
RL Plant Mol. Biol. 14:513-526(1990).

CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.

CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOSOLIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORANELLE MOVEMENT AND EXTENSION GROWTH.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.

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 CC
 CC EMBL: X17120; CAA34980.1; -
 CC PIR: S15755; S15755.
 CC INTERPRO: IPR000279; -
 CC PROSITE: PS00406; ACTINS_1; PARTIAL.
 CC PROSITE: PS00432; ACTINS_2; PARTIAL.
 CC PROSITE: PS01132; ACTINS_ACT-LIKE; PARTIAL.
 CC Structural protein; Multigene family.
 CC FT NON_TER 13
 CC SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;
 CC
 CC Query Match 18.6%; Score 20.5; DB 1; Length 13;
 CC Best Local Similarity 50.0%; Pred. No. 1.8e+03;
 CC Matches 5; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 CC
 CC QY 9 ATDLP-ACD 17
 CC 1 1 1 1 1 1
 CC Db 4 AEDIQPLVCD 13
 CC
 CC RESULT 18
 CC ACT6-SOYBN STANDARD; PRT; 17 AA.
 CC ID ACT6-SOYBN
 CC AC P15966;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 01-APR-1990 (Rel. 14, Last sequence update)
 CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
 CC DE ACTIN 6 (FRAGMENT).
 CC GN SACS.
 CC OS Glycine max (Soybean).
 CC OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 CC Fabales; Fabaceae; Papilionoideae; Glycine.
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-CV, WAYNE;
 CC RX MEDLINE-91346640; PubMed-2102831;
 CC RA Pearson L., Mesgher R.B.;
 CC RT "Diverse soybean actin transcripts contain a large intron in the 5'
 CC RT untranslated leader: structural similarity to vertebrate muscle actin
 CC RT genes.";
 CC RL Plant Mol. Biol. 14:513-526(1990).
 CC
 CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED
 CC IN ALL EUKARYOTIC CELLS.
 CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
 CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
 CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
 CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
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 CC or send an email to license@lsb-sib.ch).
 CC
 CC EMBL: X17119; CAA34979.1; -
 CC PIR: S15754; S15754.
 CC INTERPRO: IPR000279; -
 CC PROSITE: PS00406; ACTINS_1; PARTIAL.
 CC PROSITE: PS00432; ACTINS_2; PARTIAL.

DR PROSITE: PS01132; ACTINS_ACT-LIKE; PARTIAL.
 KW Structural protein; Multigene family.
 FT* NON_TER 17
 SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;
 CC
 CC Query Match 18.6%; Score 20.5; DB 1; Length 17;
 CC Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 CC Matches 5; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 CC
 CC QY 9 ATDLP-ACD 17
 CC 1 1 1 1 1 1
 CC Db 4 AEDIQPLVCD 13
 CC
 CC RESULT 19
 CC FLAA-TREPH STANDARD; PRT; 25 AA.
 CC ID FLAA-TREPH
 CC AC P21983;
 CC DT 01-AUG-1991 (Rel. 19, Created)
 CC DT 01-AUG-1991 (Rel. 19, Last sequence update)
 CC DT 01-AUG-1991 (Rel. 19, Last annotation update)
 CC DE FLAGELLAR FILAMENT OUTER LAYER PROTEIN (SHEATH PROTEIN) (FRAGMENT).
 CC GN FLAA.
 CC OS Treponema phagedentis.
 CC OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 CC [1]
 CC RP SEQUENCE.
 CC RX MEDLINE-88314903; PubMed-3045083;
 CC RA Norris S.J., Charon N.W., Cook R.G., Fuentes M.D., Limberger R.J.;
 CC RT "Antigenic relatedness and N-terminal sequence homology define two
 CC RT classes of periplasmic flagellar proteins of Treponema pallidum
 CC RT subsp. pallidum and Treponema phagedentis.";
 CC RL J. Bacteriol. 170:4072-4082(1988).
 CC CC -1- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
 CC -1- SUBUNIT: OUTER LAYER COMPOSED OF REPEATING UNITS OF FLAA AND A
 CC CORE THAT CONTAINS ONE OR ALL OF FIVE ANTIGENICALLY RELATED
 CC POLYPEPTIDE.
 CC CC -1- SUBCELLULAR LOCATION: PERIPLASMIC FLAGELLUM.
 CC DR PIR: B32351; B32351.
 CC KW Flagella; Periplasmic.
 CC FT NON_TER 25
 CC SQ SEQUENCE 25 AA; 2676 MW; EB3841091FDBDAB3 CRC64;
 CC
 CC Query Match 18.6%; Score 20.5; DB 1; Length 25;
 CC Best Local Similarity 29.4%; Pred. No. 3.4e+03;
 CC Matches 5; Conservative 7; Mismatches 4; Indels 1; Gaps 1;
 CC
 CC QY 2 VYAFHARDLPACDG 18
 CC 1 1 1 1 1 1
 CC Db 6 IDEGKLA-DIVPKNG 21
 CC
 CC RESULT 20
 CC FARP-MANSE STANDARD; PRT; 10 AA.
 CC ID FARP-MANSE
 CC AC P18523;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
 CC DT 01-NOV-1995 (Rel. 32, Last annotation update)
 CC DE FMRFAMIDE-LIKE NEUROPEPTIDE.
 CC OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 CC OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
 CC [1]
 CC RP SEQUENCE.
 CC RX MEDLINE-91045350; PubMed-2235684;
 CC RX Kinsan T.G., Teplow D.B., Phillips J.M., Rihm J.P., Rao K.R.,
 CC RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
 CC RA Hunt D.F.;
 CC "A new peptide in the FMRFamide family isolated from the CNS of the

```

RT hawkmoth, Manduca sexta.
RL Peptides 11:849-856(1990).
CC -1- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
CC MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
CC FLIGHT BEHAVIOR PATTERNS.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A43977; A43977.
KW Amidation; Neuropeptide.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SO SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;

Query Match
Best Local Similarity 57.1%; Score 20; DB 1; Length 10;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DYNVAF 7
   1 1 1 1
Db 2 DVVHSE 8

RESULT 21
CXAL_CONST STANDARD; PRT: 13 AA.
ID CXAL_CONST
AC P15471;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALPHA-CONOTOXIN SI (S1).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE-89062448; PubMed-3196703;
RA Zafarella G.C., Ramillo C., Gray W.R., Karlstrom R., Olivera B.M.,
RA Cruz L.J.;
RT "Phylogenetic specificity of cholinergic ligands: alpha-conotoxin
RT SI.":
RL Biochemistry 27:7102-7105(1988).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
DR PIR: A28953; A28953.
KW HSSP; P01519; INOT.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD_RES 13 13 AMIDATION.
FT SEQUENCE 13 AA; 1359 MW; DEE90F8EF2457EBD CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 PAC 16
   1 1 1
Db 5 PAC 7

RESULT 22
CXAX_CONGE STANDARD; PRT: 13 AA.
ID CXAX_CONGE
AC P01520;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last annotation update)
DE ALPHA-CONOTOXIN GII.

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OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE-81191854; PubMed-7014556;
RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;
RT "Peptide toxins from Conus geographus venom.":
RL J. Biol. Chem. 256:4734-4740(1981).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE-84032400; PubMed-6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin M1. Disulfide bonding and conformational states.":
RL J. Biol. Chem. 258:12247-12251(1983).
RN [3]
RP REVIEW.
RX MEDLINE-89024586; PubMed-3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous conus snails.":
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
DR PIR: A01783; NTKN2G.
DR HSSP; P01519; INOT.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD_RES 13 13 AMIDATION.
FT SEQUENCE 13 AA; 1422 MW; DEEE831C39297EBD CRC64;

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 PAC 16
   1 1 1
Db 5 PAC 7

RESULT 23
CXAX_CONST STANDARD; PRT: 13 AA.
ID CXAX_CONST
AC P28878;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE ALPHA-CONOTOXIN SIA (S1A).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE-91369955; PubMed-1892838;
RA Myers R.R., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
RA Olivera B.M.;
RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
RT receptors.":
RL Biochemistry 30:9370-9377(1991).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM.
DR PIR: A40312; NTKN4S.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD_RES 13 13 AMIDATION.
FT SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

```

Query Match 18.2%; Score 20; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 PAC 16
 |||
 DB 5 PAC 7

RESULT 24

CXAL_CONCN STANDARD: PRT: 14 AA.
 ID CXAL_CONCN
 AC P56973;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE ALPHA-CONOTOXIN CNIA [CONTAINS: ALPHA-CONOTOXIN CNIB].
 OS Conus consors.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conus.
 RN [1]
 RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.
 RC TISSUE-VENOM;
 RX MEDLINE-99255390; PubMed-10320362;
 RA Favreau P., Kimm I., Le Gall F., Bobenrieth M.J., Lamthanh H.,
 RA Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,
 RA Lancelin J.-M.;
 RT "Biochemical characterization and nuclear magnetic resonance
 structure of novel alpha-conotoxins isolated from the venom of Conus
 consors.";
 RT Biochemistry 38:6317-6326(1999).
 RL -I- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 INHIBIT THEM. THIS PEPTIDE SEEMS TO BE A POTENT AND SELECTIVE
 BLOCKER OF MUSCULAR SUBTYPE OF NACHR.
 CC PDB: 1845; 09-JUL-99.
 DR Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KW Venom; 3D-structure.
 KM PEPTIDE 1 14 ALPHA-CONOTOXIN CNIA.
 FT PEPTIDE 3 14 ALPHA-CONOTOXIN CNIB.
 FT DISULFID 3 8
 FT DISULFID 4 14
 FT MOD.RES 14 14
 FT MOD.RES 14 14
 SQ SEQUENCE 14 AA; 1548 MW; DEE91969BF5E5BD CRC64;

Query Match 18.2%; Score 20; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 PAC 16
 |||
 DB 6 PAC 8

RESULT 25

CXAL_CONCN STANDARD: PRT: 14 AA.
 ID CXAL_CONCN
 AC P01521;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE ALPHA-CONOTOXIN MI (M1).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conidae; Conus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-83073458; PubMed-7149738;
 RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
 RT "Isolation and structure of a peptide toxin from the marine snail

RT Conus magus";
 RL Arch. Biochem. Biophys. 218:329-334(1982).

RN [2]
 RP DISULFIDE BONDS.
 RX MEDLINE-84032400; PubMed-6630187;
 RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
 RT "Conotoxin MI. Disulfide bonding and conformational states.";
 RL J. Biol. Chem. 258:12247-12251(1983).

RN [3]
 RP REVIEW.
 RX MEDLINE-89024586; PubMed-3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -I- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 INHIBIT THEM.
 DR PIR: A01784; NTKNIM.
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KM Venom.
 FT DISULFID 3 8
 FT DISULFID 4 14
 FT DISULFID 14 14
 FT MOD.RES 14 14
 FT MOD.RES 14 14
 SQ SEQUENCE 14 AA; 1499 MW; DEE91898BF5E5BD CRC64;

Query Match 18.2%; Score 20; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 PAC 16
 |||
 DB 6 PAC 8

Search completed: February 5, 2001, 10:55:56
 Job time: 496 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:47:34 : Search time 68.99 Seconds
(without alignments)
9.913 Million cell updates/sec

Title: US-08-981-824-7
Sequence: 103
1 FFRWISNPATHTQDIDFLI 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 141170

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A_Geneseq_36.*
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
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5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	95	92.2	20	16	R72297	Glutamic acid deca
2	95	92.2	20	21	Y59560	GAD65 fragment, pe
3	73	70.9	14	16	R76662	Peptide derived fr
4	73	70.9	14	18	W18870	65 kD glutamic aci
5	52	50.5	20	16	R72298	Glutamic acid deca
6	52	50.5	20	21	Y59547	GAD65 fragment, pe
7	52	50.5	20	21	Y59589	GAD65 fragment, pe
8	35	34.0	19	13	R28755	Synthetic rabbit G
9	35	34.0	19	16	R71643	Human GAD C-termin
10	34	33.0	18	21	Y85070	Immunogenic peptid
11	33	32.0	18	19	W44912	Spacer peptide for
12	33	32.0	19	19	W44924	Pro-Tich spacer fo

13	33	32.0	20	15	R56619	Alginic acid Al-II
14	33	32.0	20	15	R61238	Alginic acid Al-II
15	33	32.0	20	16	R67426	N-terminal fragmen
16	32	31.1	20	15	R56620	Alginic acid Al-II
17	32	31.1	20	15	R61236	Alginic acid Al-II
18	32	31.1	20	15	R61237	Alginic acid Al-II
19	32	31.1	20	16	R67427	N-terminal fragmen
20	31	30.1	19	13	R26891	HIV epitope #13.
21	31	30.1	23	13	R26894	HIV epitope #6. S
22	30	29.1	17	12	R13289	C-terminal of soma
23	30	29.1	17	19	W87486	HIV-1 MO/LAI Nef p
24	30	29.1	18	16	R66373	Chlamydial KOMP VD
25	30	29.1	18	16	R66374	Chlamydial KOMP VD
26	30	29.1	25	8	P70377	Sequence of N-term
27	30	29.1	25	11	R00581	Partial N-terminal
28	29	28.2	17	21	Y59291	Human MUC11 tandem
29	29	28.2	20	15	R63268	Thrombin inhibitor
30	29	28.2	20	18	W42899	Immunogenic Hepati
31	29	28.2	25	20	Y45345	Human secreted pro
32	28	27.2	8	19	W59312	Non-polio enterovi
33	28	27.2	9	21	Y69593	Monoclonal antibod
34	28	27.2	13	19	W50884	Antibody 15A.2 bin
35	28	27.2	14	16	W87480	HIV-1 mutant Nef p
36	28	27.2	14	16	R71030	HSV-2 protease sub
37	28	27.2	20	15	R74077	Thrombin inhibitor
38	28	27.2	20	15	R74078	Thrombin inhibitor
39	28	27.2	20	16	R67425	N-terminal fragmen
40	28	27.2	21	19	W65674	Fibronectin bindin
41	28	27.2	22	13	R28278	Sequence of cowpea
42	27	26.2	9	20	Y36471	Fragment of human
43	27	26.2	10	21	Y51451	AAV VP3 derived pe
44	27	26.2	15	14	R42732	Murine Tgase3 27 k
45	27	26.2	15	14	R42733	Guinea pig Tgase3

ALIGNMENTS

RESULT 1
ID R72297 standard; Peptide: 20 AA.
AC R72297;
DT 13-NOV-1995 (first entry)
XX
DE Glutamic acid decarboxylase (GAD65) fragment.
XX
KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
KW Insulin-dependent diabetes mellitus; stiff man disease.
XX
OS Homo sapiens.
XX
PN W09507992-A-
XX
PD 23-MAR-1995.
XX
PF 24-AUG-1994; 94WO-US09478.
XX
PR 17-SEP-1993; 93US-0123859.
XX
XX (REGC) UNIV CALIFORNIA.
PA Clare-Saltzer MJ, Erlander MG, Kaufman DL, Toblin AJ;
PI WPI; 1995-131360/17.
DR
XX
XX New polypeptide fragments of glutamic acid decarboxylase - for
PT diagnosis and treatment of autoimmune disease, esp. insulin
PT dependent diabetes; also related nucleic acid, vectors,
PT antihodies, hydrioma(s) etc.
XX
PS Claim 1; Page 77; 100pp; English.

CC 086481 and 086482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65), respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependent diabetes mellitus or stiff man disease.
 CC
 XX Sequence 20 AA:

Query Match 92.2%; Score 95; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.2e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFRWISNPATHTQDIDF 18
 |||||||
 DB 3 ffrwvsnpathqdidf 20

RESULT 2
 ID Y59560 standard; peptide: 20 AA.
 Y59560:

AC Y59560:
 DT 03-APR-2000 (first entry)
 DE GAD65 fragment, peptide #37.
 KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KM insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
 KW therapy.

OS Homo sapiens.
 PN US5998366-A.
 PD 07-DEC-1999.
 PE 09-APR-1997; 97US-0827618.
 PR 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0586536.
 PR 18-JUN-1991; 91US-0716909.

PA (REGC) UNIV CALIFORNIA.

PI Tobin AJ, Kaufman DL, Erlander MG;

DR WPI; 2000-095930/08.

PT Ameliorating glutamic acid decarboxylase associated autoimmune
 PT disorders such as insulin dependent diabetes mellitus and Stiff man
 PT disease -

PS Claim 1; Column 43; 61pp; English.

CC This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorders by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 CC and Stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunosays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.

CC Sequence 20 AA:

Query Match 92.2%; Score 95; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.2e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFRWISNPATHTQDIDF 18
 |||||||
 DB 3 ffrwvsnpathqdidf 20

RESULT 3

ID R76662 standard; peptide: 14 AA.

AC R76662:

DT 05-MAR-1996 (first entry)

DE Peptide derived from human glutamic acid decarboxylase 21.

KW diabetes; T-cell subpopulation; detection; antigen production;
 KM diagnosis; autoimmune disease.

OS Homo sapiens.

PN DE4418091-A1.

PD 27-JUL-1995.

PE 24-MAY-1994; 94DE-4418091.

PR 04-FEB-1994; 94DE-4403522.

PR 20-JAN-1994; 94DE-4401629.

PA (ENDL/) ENDL J.

PI Albert W, Dormair K, Endl J, Jung G, Meinel E;

PI Stanzl P, Schendel D;

DR WPI; 1995-264505/35.

PT Antigen-specific activated T-lymphocytes and their detection - by
 PT interaction with inventive peptide(s) of peptide-MHC complexes;
 PT useful in diagnosis of e.g. diabetes and autoimmune diseases

PS Claim 1; Fig 2; 21pp; German.

CC R76642-62 are derived from human glutamic acid decarboxylase and
 CC specifically react with T-cell sub-populations isolated from recently
 CC diagnosed Type-I diabetes. Pharmaceutical compns. contg. these
 CC peptides and those shown in R77571-72, are useful for the diagnosis of
 CC a disease or predispositions of immune system diseases, tumours, and
 CC autoimmune diseases, including diabetes. The peptides are able to detect
 CC specific T-cell subpopulations that are then used for antigen prodn.,
 CC e.g. by reinjection.

PS Sequence 14 AA:

Query Match 70.9%; Score 73; DB 16; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VISNPATHTQDIDF 18
 |||||||
 DB 1 visnpathtqdidf 14

RESULT 4

ID W18870 standard; peptide: 14 AA.

AC W18870:

XX 05-JAN-1998 (first entry)
 DT 65 kD Glutamic acid decarboxylase peptide fragment 21.
 XX
 DE
 XX
 XX
 KM GAD, 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
 KM Insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
 KM Predisposition; autoimmune; tumour; rheumatoid arthritis;
 KM multiple sclerosis.
 XX
 OS Synthetic.
 XX
 PN DE19526561-A1.
 XX
 XX
 PD 23-JAN-1997.
 XX
 PF 20-JUL-1995; 95DE-1026561.
 XX
 PR 20-JUL-1995; 95DE-1026561.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Donie F, Endl J, Ganz M, Jung G, Kientsch-engel R;
 PI Pozzilli P, Stahl P;
 XX
 DR WPI; 1997-088254/09.
 XX
 PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
 PT Involving intradermal admin. of auto:reactive substances
 XX
 PS Claim 11; Fig 2; 12pp; German.
 XX
 CC W1842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 70.9%; Score 73; DB 18; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.7e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VISNPATHDIDF 18
 |||||||||
 Db 1 visnpatqdidf 14
 RESULT 5
 R72298 R72298 standard; Peptide; 20 AA.
 XX
 AC R72298;
 DT 13-NOV-1995 (first entry)
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX
 KM Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KM Insulin-dependent diabetes mellitus; stiff man disease.
 OS Homo sapiens.
 XX
 PN WO9507992-A.
 XX
 PD 23-MAR-1995.

XX 24-AUG-1994; 94MO-US09478.
 PF
 XX
 PR 17-SEP-1993; 93US-0123859.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
 PI WPI; 1995-131360/17.
 DR
 XX
 PT New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hydridoma(s) etc.
 XX
 PS Claim 1; Page 77; 100pp; English.
 XX
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependant diabetes mellitus or stiff man disease.
 CC
 XX
 SQ Sequence 20 AA;
 Query Match 50.5%; Score 52; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.015; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;
 QY 11 ATHODIDFLI 20
 |||||||||
 Db 1 ethqdidf11 10
 RESULT 6
 Y59547
 ID Y59547 standard; peptide; 20 AA.
 XX
 AC Y59547;
 DT 03-APR-2000 (first entry)
 XX
 DE GAD65 fragment, peptide #38.
 XX
 KM GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KM Insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
 KM therapy.
 XX
 OS Homo sapiens.
 XX
 PN US5998366-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 09-APR-1997; 97US-0827618.
 XX
 PR 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0586536.
 PR 18-JUN-1991; 91US-0716909.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Tobin AJ, Kaufman DL, Erlander MG;
 PI WPI; 2000-095930/08.
 DR
 XX
 PT Ameliorating glutamic acid decarboxylase associated autoimmune
 PT disorders such as insulin dependent diabetes mellitus and Stiff man
 PT disease -
 XX

PS Claim 1; Column 33; 61pp; English.

CC This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorders by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 CC and Stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.

CC Sequence 20 AA;

Query Match 50.5%; Score 52; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ATHODIDFLI 20
 ||||||||
 Db 1 atgqdidfli 10

RESULT 7

Y59589 standard; peptide; 20 AA.

Y59589;

03-APR-2000 (first entry)

GAD65 fragment, peptide #38.

GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
 therapy.

Homo sapiens.

US5998366-A.

07-DEC-1999.

09-APR-1997; 97US-0827618.

07-JUN-1995; 95US-0485725.

21-SEP-1990; 90US-0586536.

18-JUN-1991; 91US-0716909.

(REGC) UNIV CALIFORNIA.

Tobin AJ, Kaufman DL, Erlander MG;

WPI; 2000-095930/08.

Ameliorating glutamic acid decarboxylase associated autoimmune
 disorders such as insulin dependent diabetes mellitus and Stiff man
 disease -

Example 11; Column 43; 61pp; English.

This sequence represents a fragment of the glutamic acid decarboxylase 65
 (GAD65) protein. The invention relates to a method of ameliorating GAD
 associated autoimmune disorders by administering a GAD65 peptide to the
 patient. The method can be used for ameliorating GAD associated
 autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 and Stiff man disease. GAD65 can also be useful for screening drugs that
 alter GAD function, for generating monoclonal antibodies and in
 immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 and the diagnosis is quite easy. It is also possible to obtain much

CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.

CC Sequence 20 AA;

Query Match 50.5%; Score 52; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ATHODIDFLI 20
 ||||||||
 Db 1 atgqdidfli 10

RESULT 8

R28755 standard; Protein; 19 AA.

R28755;

20-APR-1993 (first entry)

Synthetic rabbit GAD antibody 1266 raising peptide.

Glutamic acid decarboxylase; rabbit; immunoreactive.

Synthetic.

WO9220811-A.

26-NOV-1992.

14-MAY-1992; 92WO-US04079.

15-MAY-1991; 91US-0702162.

(UNIW) UNIV WASHINGTON.

(ZYMO) ZYMOGENETICS INC.

Foster DC, Grubin CE, Hagopian W, Karlsen AE, Lernmark A, O'Hara PJ;

WPI; 1992-415789/50.

Polynucleotide encoding human islet glutamic acid decarboxylase -

used to test for auto-antibodies against itself to diagnose

insulin dependent diabetes mellitus

Example; Page 33; 45pp; English.

The peptide was synthesized based on the C-terminal sequence of
 human islet glutamic acid decarboxylase (GAD). It was used to raise
 antibody 1266 in rabbits, the antibody was used to test transfectants
 for production of human GAD by immunocytochemistry.

Sequence 19 AA;

Query Match 34.0%; Score 35; DB 13; Length 19;

Best Local Similarity 77.8%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 THODIDFLI 20
 | |||||
 Db 1 tgsdidfli 9

RESULT 9

R71643 standard; Peptide; 19 AA.

R71643;

DT 21-SEP-1995 (first entry)
 XX Human GAD C-terminal peptide.
 DE
 XX
 KW GAD; glutamic-acid-decarboxylase; glutamate-decarboxylase;
 KM non-insulin-dependent diabetes; NIDDM; diagnosis; autoantibody;
 XX pancreas; islet.
 OS Homo sapiens.
 XX
 PN W09507464-A.
 XX
 PD 16-MAR-1995.
 XX
 PE 02-SEP-1994; 94WO-US09937.
 XX
 PR 07-SEP-1993; 93US-0117907.
 XX
 PA (UNIW) UNIV WASHINGTON.
 PI Hagopian W, Karlisen AE, Landin-Olsson M, Lernmark A;
 DR WPI: 1995-123512/16.
 XX
 PT Predicting the clinical course of diabetes in patients with
 PT non-insulin dependent diabetes mellitus - by detecting the
 PT presence of autoantibodies to human islet cell glutamic acid
 PT decarboxylase.
 XX
 PS Example II: Page 26; 62pp; English.
 CC Human islet cDNA (Q86046) was expressed in tk- ts13 BHK cells
 CC (ATCC CRL 1632). Transfectants were selected in methotrexate
 CC medium. The immunoreactivity of the human GAD protein obtained
 CC was tested using antibodies raised in rabbits against a C-terminal
 CC peptide (R71643) of human GAD.
 XX
 SQ Sequence 19 AA:
 Query Match 34.0%; Score 35; DB 16; Length 19;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 12 THQDIDFLI 20
 Db 1 tgsdldfl 9
 RESULT 10
 Y85070
 ID Y85070 standard; peptide; 18 AA.
 XX
 AC Y85070;
 XX
 DT 20-JUN-2000 (first entry)
 XX
 DE Immunogenic peptide #8 derived from FMDV non-structural protein 3C.
 XX
 KM Foot and mouth disease; FMDV; epitope; anti-FMDV antibody; diagnosis;
 KW vaccine; immunoreagent; non-structural protein.
 XX
 OS Foot and mouth disease virus.
 XX
 PN US6048538-A.
 XX
 PD 11-APR-2000.
 XX
 PE 03-OCT-1997; 97US-0943173.
 XX
 PR 03-OCT-1997; 97US-0943173.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.

XX
 PI Y1 Wang C, De Chen P, Shen F;
 XX
 DR WPI: 2000-328034/28.
 XX
 PT Peptide from non-structural proteins useful for detecting
 PT foot-and-mouth disease virus infection in animal comprises an
 PT immunogenic epitope specific to antibodies
 XX
 PS Claim 1; Column 25-26; 23pp; English.
 XX
 CC This sequence represents a peptide derived from the non-structural
 CC protein 3C of the foot and mouth disease virus (FMDV). The amino acid
 CC sequence of the peptide corresponds to an immunodominant region of the
 CC FMDV non-structural protein and is an immunogenic epitope specific for
 CC anti-FMDV antibodies. The invention relates to peptides derived from
 CC three non-structural FMDV proteins. The peptides are useful as
 CC immunoreagents i.e. reagent in an immunoassay in detecting antibodies to
 CC FMDV or diagnosis of FMDV infection. The immunoassays are used to screen
 CC body fluids and tissues for the presence of FMDV-reactive antibodies and
 CC aid in the diagnosis of FMDV infection and differentiate infected from
 CC the vaccinated animals.
 XX
 SQ Sequence 18 AA:
 Query Match 33.0%; Score 34; DB 21; Length 18;
 Best Local Similarity 42.9%; Pred. No. 16;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 3 RMVTSNPATRHQDI 16
 Db 3 rllfsgaelytkd 16
 RESULT 11
 W44912
 ID W44912 standard; peptide; 18 AA.
 XX
 AC W44912;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Spacer peptide for chimeric glycoprotein AMO-Delta-Pro2.
 XX
 KM Chimeric; polypeptide; beta-turn helix; facilitation; inhibition;
 KW retrovirus; envelope glycoprotein; gene therapy; cystic fibrosis;
 KW myopathy; lysosomal disorder; cancer; human immunodeficiency virus.
 XX
 OS Synthetic.
 XX
 PN W09744474-A2.
 XX
 PD 27-NOV-1997.
 XX
 PE 16-MAY-1997; 97WO-FR00870.
 XX
 PR 20-MAY-1996; 96FR-0006234.
 XX
 PA (CNRS) CENT NAT RECH SCI.
 PI Cosset FL, Russell SJ, Valsesia S;
 XX
 DR WPI: 1998-018526/02.
 XX
 PT Introducing genes into eukaryotic cells using peptide with two
 PT receptor binding regions - especially as part of a viral
 PT glyco-protein, used in gene therapy to ensure precise targeting of
 PT vectors to particular cell types
 XX
 PS Example 2; Page 40; 117pp; French.
 CC A novel chimeric protein for gene transfer comprises, at the N-terminus,

SQ Sequence 20 AA:

Query Match

Best Local Similarity 32.0%; Score 33; DB 15; Length 20;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 PAATHODID 17
||| |
Db 2 paaahsids 10

RESULT 14

R61238
ID R61238 standard; Protein; 20 AA.

XX R61238;

DT 27-APR-1995 (first entry)

DE Alginate lyase II N-terminal sequence.

XX N-terminal; alginate lyase; Al-I; Al-III; enzyme; alginic acid;

XX cystic fibrosis.

OS Pseudomonas sp.

XX Key Location/Qualifiers
FT Misc-difference 14 /label= Undefined amino acid

XX WO9419006-A.

XX 01-SEP-1994.

XX 24-FEB-1993; 93WO-JP00227.

XX 24-FEB-1993; 93WO-JP00227.

XX (GNZE) GUNZE LTD.

XX (SAKB) OTSUKA KAGAKU KK.

PI Abe S, Hisano T, Kimura A, Murata K, Nishimura M;

PI Okayama K, Yamaguchi H, Yamashita T, Yonemoto Y;

DR WPI; 1994-293999/36.

XX New alginate lyase from Pseudomonas sp. - useful for the

PT treatment of cystic fibrosis

XX Disclosure; Page 25; 36pp; Japanese.

XX This sequence represents the N-terminal fragment of alginate lyase II.

CC Alginate lyase I and III (Al-I and Al-III) have molecular weights of 60

CC and 38 kD. The alginate lyases break down alginic acid or viscous

CC substances formed by cystic fibrosis sufferers.

XX Sequence 20 AA;

OY 9 PAATHODID 17
||| |
Db 2 paaahsids 10

RESULT 15

R67426
ID R67426 standard; Peptide; 20 AA.

AC R67426;

DT 31-AUG-1995 (first entry)

XX N-terminal fragment of alginic acid lyase. Al-II-2.

DE alginic acid lyase; flavobacterium; recombinant production;

XX N-terminal fragment.

XX Flavobacterium sp.

XX Key Location/Qualifiers

FT Misc-difference 14 /note= "unknown, not identified in the specification"

XX JP06319569-A.

XX 22-NOV-1994.

XX 14-MAY-1993; 93JP-0113149.

XX 14-MAY-1993; 93JP-0113149.

XX (GNZE) GUNZE KK.

XX (SAKB) OTSUKA KAGAKU YAKUHIN KK.

DR WPI; 1995-040321/06.

XX alginic acid lyase expression gene - used in the prepn. of

PT alginic acid lyase

XX Disclosure; Page 3; 16pp; Japanese.

XX R67425-27 are the N-terminal fragments of alginic acid lyase (Al) -I,

CC -II-2 and -III respectively. The amino acid sequence of alginic acid

CC lyase is shown in R67424 and is encoded by the gene shown in Q75342.

CC It was isolated from Flavobacterium sp. by standard genetic techniques.

CC It is used to produce the recombinant enzyme in large quantities.

XX Sequence 20 AA;

OY 9 PAATHODID 17
||| |
Db 2 paaahsids 10

RESULT 16

R56620
ID R56620 standard; peptide; 20 AA.

XX R56620;

XX 24-MAR-1995 (first entry)

DE alginic acid Al-III lyase N-terminal sequence.

XX alginic acid lyase; Al-III; 4-deoxy-5-ketonic acid;

XX pulmonary cystic fibrosis; Pseudomonas aeruginosa.

XX Flavobacterium sp. ORC-6 (FERM P-12159).

XX JP06197760-A.

XX 19-JUL-1994.

XX 28-DEC-1992; 92JP-0348465.

XX 28-DEC-1992; 92JP-0348465.

XX (GNZE) GUNZE KK.
 PA (SAKB) OTSUKA KAGAKU YAKUHIN KK.
 XX WPI: 1994-268676/33.
 DR
 XX Alginic acid lyase(s) which decompose alginic acid into sugar and
 PT then 4-deoxy-5-keto:uronic acid - is used for treatment of
 XX pulmonary cystic fibrosis
 PS Claim 2; Page 9; 11pp; Japanese.
 XX
 CC Alginic acid Al-III lyase has the N-terminal sequence R56620 and
 CC decomposes alginic acid into a sugar having a double bond between C4
 CC and C5 and finally into 4-deoxy-5-ketouronic acid. The enzyme has
 CC optimal pH 8.0, optimal temp. 70 deg C and mol.wt. 38000 and is
 CC useful for treating pulmonary cystic fibrosis caused by Pseudomonas
 CC aeruginosa.
 XX
 SQ Sequence 20 AA;
 Query Match 31.1%; Score 32; DB 15; Length 20;
 Best Local Similarity 31.2%; Pred. No. 39;
 Matches 5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 FFRWISNPATHODI 16
 I : I : I : I : I : I :
 DB 3 fdgavvkdpkptasyvdr 18
 RESULT 17
 R61236
 ID R61236 standard; peptide; 20 AA.
 XX
 AC R61236;
 XX
 DT 27-APR-1995 (first entry)
 XX
 DE Alginic acid lyase I N-terminal sequence.
 XX
 KM N-terminal: alginic acid; Al-I; Al-III; enzyme; alginic acid;
 KM cystic fibrosis.
 XX
 OS Pseudomonas sp.
 XX
 PN WO9419006-A.
 XX
 PD 01-SEP-1994.
 XX
 PF 24-FEB-1993; 93WO-JP00227.
 XX
 PR 24-FEB-1993; 93WO-JP00227.
 XX
 PA (GNZE) GUNZE LTD.
 PA (SAKB) OTSUKA KAGAKU KK.
 XX
 PI Abe S, Hisano T, Kimura A, Murata K, Nishimura M;
 PI Okayama K, Yamaguchi H, Yamashita T, Yonemoto Y;
 XX
 DR WPI: 1994-293999/36.
 XX
 PT New alginic acid lyase from Pseudomonas sp. - useful for the
 PT treatment of cystic fibrosis
 XX
 PS Claim 2; Page 24; 36pp; Japanese.
 XX
 CC The sequences given in R61236-37 represent the N-terminal fragments
 CC of alginic acid lyase I and III (Al-I and Al-III), respectively. These
 CC enzymes have molecular weights of 60 and 38 kD. The alginic acid
 CC break down alginic acid or viscous substances formed by
 CC cystic fibrosis sufferers.

SQ Sequence 20 AA;
 Query Match 31.1%; Score 32; DB 15; Length 20;
 Best Local Similarity 31.2%; Pred. No. 39;
 Matches 5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 FFRWISNPATHODI 16
 I : I : I : I : I : I :
 DB 3 fdgavvkdpkptasyvdr 18
 RESULT 18
 R61237
 ID R61237 standard; peptide; 20 AA.
 XX
 AC R61237;
 XX
 DT 27-APR-1995 (first entry)
 XX
 DE Alginic acid lyase III N-terminal sequence.
 XX
 KM N-terminal: alginic acid; Al-I; Al-III; enzyme; alginic acid;
 KM cystic fibrosis.
 XX
 OS Pseudomonas sp.
 XX
 PN WO9419006-A.
 XX
 PD 01-SEP-1994.
 XX
 PF 24-FEB-1993; 93WO-JP00227.
 XX
 PR 24-FEB-1993; 93WO-JP00227.
 XX
 PA (GNZE) GUNZE LTD.
 PA (SAKB) OTSUKA KAGAKU KK.
 XX
 PI Abe S, Hisano T, Kimura A, Murata K, Nishimura M;
 PI Okayama K, Yamaguchi H, Yamashita T, Yonemoto Y;
 XX
 DR WPI: 1994-293999/36.
 XX
 PT New alginic acid lyase from Pseudomonas sp. - useful for the
 PT treatment of cystic fibrosis
 XX
 PS Claim 4; Page 24-25; 36pp; Japanese.
 XX
 CC The sequences given in R61236-37 represent the N-terminal fragments
 CC of alginic acid lyase I and III (Al-I and Al-III), respectively. These
 CC enzymes have molecular weights of 60 and 38 kD. The alginic acid
 CC break down alginic acid or viscous substances formed by
 CC cystic fibrosis sufferers.
 XX
 SQ Sequence 20 AA;
 Query Match 31.1%; Score 32; DB 15; Length 20;
 Best Local Similarity 31.2%; Pred. No. 39;
 Matches 5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 FFRWISNPATHODI 16
 I : I : I : I : I : I :
 DB 3 fdgavvkdpkptasyvdr 18
 RESULT 19
 R67427
 ID R67427 standard; Peptide; 20 AA.
 XX
 AC R67427;
 XX
 DT 31-AUG-1995 (first entry)

DE N-terminal fragment of alginic acid lyase, Al-III.
 XX
 KW alginic acid lyase; flavobacterium; recombinant production;
 KW N-terminal fragment.
 XX
 OS Flavobacterium sp.
 XX
 PN JP06319569-A.
 XX
 PD 22-NOV-1994.
 XX
 PF 14-MAY-1993; 93JP-0113149.
 XX
 PR 14-MAY-1993; 93JP-0113149.
 XX
 PA (GNZE) GUNZE KK.
 PA (SANKB) OTSUKA KAGAKU YAKUHIN KK.
 XX
 DR WPI: 1995-040321/06.
 XX
 PT Alginic acid lyase expression gene - used in the prepn. of
 PT alginic acid lyase
 XX
 PS Disclosure: Page 3; 16pp; Japanese.
 XX
 CC R67425-27 are the N-terminal fragments of alginic acid lyase (Al)-I,
 CC -II-2 and -III respectively. The amino acid sequence of alginic acid
 CC lyase is shown in R67424 and is encoded by the gene shown in 075342.
 CC It was isolated from Flavobacterium sp. by standard genetic techniques
 CC It is used to produce the recombinant enzyme in large quantities.
 XX
 SQ Sequence 20 AA:

Query Match	31.1%	Score 33	DB 16	Length 20
Best Local Similarity	31.2%	Pred. No. 39		
Matches	5	Conservative	6	Mismatches 5
				Indels 0
				Gaps 0
Qy	1	FFRWYISNPATHTODI	16	
	1	1	1	1
Db	3	fdqavvkptasyadv	18	

PT Hybrid polio virus useful as vaccine against HIV-1 infections -
PT contains epitope of heterologous protein inserted into the BC
PT loop of polio virus
XX
PS Disclosure; Page 22; 35pp; English.
XX
The sequences given in R26879-93 are portions of the HIV-1 principle
CC neutralising domain (PND) protein which were used as neutralising
CC epitopes. HIV-1 PND is an approx. 40 amino acid region of the
CC external envelope protein gp120 which forms a looped structure in
CC native gp120. The epitopes were inserted into the BC loop of a hybrid
CC poliovirus. This construct could be used as a vaccine. The vaccine
CC may be used for prophylaxis or treatment of human patients infected
CC with HIV-1.
XX
XX Sequence 19 AA;
SQ

Query Match	30.1%	Score 31:	DB 13:	Length 19:
Best Local Similarity	55.6%	Pred. No.	55:	
Matches	5:	Conservative	2:	Mismatches
				Indels
				Gaps
				0:

```
QY      4 MVISNPAAT 12
        | : ||| : |
Db      5 mtvdnpast 13
```

Query Match 30.1%; Score 31; DB 13; Length 23;
 Best Local Similarity 55.6%; Pred. No. 69;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 WVISNPAT 12
 1 : |||:1
 DB 5 mtvdpast 13

RESULT 22

R13289
 ID R13289 standard; Protein; 17 AA.

XX R13289;

XX 10-OCT-1991 (first entry)

XX C-terminal of somatotropin binding protein.

XX MAb; receptor; GHBP; monoclonal antibodies; epitope.

XX Synthetic.

XX EP439797-A.

XX 07-AUG-1991.

XX 20-DEC-1990: 90EP-0125021.

XX 31-JAN-1990: 90US-0473086.

XX (AMCY) AMERICAN CYANAMID CO.

XX Baumach WR, Wang BS, Sadeghi H, Logan JS, Hart IC;

XX WPI: 1991-231627/32.

XX Monoclonal antibodies to somatotropin binding protein in animals
 PT - do not bind to receptor and can be used alone, or with
 PT somatotropin to potentiate growth as well as in assays.

XX Disclosure; Page 11; 17pp; English.

XX The C-terminal of mouse SBP was prepared by solid phase peptide
 CC synthesis with the addition of Cys residue for coupling to an
 CC antigenic carrier protein. The conjugate was then used to raise
 CC MAb GHBP 4.3 which can be used to enhance animal growth or used
 CC with somatotropin to potentiate the effect of somatotropin in
 CC animals. It can also be used to distinguish between somatotropin
 CC binding protein and receptors.
 CC See also R13288.

XX Sequence 17 AA;

Query Match 29.1%; Score 30; DB 12; Length 17;
 Best Local Similarity 54.5%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 SNPAATHQDID 17
 1 : |||:1
 DB 4 snsqbphgeid 14

RESULT 23

W87486
 ID W87486 standard; peptide; 17 AA.

XX W87486;

XX 11-FEB-1999 (first entry)

XX

DE HIV-1 MO/LAI Nef protein amino acid fragment.

XX Human immunodeficiency virus-1; HIV-1; protease; provirus; L-2 cell;

XX mutation; Nef protein; immunogen; apoptosis; treatment; hybridisation;

XX cell lysis; chemotherapeutic; toxin; HIV infection; MO/LAI.

XX Human immunodeficiency virus type 1.

XX WO9844945-A1.

XX 15-OCT-1998.

XX 03-APR-1998: 98WO-US06690.

XX 04-APR-1997: 97US-0043047.

XX (IMMU-) IMMUNE RESPONSE CORP.

XX Luftig RB;

XX WPI: 1998-568304/48.

XX N-PSDB; V71869.

XX New nucleic acid encoding mutant or truncated forms of human immune
 PT deficiency virus proteins - used to generate non-infectious
 PT particles useful as therapeutic or prophylactic immunogens, also for
 PT diagnosis

XX Example 1; Fig 1; 66pp; English.

XX W87481 to W87486 represent human immunodeficiency virus-1 (HIV-1)
 CC sequences in MO/LAI cells that were used for comparing the mutant amino
 CC acid sequences of the defective HIV provirus in L-2 cells. V71858 to
 CC V71863 represent the portions of pol protease (prot.), vpr, env (gp120
 CC and gp41), and nef gene regions that were mutated as compared to wild-
 CC type HIV-1 in LAI or MO/LAI cells. The invention relates to mutated
 CC DNA, proteins or fragments of defective HIV-1 provirus in L-2 cell line.
 CC The mutations result in non-infectious HIV-1 particles. Inactive,
 CC protease-deficient HIV-1 particles containing at least one of Nef
 CC truncated protein fragments are used as immunogens, particularly for
 CC reducing or preventing apoptosis in HIV-1 sero-negative or -positive
 CC subjects, specifically those with HIV-1 infection, both for prevention
 CC and treatment. Fragments of nef gene and fragments encoding specific
 CC mutant Nef proteins are also useful in hybridisation tests for diagnostic
 CC detection of mutated genes in (lysed) cells or body fluids, while the
 CC corresponding mutant proteins are detected in immunoassays using
 CC antibodies. The protease-deficient HIV-1 particles and antibodies,
 CC optionally attached to a radioisotope, chemotherapeutic agent or toxin,
 CC can be used to reduce the severity of HIV infections.

XX Sequence 17 AA;

Query Match 29.1%; Score 30; DB 19; Length 17;
 Best Local Similarity 53.8%; Pred. No. 72;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 7 SNPAATHQDIDFL 19
 1 : |||:1 :1
 DB 3 snlaatnadcaavl 15

RESULT 24

R66373
 ID R66373 standard; peptide; 18 AA.

XX R66373;

XX 27-JUN-1995 (first entry)

XX Chlamydial MOMP VDI epitope.

XX Chlamydial epitope; variable domain; MOMP;

KW	major outer membrane protein; picornavirus; poliovirus; PV1;
KV	diagnostic; therapeutic; capsid protein.
XX	
XX	Chlamydia trachomatis serovar A.
OS	
PN	MO9426900-A.
XX	
PD	24-NOV-1994.
XX	
PF	12-MAY-1994; 94WO-CA00262.
XX	
PR	13-MAY-1993; 93US-0060978.
XX	
PA	(CONN-) CONNAUGHT LAB LTD.
XX	
PI	Caldwell HD, Klein MH, Mardin AD, Oomen RP;
XX	
DR	WPI: 1995-006796/01.
XX	
PT	New hybrid picornaviruses expressing chlamydial epitopes - used
XX	to develop prods. for vaccination, diagnosis, treatment of
PT	chlamydial infections and prodn. of immunological reagents
XX	
PS	Disclosure: Page 15; 99pp; English.
XX	
CC	To obtain a poliovirus-1 (PV1)/chlamydial hybrid, the PV1
CC	Mahoney cDNA clone PT7XLD was modified to encode epitopes from
CC	C. trachomatis ser. A MOMP VDI. The mutagenesis cartridge was
CC	contained between PV nucleotides 2753-91 (given in 079003) which
CC	encode PV amino acids 1092-1104 (R66375) which include the BC loop
CC	of capsid protein VP1 (R66386). The polio-specific DNA within the
CC	cartridge, encoding the sequence given in R66369, was replaced by
CC	oligonucleotides encoding VDI peptides R66370-74. Viable PV
CC	expressing chlamydial immunostimulatory epitope was expressed in
CC	Vero cells.
XX	
SO	Sequence 18 AA:
XX	
QY	Query Match 29.1%; Score 30; DB 16; Length 18;
XX	Best Local Similarity 55.6%; Pred. No. 77;
XX	Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0
DB	8 NPATRHODI 16
XX	
XX	1 npaststdv 9
XX	
RESULT 25	
ID	R66374 standard; peptide: 18 AA.
XX	
AC	R66374;
XX	
DT	27-JUN-1995 (first entry)
XX	
DE	Chlamydial MOMP VDI epitope.
XX	
XX	Chlamydial epitope; variable domain; MOMP;
KW	major outer membrane protein; picornavirus; poliovirus; PV1;
KV	diagnostic; therapeutic; capsid protein.
XX	
OS	Chlamydia trachomatis serovar A.
XX	
PN	MO9426900-A.
XX	
PD	24-NOV-1994.
XX	
PF	12-MAY-1994; 94WO-CA00262.
XX	
PR	13-MAY-1993; 93US-0060978.
XX	
PA	(CONN-) CONNAUGHT LAB LTD.

xx	Caldwell HD, Klein MH, Murdin AD, Oomen RP;
pi	
xx	WPI: 1995-006796/01.
DR	
xx	New hybrid picornaviruses expressing chlamydial epitopes - used
Ft	to develop prods. for vaccination, diagnosis, treatment of
Pt	chlamydial infections and prodn. of immunological reagents
xx	
PS	Disclosure; Page 15; 99pp; English.
xx	
CC	To obtain a poliovirus-1 (PV1)/chlamydial hybrid, the PV1
CC	Mahoney cDNA clone pT7XLD was modified to encode epitopes from
CC	C. trachomatis ser. A ROMP VDI. The mutagenesis cartridge was
CC	contained between PV nucleotides 2753-91 (given in Q79003) which
CC	encode PV amino acids 1092-1104 (R66375) which include the BC loop
CC	of capsid protein VP1 (R66386). The polio-specific DNA within the
CC	cartridge, encoding the sequence given in R66369, was replaced by
CC	oligonucleotides encoding VDI peptides R66370-74. Viable PV
CC	expressing chlamydial immunostimulatory epitope was expressed in
CC	Vero cells.
XX	
SQ	Sequence 18 AA;
Query Match	29.1%; Score 30; DB 16; Length 18;
Best Local Similarity	55.6%; Pred. No. 77;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
QY	8 NPAAHQDI 16 :: :
DB	1 npastsdv 9

```
Search completed: February 5, 2001, 10:47:36
Job time: 630 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:40:11 ; Search time 93.77 Seconds

(without alignments)
24.999 Million cell updates/sec

Title: US-08-981-824-1

Sequence: 1 DVNVAFLHATDLPACDGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_NHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.5	27.7	22	12_085712	085712 rous sarcom
2	30	27.3	23	8_09TJ56	09TJ56 abies fabri
3	30	27.3	23	8_09TJ54	09TJ54 abies farge
4	30	27.3	23	8_09TJ52	09TJ52 abies flama
5	30	27.3	23	8_09TJ50	09TJ50 abies frase
6	30	27.3	23	8_09TJ48	09TJ48 abies holop
7	30	27.3	23	8_09TJ46	09TJ46 abies homol
8	30	27.3	23	8_09TJ44	09TJ44 abies korea
9	30	27.3	23	8_09TJ42	09TJ42 abies lasio
10	30	27.3	23	8_09TJ40	09TJ40 abies marie
11	30	27.3	23	8_09TJ38	09TJ38 abies neph
12	30	27.3	23	8_09TJ36	09TJ36 abies sach
13	30	27.3	23	8_09TJ34	09TJ34 abies sibit
14	30	27.3	23	8_09TJ32	09TJ32 abies veitc
15	30	27.3	25	2_007916	007916 mycobacteri
16	29	26.4	20	4_015988	015988 homo sapien
17	29	26.4	22	2_034195	034195 ehrlichia r
18	28	25.5	15	12_085713	085713 rous sarcom
19	28	25.5	21	10_0958J0	0958J0 bryonia dlo

20	28	25.5	23	6_09TRC6	09TRC6 cants fam11
21	28	25.5	24	5_094377	094377 caenorhabd1
22	27	24.5	21	6_09TJ55	09TJ55 cebus apell1
23	26	23.6	18	7_030216	030216 homo sapien
24	26	23.6	19	4_09UMM9	09umm9 homo sapien
25	26	23.6	20	11_09OV03	09ov03 rattus sp.
26	26	23.6	21	11_088229	088229 mus muschlu
27	26	23.6	21	11_09RIH1	09rih1 rattus norv
28	26	23.6	24	2_052388	052388 anabaena fl
29	26	23.6	24	5_094369	094369 caenorhabd1
30	26	23.6	24	5_094374	094374 caenorhabd1
31	25.5	23.2	20	5_09TJNO	09tjno macrobellea
32	25.5	23.2	22	8_09TJ27	09tj27 pisum sativ
33	25	22.7	14	10_09SAP8	09sap8 pisum sativ
34	25	22.7	18	4_014009	014009 homo sapien
35	25	22.7	20	4_09UCA0	09uca0 homo sapien
36	25	22.7	21	11_09OV03	09ov03 rattus sp.
37	25	22.7	22	4_09MS53	09ms53 homo sapien
38	25	22.7	24	5_094373	094373 caenorhabd1
39	25	22.7	24	6_09TJ50	09tj50 bos taurus
40	24	21.8	13	12_09WMG5	09wmg5 sigma virus
41	24	21.8	15	6_09MYT7	09myt7 sus scrofa
42	24	21.8	19	2_031045	031045 streptomyce
43	24	21.8	19	8_099724	099724 dryocopus
44	24	21.8	19	8_099728	099728 buteo jama1
45	24	21.8	19	13_P87468	P87468 xenopus lae

ALIGNMENTS

RESULT 1					
ID 085712	PRELIMINARY:	PRT:	22 AA.		
AC 085712:					
DT 01-NOV-1996 (TREMBLrel. 01, Created)					
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)					
DE (BRYAN HIGH-TITER STRAIN) SRC (FRAGMENT).					
OS Rous sarcoma virus.					
OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.					
OX NCBI_Taxid-11886;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE-84115080; PubMed-6319754;					
RA Lerner T.L., Hanafusa H.;					
RT "DNA sequence of the Bryan high-titer strain of Rous sarcoma virus: extent of env deletion and possible genealogical relationship with other viral strains."					
RL J. VIROL. 49:549-556(1984).					
DR EMBL; K03366; AAA42559.1; -.					
FT NON_TER					
FT NON_TER					
SQ SEQUENCE	22 AA;	2519 MW;	EOBB3BB6F1DE4F3F CRC64;		
Query Match	27.7%;	Score 30.5;	DB 12;	Length 22;	
Best Local Similarity	53.8%;	Pred. No. 2e+02;			
Matches	7;	Conservative	2;	Mismatches	3;
				Indels	1;
				Gaps	1;
DB	5	FAYLQA-QULPAC	16		
QY	4	YAFLLHATDLPAC	16		
DB	5	FAYLQA-QULPAC	16		
RESULT 2					
ID 09TJ56	PRELIMINARY:	PRT:	23 AA.		
AC 09TJ56:					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)					
DE P700 APOPROTEIN IB (FRAGMENT).					
GN PSAB.					

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OS Abies fabri.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCB1_TaxID=97166;
RN [1]
RP SEQUENCE FROM N.A.
RA Suyama Y., Tsumura Y., Yoshimaru H.;
RT "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
RT chloroplast DNA sequences."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029670; BAA87992.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 23 AA: 2485 MW: C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 VNVAFLHATDLPACDGE 19
DB 4 VGIFTYAFLIASTSGK 21

RESULT 3
ID 09TJ54 PRELIMINARY; PRT; 23 AA.
AC 09TJ54:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE P700 APOPROTEIN IB (FRAGMENT).
GN PSAB.
OS Abies fargesii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCB1_TaxID=97167;
RN [1]
RP SEQUENCE FROM N.A.
RA Suyama Y., Tsumura Y., Yoshimaru H.;
RT "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
RT chloroplast DNA sequences."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029671; BAA87994.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 23 AA: 2485 MW: C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 VNVAFLHATDLPACDGE 19
DB 4 VGIFTYAFLIASTSGK 21

RESULT 4
ID 09TJ52 PRELIMINARY; PRT; 23 AA.
AC 09TJ52:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE P700 APOPROTEIN IB (FRAGMENT).
GN PSAB.
OS Abies firma.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

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OC Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCB1_TaxID=78260;
RN [1]
RP SEQUENCE FROM N.A.
RA Suyama Y., Tsumura Y., Yoshimaru H.;
RT "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
RT chloroplast DNA sequences."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029672; BAA87996.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 23 AA: 2485 MW: C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 VNVAFLHATDLPACDGE 19
DB 4 VGIFTYAFLIASTSGK 21

RESULT 5
ID 09TJ50 PRELIMINARY; PRT; 23 AA.
AC 09TJ50:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE P700 APOPROTEIN IB (FRAGMENT).
GN PSAB.
OS Abies fraseri.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCB1_TaxID=97172;
RN [1]
RP SEQUENCE FROM N.A.
RA Suyama Y., Tsumura Y., Yoshimaru H.;
RT "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
RT chloroplast DNA sequences."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029673; BAA87998.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 23 AA: 2485 MW: C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;
Best Local Similarity 33.3%; Pred. No. 2.5e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 VNVAFLHATDLPACDGE 19
DB 4 VGIFTYAFLIASTSGK 21

RESULT 6
ID 09TJ48 PRELIMINARY; PRT; 23 AA.
AC 09TJ48:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE P700 APOPROTEIN IB (FRAGMENT).
GN PSAB.
OS Abies holophylla.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCB1_TaxID=97168;
RN [1]

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RP      SEQUENCE FROM N.A.
RA      Suyama Y., Tsunmura Y., Yoshimaru H.;
RT      "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
RT      chloroplast DNA sequences."
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB029674; BAA88000.1; -.
KW      Chloroplast.
FT      NON TER
SO      SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;

Query Match
Best Local Similarity 33.3%; Score 30; DB 8; Length 23;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 VNVAFLHATDLLPACDGE 19
      | | | | | : : | :
Db      4 VGIIPTVA AFLIASTSGK 21

RESULT 7
ID      Q9TJ46      PRELIMINARY;      PRT;      23 AA.
AC      Q9TJ46;
DT      01-MAY-2000 (TREMBLrel. 13; Created)
DT      01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DT      01-MAY-2000 (TREMBLrel. 13; Last annotation update)
DE      P700 APOPROTEIN IB (FRAGMENT).
GN      PSAB.
OS      Abies homolepis.
OG      Chloroplast.
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Coniferopsida; Coniferales; Pinaceae; Abies.
OX      NCBL_taxonomy=78261;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Suyama Y., Tsunmura Y., Yoshimaru H.;
RT      "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
RT      chloroplast DNA sequences."
RL      Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB029675; BAA88002.1; -.
KW      Chloroplast.
FT      NON TER
SO      SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;

Query Match
Best Local Similarity 33.3%; Score 30; DB 8; Length 23;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      2 VNVAFLHATDLLPACDGE 19
      | | | | | : : | :
Db      4 VGIIPTVA AFLIASTSGK 21

RESULT 8
ID      Q9TJ44      PRELIMINARY;      PRT;      23 AA.
AC      Q9TJ44;
DT      01-MAY-2000 (TREMBLrel. 13; Created)
DT      01-MAY-2000 (TREMBLrel. 13; Last sequence update)
DT      01-MAY-2000 (TREMBLrel. 13; Last annotation update)
DE      P700 APOPROTEIN IB (FRAGMENT).
GN      PSAB.
OS      Abies koreana.
OG      Chloroplast.
OC      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC      Coniferopsida; Coniferales; Pinaceae; Abies.
OX      NCBL_taxonomy=97170;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Suyama Y., Tsunmura Y., Yoshimaru H.;
RT      "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on

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DR	chloroplast DNA sequences."
RL	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
KW	Chloroplast.
FT	NON_TER
SQ	SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;
OY	2 VNYAFLHATDLLPACDGE 19 : : - :
DB	4 VGITFYAAFLIASTSGK 21
RESULT 9	
ID	09TU42 PRELIMINARY; PRT; 23 AA.
AC	09TU42:
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DM	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DZ	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	P700 APOPROTEIN IB (FRAGMENT).
GN	PSAB.
OS	Abies lasiocarpa.
OC	Chloroplast.
CC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OX	NCB1_TaxID=34340;
RN	[1]
RA	SEQUENCE FROM N.A.
RP	Suyama Y., Tsunuma Y., Yoshimaru H.;
RT	"Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
RL	chloroplast DNA sequences.";
DR	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
KW	Chloroplast.
FT	NON_TER
SQ	SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;
OY	2 VNYAFLHATDLLPACDGE 19 : : - :
DB	4 VGITFYAAFLIASTSGK 21
RESULT 10	
ID	09TU40 PRELIMINARY; PRT; 23 AA.
AC	09TU40:
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DM	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DZ	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	P700 APOPROTEIN IB (FRAGMENT).
GN	PSAB.
OS	Abies mariesii.
OC	Chloroplast.
CC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OX	NCB1_TaxID=78263;
RN	[1]
RA	SEQUENCE FROM N.A.
RP	Suyama Y., Tsunuma Y., Yoshimaru H.;
RT	"Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
RL	chloroplast DNA sequences.";
DR	Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
KW	Chloroplast.
FT	NON_TER
SQ	SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;
OY	2 VNYAFLHATDLLPACDGE 19 : : - :
DB	4 VGITFYAAFLIASTSGK 21
Query Match	27.3%; Score 30; DB 8; Length 23;
Best Local Similarity	33.3%; Pred. No. 2.5e+02;
Matches 6; Conservative	4; Mismatches 8; Indels 0; Gaps 0;

KW Chloroplast. 1
 FT NON_TER 1
 SO SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;
 Best Local Similarity 33.3%; Pred. No. 2.5e+02;
 Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 2 VNVAFLHATDLPACDGE 19
 | | | | | : : : : :
 Db 4 VGIFTYAFLIASTSGK 21

RESULT 11

O9TJ38 PRELIMINARY; PRT; 23 AA.

AC O9TJ38;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE P700 APOPROTEIN IB (FRAGMENT).
 GN PSAB.

OS Abies nephrolepis.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Abies.

OX NCB1_TaxID=97171;

RN [1]
 RP SEQUENCE FROM N.A.

RA Suyama Y., Tsumura Y., Yoshimaru H.;
 RT "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
 RT chloroplast DNA sequences.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB029679; BAA88010.1; -
 KW Chloroplast.

FT NON_TER 1
 SQ SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;
 Best Local Similarity 33.3%; Pred. No. 2.5e+02;
 Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 2 VNVAFLHATDLPACDGE 19
 | | | | | : : : : :
 Db 4 VGIFTYAFLIASTSGK 21

RESULT 12

O9TJ36 PRELIMINARY; PRT; 23 AA.

AC O9TJ36;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE P700 APOPROTEIN IB (FRAGMENT).
 GN PSAB.

OS Abies sachalinensis.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Abies.

OX NCB1_TaxID=78264;

RN [1]
 RP SEQUENCE FROM N.A.

RA Suyama Y., Tsumura Y., Yoshimaru H.;
 RT "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
 RT chloroplast DNA sequences.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB029680; BAA88012.1; -
 KW Chloroplast.

FT NON_TER 1
 SQ SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;
 Best Local Similarity 33.3%; Pred. No. 2.5e+02;
 Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 2 VNVAFLHATDLPACDGE 19
 | | | | | : : : : :
 Db 4 VGIFTYAFLIASTSGK 21

RESULT 13

O9TJ34 PRELIMINARY; PRT; 23 AA.

AC O9TJ34;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE P700 APOPROTEIN IB (FRAGMENT).
 GN PSAB.

OS Abies sibirica.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Abies.

OX NCB1_TaxID=97169;

RN [1]
 RP SEQUENCE FROM N.A.

RA Suyama Y., Tsumura Y., Yoshimaru H.;
 RT "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
 RT chloroplast DNA sequences.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB029681; BAA88014.1; -
 KW Chloroplast.

FT NON_TER 1
 SQ SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;
 Best Local Similarity 33.3%; Pred. No. 2.5e+02;
 Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 2 VNVAFLHATDLPACDGE 19
 | | | | | : : : : :
 Db 4 VGIFTYAFLIASTSGK 21

RESULT 14

O9TJ32 PRELIMINARY; PRT; 23 AA.

AC O9TJ32;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE P700 APOPROTEIN IB (FRAGMENT).
 GN PSAB.

OS Abies velutichii.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Abies.

OX NCB1_TaxID=78262;

RN [1]
 RP SEQUENCE FROM N.A.

RA Suyama Y., Tsumura Y., Yoshimaru H.;
 RT "Molecular phylogenetic position of Japanese Abies (Pinaceae) based on
 RT chloroplast DNA sequences.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB029682; BAA88016.1; -
 KW Chloroplast.

FT NON_TER 1
 SQ SEQUENCE 23 AA; 2485 MW; C19201F5B9BE67C8 CRC64;

Query Match 27.3%; Score 30; DB 8; Length 23;

Best Local Similarity: 33.3%; Pred. No. 2.5e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 2 VNAYFLATDLPACDGE 19
1 | | | : | : | :
4 VGIYTYAFLASTSGK 21

RESULT 15
007916

ID 007916 PRELIMINARY: PRT: 25 AA.

AC 007916;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE HYPOTHETICAL 2.6 KDA PROTEIN.
OS Mycobacterium tuberculosis, and Mycobacterium bovis BCG.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 33892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-2296207, AND PASTEUR;
RA Supply P., Magdalena J., Himpens S., Loch C.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y13628; CAA73960.1; -
DR EMBL: Y13627; CAA73955.1; -
DR EMBL: Y13628; CAA73959.1; -
KW Hypothetical protein.
SQ SEQUENCE 25 AA: 2639 MW: 036E7271A33D1CF2 CRC64;

Query Match 27.3%; Score 30; DB 2; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 14 PACDGE 19
1 | | | : | : | :
18 PACGGE 23

RESULT 16
015988 PRELIMINARY: PRT: 20 AA.

ID 015988;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE HLX1 PROTEIN (FRAGMENT).
GN HLX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93194183; PubMed=8095486;
RA Nishimura D.Y., Purchio A.F., Murray J.C.;
RT "Linkage localization of TGFB2 and the human homeobox gene HLX1 to
chromosome 1q."
RL Genomics 15:357-364(1993).
DR EMBL: S56767; AAD13885.1; -
FT NON_TER 1 1
SQ SEQUENCE 20 AA: 2012 MW: 6BB655F09B5B5A64 CRC64;

Query Match 26.4%; Score 29; DB 4; Length 20;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 14 PACDGER 20
1 | | | : | : | :
7 PAADGEG 13

RESULT 17
034195 PRELIMINARY: PRT: 22 AA.

ID 034195;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE GROES (FRAGMENT).
GN GROES.
OS Ehrlichia risticii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Ehrlichiae; Ehrlichia.
OX NCBI_TaxID=950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373904; PubMed=9230387;
RA Sumner J.W., Nicholson W.L., Massung R.F.;
RT PCR amplification and comparison of nucleotide sequences from the
groEL heat shock operon of Ehrlichia species."
RL J. Clin. Microbiol. 35:2087-2092(1997).
DR EMBL: U96732; AAB65632.1; -
DR INTERPRO: IPR001476; -
DR PFM: PFM00166; cpn10; 1.
FT NON_TER 1 1
SQ SEQUENCE 22 AA: 2504 MW: 21D959D75191F620 CRC64;

Query Match 26.4%; Score 29; DB 2; Length 22;
Best Local Similarity 27.8%; Pred. No. 3.6e+02;
Matches 5; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 2 VNAYFLATDLPACDGE 19
1 | | | : | : | :
5 VEVYVMEKEDIIRKESK 22

RESULT 18
085713 PRELIMINARY: PRT: 15 AA.

ID 085713;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE 29 (RSV-29) SRC (FRAGMENT).
OS Rous sarcoma virus.
OC Viruses; Retroviruses; Retroviridae; Avian type C retroviruses.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85265036; PubMed=2991593;
RA Dutta A., Wang L.H., Hanafusa T., Hanafusa H.;
RT "Partial nucleotide sequence of Rous sarcoma virus-29 provides
evidence that the original Rous sarcoma virus was replication
defective."
RL J. Virol. 55:728-735(1985).
DR EMBL: M1117; AAA42556.1; -
FT NON_TER 1 1
SQ SEQUENCE 15 AA: 1597 MW: DB53E0F31273C5C1 CRC64;

Query Match 25.5%; Score 28; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LIPAC 16
1 | | | : | : | :
5 LIPAC 9

RESULT 19
09S8J0

ID 095830 PRELIMINARY; PRT; 21 AA.
 AC 095830;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
 DE 27 KDA RIBOSOME-INACTIVATING PROTEIN (FRAGMENT).
 OS Bryonia dioica (Red bryon).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Cucurbitales; Cucurbitaceae; Bryonia.
 NCBI_TaxID=3652;
 RX MEDLINE=95151812; PubMed=7849072;
 RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
 Marquardt H.;
 RT "Characterization of ribosome-inactivating proteins isolated from
 RT Bryonia dioica and their utility as carcinoma-reactive
 RT immunocytogenetics";
 RL Bioconjug. Chem. 5:423-429(1994).
 SQ SEQUENCE 21 AA; 2302 MW; 54ED5E00AD12787B CRC64;

Query Match 25.5%; Score 28; DB 10; Length 21;
 Best Local Similarity 40.0%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYNATFLHAT 10
 ID 09TRC6 PRELIMINARY; PRT; 23 AA.
 AC 09TRC6;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
 DE CITOCHROME P450 DPB-1 ISOFORM (FRAGMENT).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RX MEDLINE=94198820; PubMed=8185738;
 RA Shiraga T., Iwasaki K., Nozaki K., Yamura T., Yamazoe Y., Kato R.,
 Takahaka A.;
 RT "Isolation and characterization of four cytochrome P450 isozymes from
 RT untreated and phenobarbital-treated beagle dogs";
 RL Biol. Pharm. Bull. 17:22-28(1994).
 SQ SEQUENCE 23 AA; 2638 MW; AF86888FE8029F8 CRC64;

Query Match 25.5%; Score 28; DB 6; Length 23;
 Best Local Similarity 55.6%; Pred. No. 5.5e+02; 2; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 DLPACDGE 19
 ID 094377 PRELIMINARY; PRT; 24 AA.
 AC 094377;
 DT 01-FEB-1997 (TRENBLREL. 02, Created)
 DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)
 DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
 DE PPI-LIKE SER/THR PROTEIN PHOSPHATASE (FRAGMENT).
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RX MEDLINE=95151812; PubMed=7849072;
 RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
 Marquardt H.;
 RT "Characterization of ribosome-inactivating proteins isolated from
 RT Bryonia dioica and their utility as carcinoma-reactive
 RT immunocytogenetics";
 RL Bioconjug. Chem. 5:423-429(1994).
 SQ SEQUENCE 21 AA; 2302 MW; 54ED5E00AD12787B CRC64;

Query Match 25.5%; Score 28; DB 5; Length 24;
 Best Local Similarity 71.4%; Pred. No. 5.7e+02; 1; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYNATFL 7
 ID 09T055 PRELIMINARY; PRT; 21 AA.
 AC 09T055;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 1A1 (FRAGMENT).
 OS Cebus apella (Brown-capped capuchin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
 NCBI_TaxID=9515;
 RX MEDLINE=94198820; PubMed=8185738;
 RA Shiraga T., Iwasaki K., Nozaki K., Yamura T., Yamazoe Y., Kato R.,
 Takahaka A.;
 RT "Isolation and characterization of four cytochrome P450 isozymes from
 RT untreated and phenobarbital-treated beagle dogs";
 RL Biol. Pharm. Bull. 17:22-28(1994).
 SQ SEQUENCE 21 AA; 2000 MW; 9887EF96C931C820 CRC64;

Query Match 24.5%; Score 27; DB 6; Length 21;
 Best Local Similarity 66.7%; Pred. No. 7.3e+02; 1; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 LPACDG 18
 ID 030216 PRELIMINARY; PRT; 18 AA.
 AC 030216;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
 DE HUMAN LEUKOCYTE ANTIGEN ALPHA CHAIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=95151812; PubMed=7849072;
 RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
 Marquardt H.;
 RT "Characterization of ribosome-inactivating proteins isolated from
 RT Bryonia dioica and their utility as carcinoma-reactive
 RT immunocytogenetics";
 RL Bioconjug. Chem. 5:423-429(1994).
 SQ SEQUENCE 21 AA; 2302 MW; 54ED5E00AD12787B CRC64;

RP SEQUENCE FROM N.A.
 RX MEDLINE=95064785; PubMed=79744465;
 RA Fogdell A., Olerup O.;
 RT "The DAI*0104 allele is carried by DRB1*1001- and DRB1*1401-positive
 RT haplotypes in Caucasians, Africans and Orientals.";
 RT Tissue Antigens 44:19-24(1994).
 DR EMBL: S75685; AAB32621.1; -
 DR INTERPRO: IPR001003; -
 DR PFM: PF00993; MHC-II_alpha: 1.
 FT NON_TER
 SQ SEQUENCE 18 AA; 1708 MW; 097492525C2252FC CRC64;

Query Match 23.6%; Score 26; DB 7; Length 18;
 Best Local Similarity 38.5%; Pred. No. 9.1e+02;
 Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 7 LHATDLPACDGE 19
 | | : | |
 Db 3 LALTTMSPCGGE 15

RESULT 24
 OSUMM9 PRELIMINARY; PRT; 19 AA.
 AC Q9UMM9:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE ARGININE VASOPRESSIN-NEUROPHYSIN II (FRAGMENT).
 GN AVP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91123474; PubMed=1840604;
 RA Ito M., Mori Y., Oiso Y., Saito H.;
 RT "A single base substitution in the coding region for neurophysin II
 RT associated with familial central diabetes insipidus.";
 RL J. Clin. Invest. 87:725-728(1991).
 DR EMBL: M63733; AAA69844.1; -
 FT NON_TER
 SQ SEQUENCE 19 AA; 1985 MW; 5FF5FCD7BD990451 CRC64;

Query Match 23.6%; Score 26; DB 4; Length 19;
 Best Local Similarity 80.0%; Pred. No. 9.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LRPAC 16
 : ||||
 Db 5 MLPAC 9

RESULT 25
 OSUMM9 PRELIMINARY; PRT; 20 AA.
 AC Q9QVG0:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE CLEAVED PROLACTIN-1, CLPRL-1-FRAGMENT A.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92143803; PubMed=1736889;
 RA Andries M., Tillemans D., Deneef C.;
 RT "Isolation of cleaved prolactin variants that stimulate DNA synthesis

RT in specific cell types in rat pituitary cell aggregates in culture.";
 RL Biochem. J. 281:393-400(1992).
 SQ SEQUENCE 20 AA; 2146 MW; 89CA019A7668CBA CRC64;

Query Match 23.6%; Score 26; DB 11; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 13 LRPACD 18
 | | | |
 Db 1 LRPVCSG 6

Search completed: February 5, 2001, 10:55:20
 Job time: 909 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:37:07; Search time 58.67 Seconds
(without alignments)
23.147 Million cell updates/sec

Title: us-08-981-824-1

Perfect score: 110

Sequence: 1 DVNRYFLHARDLPACDGER 20

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 5001

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR66:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	28.2	25	2	S10850
2	29	26.4	16	2	PH1640
3	28	25.5	20	2	S15861
4	28	25.5	24	2	T42014
5	26	23.6	18	2	I59649
6	26	23.6	19	2	H27480
7	26	23.6	24	2	T42257
8	26	23.6	24	2	T42441
9	25	22.7	18	2	S58277
10	25	22.7	20	2	S65884
11	25	22.7	23	2	B39855
12	25	22.7	23	2	S38991
13	25	22.7	24	2	T42258
14	25	22.7	25	2	S13996
15	25	22.7	25	2	S11351
16	24	21.8	11	2	S61797
17	24	21.8	16	2	S68730
18	24	21.8	18	1	QHRC2
19	24	21.8	18	2	A60103
20	24	21.8	18	2	I51427
21	24	21.8	19	2	S63489
22	24	21.8	20	2	S63490
23	24	21.8	23	2	A39855
24	24	21.8	24	2	T42259
25	23	20.9	10	2	A32543
26	23	20.9	10	2	A32543
27	23	20.9	17	2	A54534
28	23	20.9	19	2	I40063
29	23	20.9	22	2	I51830

30	23	20.9	24	2	T42256
31	23	20.9	24	2	I54750
32	22	20.0	12	2	S16204
33	22	20.0	14	2	PL0040
34	22	20.0	15	2	S30608
35	22	20.0	15	2	S55312
36	22	20.0	17	2	J02310
37	22	20.0	17	2	J02320
38	22	20.0	19	1	EW5MAN
39	22	20.0	23	2	D34047
40	22	20.0	23	2	B42382
41	22	20.0	24	2	T42378
42	22	20.0	25	2	S20257
43	21	19.1	11	2	B49164
44	21	19.1	12	2	S01122
45	21	19.1	13	2	S01119

ALIGNMENTS

RESULT 1
S10850
alpha-amylase inhibitor - durum wheat (fragment)
N:Alternate names: glutenin low molecular weight chain
C:Species: Triticum durum (durum wheat)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C:Accession: S10850
R:Kobrehel, K.; Alary, R.
J. Sci. Food Agric. 48, 441-452, 1989
A:Title: Isolation and partial characterization of two low molecular weight durum whe
A:Reference number: S10849
A:Accession: S10850
A:Molecule type: protein
A:Residues: 1-25 <KOB>
C:Superfamily: wheat alpha-amylase inhibitor
C:Keywords: alpha-amylase inhibitor

Query Match 28.2%; Score 31; DB 2; Length 25;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 TDLTPAC 16

DB 12 TBLPAC 18

RESULT 2

PH1640
Ig H chain V-D-J region (clone B-lees 235) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1640

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-lees m

A:Reference number: PH1580; MUID:93301609

A:Accession: PH1640

A:Molecule type: DNA

A:Residues: 1-16 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: Immunoglobulin

QY 5 AFLHATDLPACDG 18

DB 2 ARLRATVPIGVG 15

Query Match 26.4%; Score 29; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

RESULT 3
S15861
estrogen receptor - p1g (fragments)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 30-May-1997
C:Accession: S15861
R:Thole, H.H.; Jungblut, P.W.; Jakob, F.
Biochem. J. 276, 709-714, 1991
A:Title: The proton-driven dissociation of oestradiol-receptor dimers as a preparative
9.
A:Reference number: S15861; MUID:91291128
A:Accession: S15861
A:Molecule type: Protein
A:Residues: 1-20 <Bio>
C:Keywords: steroid hormone receptor

Query Match 25.5%; Score 28; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VNVAFLHA 9
||| |||
Db 6 INMAKLHA 13

RESULT 4
T42014
Ser/Thr protein phosphatase, PP1-like - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T42014
R:Zeke, T.; Gergely, P.; Dombradi, V.
submitted to the EMBL Data Library, July 1996
A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis
A:Reference number: 222025
A:Accession: T42014
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <Zek>
A:Cross-references: EMBL:277740; PIDN:CAB01299.1
A:Experimental source: strain Bristol; clone C-1
C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein

Query Match 25.5%; Score 28; DB 2; Length 24;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVNVAFL 7
||| |||
Db 17 DVNVAFL 23

RESULT 5
I59649
human leukocyte antigen alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I59649
R:Fogdell, A.; Olerup, O.
Tissue Antigens 44, 19-24, 1994
A:Title: The DOA1*0104 allele is carried by DRB1*1001- and DRB1*1401-positive haplotypes
A:Reference number: I59649; MUID:35064785
A:Accession: I59649
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: GB:S75665; MID:g913771; PIDN:AA32621.1; PID:g913772
C:Genetics:
A:Gene: GDB:HLA-DOA1
A:Cross-references: GDB:120638; OMIM:146880

A:Map position: 6p21.3-6p21.3

Query Match 23.6%; Score 26; DB 2; Length 18;
Best Local Similarity 38.5%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 7 LHAIDLPAADGE 19
||| |||
Db 3 LALTRMSPGGE 15

RESULT 6
H27480
hydrogenase (EC 1.18.99.1) large chain - Desulfovibrio baculatus (strain Norway 4) (f
N:Alternate names: hydrogenase; Nifese hydrogenase
C:Species: Desulfovibrio baculatus
C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 30-Sep-1993
C:Accession: H27480
R:Prickrill, B.C.; He, S.H.; Li, C.; Menon, N.; Chol, E.S.; Przybyla, A.E.; DerVartan
Biochem. Biophys. Res. Commun. 149, 369-377, 1987
A:Title: Identification of three classes of hydrogenase in the genus, Desulfovibrio.
A:Reference number: A27480; MUID:88106446
A:Accession: H27480
A:Molecule type: protein
A:Residues: 1-19 <PRIT>
C:Keywords: oxidoreductase

Query Match 23.6%; Score 26; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 6.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 14 PACDGER 20
||| |||
Db 6 PAADGKR 12

RESULT 7
T42257
phosphoprotein phosphatase (EC 3.1.3.16) - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T42257
R:Zeke, T.; Gergely, P.; Dombradi, V.
submitted to the EMBL Data Library, July 1996
A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabd
A:Reference number: 222131
A:Accession: T42257
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <Zek>
A:Cross-references: EMBL:277735; PIDN:CAB01294.1
C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprot
C:Keywords: phosphoric monoester hydrolase

Query Match 23.6%; Score 26; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VNVAFL 7
||| |||
Db 18 VNVAFL 23

RESULT 8
T42441
protein phosphatase - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T42441
R:Zeke, T.; Gergely, P.; Dombradi, V.

submitted to the EMBL Data Library, July 1996

A:Description: The catalytic subunits of Ser/Thr protein phosphatases from *Caenorhabditis*

A:Reference number: 222131

A:Accession: T42441

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-24 <ZK>

A:Cross-references: EMBL:277729; PIDN:CA01288.1

C:Superfamily: phosphoprotein phosphatase; phosphodiesterase core homology; phosphoprotein

Query Match 23.6%; Score 26; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 VNPAFL 7
|||
18 VNYLFL 23

RESULT 9
S58277
Insulin-like growth factor receptor type II - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999

C:Accession: S58277

R:Smrka, O.W.; Stoger, R.; Kurzbauer, R.; Fae, I.; Fischer, G.F.; Barlow, D.P.

submitted to the EMBL Data Library, January 1995

A:Description: Conservation of a methylation imprint and a putative imprinting box at th

A:Reference number: S58277

A:Accession: S58277

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-18 <SKR>

A:Cross-references: EMBL:X83702; NID:g929644; PIDN:CA58675.1; PID:g929645

C:Keywords: growth factor receptor

Query Match 22.7%; Score 25; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 8.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 13 LPACDGE 19
|||
11 LPSCVCK 17

RESULT 10
S55884
translational initiation factor eIF-1 - rabbit (fragments)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S55884

R:Kasperaitis, M.A.M.; Voorma, H.O.; Thomas, A.A.M.

FEBS Lett. 365, 47-50, 1995

A:Title: The amino acid sequence of eukaryotic translation initiation factor 1 and its s

A:Reference number: S55884; MUID:95293122

A:Accession: S55884

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9;10-16;17-20 <KAS>

Query Match 22.7%; Score 25; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 DLPPA 15
|||||
2 DLPPA 6

RESULT 11

B39855

paralytic peptide II - tobacco hornworm

C:Species: Manduca sexta (tobacco hornworm)

C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 03-Feb-1994

C:Accession: B39855

R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Qvistad, G.B

J. Biol. Chem. 266, 12873-12877, 1991

A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep

A:Reference number: A39855; MUID:91302298

A:Accession: B39855

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-23 <SKI>

C:Superfamily: paralytic peptide I

Query Match 22.7%; Score 25; DB 2; Length 23;
Best Local Similarity 43.8%; Pred. No. 1.1e+03;
Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 NYAFLHATDLPACDG 18
|:|:|:|:|:|:|
2 NFAGCATGFLRTADG 17

RESULT 12
S38991
glycine reductase (EC 1.4.99.-) sulphydryl protein C - *Eubacterium acidaminophilum* (f

N:Alternate names: glycyl reductase 57K protein

C:Species: *Eubacterium acidaminophilum*

C:Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 15-Aug-1997

C:Accession: S38991; S21250

R:Lueneburg, M.; Andreesen, J.R.

Eur. J. Biochem. 217, 791-798, 1993

A:Title: Components of glycine reductase from *Eubacterium acidaminophilum*. Cloning, s

A:Reference number: S38988; MUID:94039119

A:Accession: S38991

A:Molecule type: DNA

A:Residues: 1-23 <LDE>

A:Cross-references: GB:L04500

R:Schraeder, T.; Andreesen, J.R.

Eur. J. Biochem. 206, 79-85, 1992

A:Title: Purification and characterization of protein P(c), a component of glycine re

A:Reference number: S21222; MUID:92267030

A:Accession: S21250

A:Molecule type: protein

A:Residues: 1-23 <SCH>

A:Genetics:

A:Gene: grdc

C:Function:

A:Description: glycine reductase complex catalyzes the reductive deamination of glyci

C:Keywords: ATP; oxidoreductase

Query Match 22.7%; Score 25; DB 2; Length 23;
Best Local Similarity 30.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 YAFLNATDGL 13
|:|:|:|:|:|:|
11 YVLVHTPDWI 20

RESULT 13
T42258
Ser/Thr protein phosphatase homolog - *Caenorhabditis elegans* (fragment)

C:Species: *Caenorhabditis elegans*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000

C:Accession: T42258

R:Zeke, T.; Gergely, P.; Dombadi, V.

submitted to the EMBL Data Library, July 1996

A:Description: The catalytic subunits of Ser/Thr protein phosphatases from *Caenorhabd*

A:Reference number: 222131

A:Accession: T42258
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-24 <ZEX>
 A:Cross-references: EMBL:277734; PIDN:CAB01293.1
 C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein

Query Match 22.7%; Score 25; DB 2; Length 24;
 Best Local Similarity 36.4%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 7 LHATDLPACD 17
 |||
 Db 3 IHLRLMTCD 13

RESULT 14
 S13996
 hypothetical protein - phage TW19 (fragment)
 C:Species: phage TW19
 C:Date: 18-Feb-1994 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
 C:Accession: S13996
 R:Inokuchi, Y.; Hirashima, A.; Matanabe, I.
 J. Mol. Biol. 158, 711-730, 1982
 A:Title: Comparison of the nucleotide sequences at the 3'-terminal region of RNAs from F
 A:Reference number: S07250; MUID:83010313
 A:Accession: S13996
 A:Status: translation not shown
 A:Molecule type: genomic RNA
 A:Residues: 1-25 <INO>
 A:Cross-references: EMBL:J0520; NID:9216180

Query Match 22.7%; Score 25; DB 2; Length 25;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 14 PACDG 18
 |||
 Db 12 PSCG 16

RESULT 15
 S11351
 spore storage protein light chain isoform M2b - ostrich fern (fragment)
 N:Alternate names: matuccin
 C:Species: Matuccia struthiopteris (ostrich fern)
 C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 01-Feb-1999
 C:Accession: S11351
 R:Roedin, J.; Rask, L.
 Eur. J. Biochem. 192, 101-107, 1990
 A:Title: Characterization of matuccin, the 2.2S storage protein of the ostrich fern.
 A:Reference number: S11350; MUID:90382429
 A:Accession: S11351
 A:Molecule type: protein
 A:Residues: 1-25 <ROE>
 C:Keywords: heterodimer; seed

Query Match 22.7%; Score 25; DB 2; Length 25;
 Best Local Similarity 62.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 LHATDLP 14
 |||
 Db 12 LHOCRLP 19

RESULT 16
 S61797
 T-cell-specific transcription factor 1 splice form F - human (fragment)
 N:Alternate names: transcription factor TCF-1F

C:Species: Homo sapiens (man)
 C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 24-Jul-1998
 C:Accession: S61797; S61879
 R:Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
 Biochim. Biophys. Acta 1263, 169-172, 1995
 A:Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel is
 A:Reference number: S61796; MUID:95367594
 A:Accession: S61797
 A:Molecule type: mRNA
 A:Residues: 1-11 <MAV>
 A:Cross-references: EMBL:247363
 A:Note: DNA was also sequenced
 C:Keywords: alternative splicing; DNA binding; transcription factor

Query Match 21.8%; Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 7.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 DLTPAC 16
 |||
 Db 1 DGLPAC 6

RESULT 17
 S68730
 bleomycin-binding protein - Streptomyces verticillius (fragment)
 C:Species: Streptomyces verticillius
 C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
 C:Accession: S68730
 R:Sugiyama, M.; Kumagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Na
 FEBS Lett. 362, 80-84, 1995
 A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing St
 al. characterization.
 A:Reference number: S68730; MUID:95212588
 A:Accession: S68730
 A:Molecule type: protein
 A:Residues: 1-16 <SUG>
 A:Experimental source: ATCC 15003
 C:Keywords: antibiotic resistance

Query Match 21.8%; Score 24; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 6 FLHATDLPACD 17
 |||
 Db 4 FLGAVPVLTAVD 15

RESULT 18
 QHEC2
 heat-stable enterotoxin ST-2 - Escherichia coli
 C:Species: Escherichia coli
 C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 31-Dec-1996
 C:Accession: A01823
 R:Chan, S.K.; Giannella, R.A.
 J. Biol. Chem. 256, 7744-7746, 1981
 A:Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli
 A:Reference number: A01823; MUID:81264141
 A:Accession: A01823
 A:Molecule type: protein
 A:Residues: 1-18 <CHA>
 A:Experimental source: strain 18D, serotype O.42:H6:H37
 C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced
 idues of the heat-stable enterotoxin ST-1.
 C:Superfamily: heat-stable enterotoxin ST
 C:Keywords: enterotoxin; heat-stable protein
 F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
 F:3-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 21.8%; Score 24; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 PACDG 18
||| |
DB 12 PACAG 16

RESULT 19

heat-stable enterotoxin ST-Ia - Citrobacter freundii
C:Species: Citrobacter freundii
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993
C:Accession: A60103
R:Guarino, A.; Giannella, R.; Thompson, M.R.
A:Title: Immun. 57, 649-652, 1989
A:Reference number: A60103; MUID:89108617
A:Molecule type: protein
A:Residues: 1-18 <CUA>
C:Superfamily: heat-stable enterotoxin ST

Query Match 21.8%; Score 24; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 PACDG 18
||| |
DB 12 PACAG 16

RESULT 20

hemoglobin alpha chain - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 19-May-2000
C:Accession: I51427
R:Patel, R.K.; Elkington, J.A.; Kay, R.M.; Williams, J.G.
Cell 21, 565-573, 1980
A:Title: Internal organization of the major adult alpha- and beta-globin genes of X.laevis
A:Reference number: I51427; MUID:81001900
A:Accession: I51427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <PAT>
A:Cross-references: GB:J00975; NID:g214198; PID:g214199
C:Superfamily: globin; globin homology
C:Keywords: blood; oxygen carrier

Query Match 21.8%; Score 24; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 LHATDL 12
||| |
DB 6 LHAYDL 11

RESULT 21

S63489
disimilatory sulfite reductase alpha chain, membrane-bound - Desulfovibrio desulfuricans
C:Species: Desulfovibrio desulfuricans
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S63489
R:Seudner, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio
A:Reference number: S63489; MUID:96085152
A:Accession: S63489

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <STE>

Query Match 21.8%; Score 24; DB 2; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 HATDL 13
||| |
DB 3 HATPL 8

RESULT 22

S63490
dissimilatory sulfite reductase alpha chain, soluble - Desulfovibrio desulfuricans (f
C:Species: Desulfovibrio desulfuricans
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S63490
R:Seudner, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
Eur. J. Biochem. 233, 873-879, 1995
A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibr
A:Reference number: S63489; MUID:96085152
A:Accession: S63490
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <STE>

Query Match 21.8%; Score 24; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 HATDL 13
||| |
DB 3 HATPL 8

RESULT 23

A39855
paralytic peptide I - tobacco hornworm
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 03-Feb-1994
C:Accession: A39855
R:Skinner, W.S.; Dennis, P.A.; Li, J.P.; Summerfelt, R.M.; Carney, R.L.; Quistad, G.B.
J. Biol. Chem. 266, 12873-12877, 1991
A:Title: Isolation and identification of paralytic peptides from hemolymph of the lep
A:Reference number: A39855; MUID:91302298
A:Accession: A39855
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <SKI>
C:Superfamily: paralytic peptide I

Query Match 21.8%; Score 24; DB 2; Length 23;
Best Local Similarity 43.8%; Pred. No. 1.7e+03;
Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 NVAFLHATDLIPACDG 18
||| |
DB 2 NFAGCATGYLRTADG 17

RESULT 24

T42259
phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain - Caenorhabditis elegans (f
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T42259
R:Zeke, T.; Gergely, P.; Dombradi, V.
submitted to the EMBL Data Library, July 1996

A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis
A:Reference number: 222131
A:Accession: T42259
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <ZEK>
A:Cross-references: EMBL:Z77733; PIDN:CAB01292.1
C:Genetics:
A:Note: PPI
C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein
C:Keywords: phosphoric monoester hydrolase

Query Match 21.8%; Score 24; DB 2; Length 24;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DVNYAFL 7
: ||||
Db 17 EANYLFL 23

RESULT 25
A32543
cardioexcitatory neuropeptide - desert locust
C:Species: Schistocerca gregaria (desert locust)
C:Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 18-Aug-2000
C:Accession: A32543
R:Robb, S.; Packman, L.C.; Evans, P.D.
Biochem. Biophys. Res. Commun. 160, 850-856, 1989
A:Title: Isolation, primary structure and bioactivity of Schistoflrf-amide, a FMRF-amide
A:Reference number: A32543; MUID:89246543
A:Accession: A32543
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <ROB>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; neuropeptide
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.9%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVNYAFL 7
||:|
Db 2 DVDHYFL 8

Search completed: February 5, 2001, 10:49:26
Job time: 739 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:37:06 ; Search time 68.99 Seconds
(without alignments)
9.913 Million cell updates/sec

Title: US-08-981-824-1

Perfect score: 110
Sequence: 1 DYNVAFRLHATDLPACDGER 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 141170

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36.*

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2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
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4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	100.0	20	18	W18842
2	110	100.0	20	18	W01793
3	73	66.4	20	16	R76649
4	73	66.4	20	18	W18857
5	73	66.4	20	16	R72267
6	73	66.4	20	21	Y59569
7	58.2	58.2	20	16	R72266
8	58.2	58.2	20	21	Y59540
9	64	58.2	20	21	Y59568
10	38	34.5	19	19	W79176
11	34	30.9	15	14	R43901
12	34	30.9	15	19	W58542

13	34	30.9	15	20	W87621
14	34	30.9	15	20	W72822
15	34	30.9	20	19	W76928
16	32	29.1	9	21	Y82873
17	32	29.1	15	19	W85260
18	32	29.1	20	9	P82057
19	31	28.2	17	13	R38839
20	31	28.2	19	13	R38840
21	31	28.2	21	20	W96277
22	30	27.3	7	18	W30416
23	30	27.3	15	17	R89429
24	30	27.3	15	19	W85278
25	30	27.3	20	16	R36614
26	30	27.3	20	16	R84360
27	30	27.3	10	19	W68470
28	29	26.4	10	20	Y25488
29	29	26.4	10	20	Y07180
30	29	26.4	15	21	Y67116
31	29	26.4	15	21	Y67117
32	29	26.4	15	21	Y54753
33	29	26.4	15	21	Y54754
34	29	26.4	15	21	Y54754
35	29	26.4	19	11	R04826
36	29	26.4	22	9	P82431
37	29	26.4	22	20	Y36422
38	29	26.4	22	20	Y37745
39	28	25.5	12	21	Y83094
40	28	25.5	19	16	R97609
41	28	25.5	21	20	Y04383
42	28	25.5	21	20	Y04385
43	28	25.5	22	6	P50362
44	28	25.5	22	9	P82432
45	28	25.5	22	18	W35329

ALIGNMENTS

RESULT 1

ID W18842

W18842 standard; peptide: 20 AA.

AC W18842;

DT 05-JAN-1998 (first entry)

DE 65 kD glutamic acid decarboxylase peptide fragment I.

DE 65 kD glutamic acid decarboxylase; autoreactive; diagnosis:

KW Insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;

KW predisposition; autoimmune; tumour; rheumatoid arthritis;

KW multiple sclerosis.

OS Synthetic.

XX DE19526561-A1.

XX 23-JAN-1997.

XX 20-JUL-1995; 95DE-1026561.

XX 20-JUL-1995; 95FR-1026561.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Donde F, Endl J, Ganz M, Jung G, Kientsch-Engel R;

XX Pozzilli P, Stahl P;

XX WPI: 1997-088254/09.

PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -

PT Involving intradermal admin. of auto-reactive substances

Epitope of HIV-1 g
HIV-1 gp120 monocl
Fusion immunoglobu
Teratocarcinoma-de
Helper T-cell pep
Pep-14 comprising
Peptide from the E
B-cell epitope of
HRE-I affinity pep
KIR-conjugated pep
Helper T-cell pep
HCV peptide NP-17.
Hepatitis C virus
Hepatitis C virus
Amino acids 250-25
Insulin-like growth
HIV binding peptide
Human protease pep
Human protease pep
Human subtilisin f
Junction of STA-re
Peptide unit of pr
Fragment of human
Human secreted pro
Cull peptide anti
Human thyroglobuli
Partial pullanase
Partial pullanase
Heparin derived cy
Peptide unit of pr
Pseudomonas HSP60

```

PS Claim 11; Page 9; 12pp; German.
CC W18842-70 are peptide fragments of the 65 kD human glutamic acid
CC decarboxylase (GAD). The fragments are autoreactive substances used for
CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
CC determined by using a claimed method for diagnosis of cell-mediated
CC diseases or a predisposition to cell-mediated diseases, which is effected
CC by administering an autoreactive substance intradermally and establishing
CC the diagnosis on the basis of the occurrence or lack of a positive
CC reaction at the site of administration. The method is used for diagnosis
CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
CC
XX Sequence 20 AA:
SQ
QY 1 DVNYAFHLNATDLLPACDGER 20
   |||||
Db 1 dvnyafhlntdlipacdger 20
RESULT 2
DE ID W01793 standard; peptide; 20 AA.
W01793
AC W01793;
XX
XX 15-OCT-1997 (first entry)
DE Human 65 kD glutamine decarboxylase peptide.
XX
XX Human; glutamine decarboxylase; GAD; diagnosis; predisposition;
KW tumour; immunological; disease; autoimmune; diabetes; reagent;
KW determination; T cell; subpopulation; medicament; treatment;
KW prevention; production; antigen; immunogen; tolerogen; isolation;
XX reinjection; inactivation.
XX Homo sapiens.
XX DEJ9525784-A1.
PN 16-JAN-1997.
PD 14-JUL-1995; 95DE-1025784.
PF 14-JUL-1995; 95DE-1025784.
PR 14-JUL-1995; 95DE-1025784.
XX (BOEF ) BOEHRINGER MANNHEIM GMBH.
PA
XX Albert W, Boltard C, Endl J, Jung G, Schendel D;
PI Stahl P, Van Enderdt P;
XX MPI; 1997-078452/08.
DR Glutamine decarboxylase peptide(s) - for diagnosis and therapy of
PT diabetes, etc.
XX
XX Claim 1; Page 12; 15pp; German.
CC The present peptide is a fragment of the human 65 kD glutamine
CC decarboxylase (GAD), which can be used to diagnose, or diagnose a
CC predisposition to, a tumour or immunological disease, preferably an
CC autoimmune disease, especially diabetes. It can also be used as a
CC reagent to determine specific T cell subpopulations, in medicaments
CC to treat or prevent immunological diseases, preferably autoimmune
CC diseases, especially diabetes, to produce antigens, especially
CC immunogens or tolerogens and to isolate specific T cell
CC subpopulations, which can be used to produce antigens or for
CC reinjection, optionally after inactivation.

```

[illegible]

W18857
 ID W18857 standard; peptide: 14 AA.
 AC W18857;
 DT 05-JAN-1998 (first entry)
 XX
 DE 65 kD Glutamic acid decarboxylase peptide fragment 8.
 XX
 KW GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
 KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
 KW predilection: autoimmune; tumour; rheumatoid arthritis;
 KW multiple sclerosis.
 XX
 OS Synthetic.
 XX
 PN DE19526561-A1.
 PD 23-JAN-1997.
 XX
 PF 20-JUL-1995; 95DE-1026561.
 XX
 PR 20-JUL-1995; 95DE-1026561.
 XX
 PA (BOER) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;
 PI Pozzilli P, Stahl P;
 XX
 DR WPI: 1997-088254/09.
 XX
 PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
 PT involving intradermal admin. of auto-reactive substances
 XX
 PS Claim 11: Fig 2; 12pp; German.
 XX
 SQ W18842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predilection to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 CC
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 66.4%; Score 73; DB 18; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 VNYAFLLHATDLP 15
 DB 1 VNYAFLLHATDLP 14
 XX
 RESULT 5
 R72267
 ID R72267 standard; Peptide: 20 AA.
 AC R72267;
 DT 13-NOV-1995 (first entry)
 XX
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX
 KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KW insulin-dependent diabetes mellitus; stiff man disease.
 XX
 OS Homo sapiens.

XX
 PN W09507992-A.
 XX
 PD 23-MAR-1995.
 XX
 PF 24-AUG-1994; 94WO-US09478.
 XX
 PR 17-SEP-1993; 93US-0123859.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
 XX
 DR WPI: 1995-131360/17.
 XX
 PT New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hybridoma(s) etc.
 XX
 PS Example 11, Page 76; 100pp; English.
 XX
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependant diabetes mellitus or stiff man disease.
 CC
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 66.4%; Score 73; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 HATDLPACDGER 20
 DB 1 hatdlpacdger 13
 XX
 RESULT 6
 Y59569
 ID Y59569 standard; peptide: 20 AA.
 XX
 AC Y59569;
 XX
 DT 03-APR-2000 (first entry)
 XX
 DE GAD65 fragment, peptide #7.
 XX
 KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependent diabetes mellitus; stiff man disease; diagnosis;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN US5998366-A.
 XX
 PD 07-DEC-1999.
 XX
 PF 09-APR-1997; 97US-0827618.
 XX
 PR 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0586536.
 PR 18-JUN-1991; 91US-0716909.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Tobin AJ, Kaufman DL, Erlander MG;
 XX
 DR WPI: 2000-095930/08.
 XX

PT Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders such as insulin dependent diabetes mellitus and stiff man
PT disease -

PS Example 11; Column 42; 61pp; English.

CC This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.

CC Sequence 20 AA;

Query Match 66.4%; Score 73; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 HATDLPACDGER 20
Db 1 hatdlpacdger 13

RESULT 7

ID R72266 standard; Peptide; 20 AA.

AC R72266;

DT 13-NOV-1995 (first entry)

DE Glutamic acid decarboxylase (GAD65) fragment.

KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;

XX Insulin-dependent diabetes mellitus; stiff man disease.

OS Homo sapiens.

PN W09507992-A.

PD 23-MAR-1995.

PE 24-AUG-1994; 94WO-US09478.

PR 17-SEP-1993; 93US-0123859.

PA (REGC) UNIV CALIFORNIA.

PI Claire-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;

DR WPL; 1995-131360/17.

PT New polypeptide fragments of glutamic acid decarboxylase - for
PT diagnosis and treatment of autoimmune disease, esp. insulin
PT dependent diabetes, also related nucleic acid, vectors,
PT antibodies, hybridoma(s) etc.

PS Claim 1; Page 76; 100pp; English.

CC 086481 and 086482 encode R71733 and R79105, rat and human glutamic
CC acid decarboxylase (GAD65) respectively, from which the GAD65
CC fragments described in R72261-R72298 were derived. These fragments
CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC and treat GAD-related autoimmune disorders, such as insulin
CC dependant diabetes mellitus or stiff man disease.

SQ Sequence 20 AA;

Query Match 58.2%; Score 64; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYNATFIHARDL 12
Db 9 dynatfihardl 20

RESULT 8

ID Y59540 standard; peptide; 20 AA.

AC Y59540;

DT 03-APR-2000 (first entry)

DE GAD65 fragment, peptide #6.

KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;

KW Insulin dependent diabetes mellitus; Stiff man disease; diagnosis;

XX therapy.

OS Homo sapiens.

PN US5998366-A.

PD 07-DEC-1999.

PE 09-APR-1997; 97US-0827618.

PR 07-JUN-1995; 95US-0485725.

PR 21-SEP-1990; 90US-0586536.

PR 18-JUN-1991; 91US-0716909.

PA (REGC) UNIV CALIFORNIA.

PI Tobin AJ, Kaufman DL, Erlander MG;

DR WPL; 2000-095930/08.

PT Ameliorating glutamic acid decarboxylase associated autoimmune

PT disorders such as insulin dependent diabetes mellitus and stiff man

PT disease -

PS Claim 1; Column 33; 61pp; English.

CC This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.

SQ Sequence 20 AA;

Query Match 58.2%; Score 64; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYNATFIHARDL 12
Db 9 dynatfihardl 20

```

RESULT 9
ID Y59568 standard; peptide: 20 AA.
XX
AC Y59568;
XX
DT 03-APR-2000 (first entry)
XX
DE GAD65 fragment, peptide #6.
XX
KM GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KM insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
KM therapy.
XX
OS Homo sapiens.
XX
PN US5998366-A.
XX
PD 07-DEC-1999.
XX
PE 09-APR-1997; 97US-0827618.
XX
PR 07-JUN-1995; 95US-0485725.
PR 21-SEP-1990; 90US-0586536.
PR 18-JUN-1991; 91US-0716909.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Tobin AJ, Kaufman DL, Erlander MG;
XX
DR WPI; 2000-095930/08.
XX
PT Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders such as insulin dependent diabetes mellitus and Stiff man
PT disease -
XX
PS Example 11; Column 42; 61pp; English.
XX
XX This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and Stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.
XX
SQ Sequence 20 AA:

```

```

Query Match 58.2%; Score 64; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 DNYAFELHATDL 12
   |||:|||||
DB 9 dnyafelhatdl 20

```

```

RESULT 10
ID W79176 standard; peptide: 19 AA.
XX
AC W79176;
XX
DT 25-JAN-1999 (first entry)
XX
DE Fusion immunoglobulin heavy chain HIV gp120 T cell epitope #54.
XX

```

```

KM B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IGH;
KM human immune deficiency virus; HIV; tolerance; treatment; therapy;
KM prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;
KM microbial infection; autoimmune disease; antibody; apoptosis;
KM antiviral T cell immunity.
XX
OS Mus sp.
XX
OS Homo sapiens.
XX
PN WO9836087-A1.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-US02766.
XX
PR 13-FEB-1997; 97US-0040581.
XX
PA (AMNA-) AMERICAN NAT RED CROSS.
XX
PI Scott D, Zambidis E;
XX
DR WPI; 1998-506315/43.
XX
PT New fusion immunoglobulin heavy chain including gp120 epitopes and
PT related complete antibodies - DNA, vectors and transformed cells,
PT used to induce tolerance to the epitopes for treatment of human
PT immune deficiency virus infection
XX
PS Disclosure; Page 49; 154pp; English.
XX
XX This sequence is an epitope used in the construction of a novel fusion
CC immunoglobulin heavy chain (IGH) protein with a mammalian, especially
CC human, IGH chain fused in frame at its N-terminus to one or more human
CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
CC transfected cells are used to tolerate subjects to gp120 epitopes and to
CC maintain this tolerance, particularly for treatment of HIV infection,
CC optionally together with other therapeutic/prophylactic agents such as
CC vaccines, chemotherapeutic agents and immune response modifiers. Such
CC proteins can be used against other diseases where an immune response is
CC deleterious, e.g. microbial infection, tumours or autoimmune disease.
CC Induction of tolerance suppresses production of antibodies against gp120,
CC so prevents or inhibits 'stander' apoptosis of uninfected T cells that
CC are bound to gp120 protein, maximising induction of protective antiviral
CC T cell immunity.
XX
SQ Sequence 19 AA:

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```

Query Match 34.5%; Score 38; DB 19; Length 19;
Best Local Similarity 42.9%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

```

OY 4 YAFELHATDLAPAC 17
   |||:|||||
DB 6 yafelhatdlapld 19

```

```

RESULT 11
ID R43901 standard; peptide: 15 AA.
XX
AC R43901;
XX
DT 06-JUN-1994 (first entry)
XX
DE HIV-1 IIB gp120 monoclonal antibody antigenic peptide VI5P.
XX
KM Human immunodeficiency virus; therapy; HIV-1 infection; diagnosis;
KM post-exposure prophylaxis; infection; cytotoxic agent targeting;
KM neutralisation domain; BAT085; G3-136.
XX
OS Synthetic.
XX

```

PN US5266478-A.
 XX
 PD 30-NOV-1993.
 XX
 XX
 PF 25-NOV-1991; 91US-0797692.
 XX
 PR 29-MAY-1987; 87US-0057445.
 PR 24-DEC-1987; 87US-0137861.
 PR 26-APR-1991; 91US-0692299.
 PR 26-SEP-1991; 91US-0767533.
 PR 25-NOV-1991; 91US-0797692.
 XX
 PA (TANO-) TANOX BIOSYSTEMS INC.
 XX
 PI Chang TW, Fung MSC, Sun BNC, Sun CRY;
 XX
 DR WPI; 1993-395339/49.
 XX
 PT Monoclonal antibody to HIV-1 gp120 - used for therapy of HIV-1
 PT Infection or AIDS, post-exposure prophylaxis and diagnosis of HIV-1
 PT HIV-1 infection
 XX
 PS Example; Page 8; 9pp; Japanese.
 XX
 CC The sequence is that of a synthetic peptide V15P corresponding to a
 CC unique neutralisation domain in the V2 region of HIV-1 gp 120. It
 CC can be used in the prodn. of monoclonal antibodies (Mabs) BAT085
 CC and G3-136. The Mabs may be used for therapy of HIV-1 infection or
 CC AIDS, post-exposure prophylaxis and diagnosis of HIV-1 infection and
 CC to reduce or eliminate virus infected T-cells by antibody-dependent
 CC cellular cytotoxicity, complement-mediated cytotoxicity or other
 CC cytolytic or regulatory immune mechanisms. The Mab can also be
 CC used for targeting cytotoxic agents to HIV-1 infected cells.
 CC
 CC Sequence 15 AA:
 XX
 SQ
 Query Match 30.9%; Score 34; DB 14; Length 15;
 Best Local Similarity 45.5%; Pred. NO. 19;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 4 YAFPLHATDLP 14
 ||| : ||:
 5 yaflykidlvp 15
 Db
 RESULT 12
 W58542 W58542 standard; peptide; 15 AA.
 XX
 AC W58542;
 XX
 DT 02-SEP-1998 (first entry)
 XX
 DE Aspergillus oryzae phospholipase A1 peptide seq ID NO:3.
 XX
 KM Aspergillus oryzae; phospholipase A1; microbe; PLAI.
 XX
 OS Aspergillus oryzae.
 XX
 PN JP10155493-A.
 XX
 PD 16-JUN-1998.
 XX
 PF 03-OCT-1997; 97JP-0270967.
 XX
 PR 04-OCT-1996; 96JP-0264241.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 1998-391046/34.
 XX
 PT Aspergillus-derived phospholipase A1 gene - used for the recombinant

PT production of phospholipase A of high purity and in a high yield
 XX
 XX Example 1; Page 18; 23pp; Japanese.
 PS
 XX
 CC The present sequence represents a phospholipase A1 (PLAI) peptide
 CC derived from Aspergillus oryzae. Phospholipase A can be prepared by
 CC culturing host cells and collecting the host cell from the culture. DNA
 CC encoding mature PLAI can be used to produce recombinant phospholipase
 CC A of high purity and in a high yield.
 XX
 XX Sequence 15 AA:
 SQ
 Query Match 30.9%; Score 34; DB 19; Length 15;
 Best Local Similarity 41.7%; Pred. NO. 19;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 3 NYAFHATDLP 14
 ||| : ||:
 3 nyrvthndlvp 14
 Db
 RESULT 13
 W87621 W87621 standard; peptide; 15 AA.
 XX
 AC W87621;
 XX
 DT 03-MAR-1999 (first entry)
 XX
 DE Epitope of HIV-1 gp120 protein which binds antibody BAT085.
 XX
 KM Epitope; gp120 protein; monoclonal antibody; HIV-1; antibody BAT123;
 KM antibody BAT267; antibody BAT085; T cell infection inhibition;
 KM syncytia formation; acquired immune deficiency syndrome; AIDS;
 KM AIDS-related complex; passive immunisation; antiviral; cytotoxic;
 KM viral load measurement; vaccine.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN US5854400-A.
 XX
 PD 29-DEC-1998.
 XX
 PF 22-SEP-1992; 92US-0950571.
 XX
 PR 22-SEP-1992; 92US-0950571.
 PR 29-MAY-1987; 87US-0057445.
 PR 27-DEC-1987; 87US-0137861.
 PR 26-SEP-1991; 91US-0767533.
 XX
 PA (TANO-) TANOX INC.
 XX
 PI Chang NT, Chang TW, Fung MSC, Sun BNC, Sun CRY;
 XX
 DR WPI; 1999-095002/08.
 XX
 PT Monoclonal antibodies directed against regions of gp120 of human
 PT immune deficiency virus-1 - are neutralising and able to inhibit
 PT infection of T cells and formation of syncytia, used for treatment,
 PT prevention or diagnosis of acquired immune deficiency syndrome
 XX
 PS Claim 8; Column 9; 16pp; English.
 XX
 CC The present sequence represents an epitope of the gp120 protein of
 CC human immune deficiency virus (HIV)-1. The sequence comprises
 CC amino acids 169 to 183 of gp120. The specification describes
 CC monoclonal antibodies which bind to epitopes of the gp120 protein.
 CC Specifically, these antibodies are designated BAT123, 267 and 085.
 CC Monoclonal antibodies neutralise HIV-1, inhibiting both infection
 CC of T cells and formation of syncytia, so are used to treat acquired
 CC immune deficiency syndrome (AIDS) and AIDS-related complex, by
 CC passive immunisation, as carriers of cytotoxic or antiviral agents,

CC and in extracorporeal systems. They can also be used as immunoassay
 CC reagents (for diagnosis or measurement of viral load) and to screen
 CC for neutralising epitopes, potentially useful in vaccine development.
 XX

SO Sequence 15 AA;

Query Match 30.9%; Score 34; DB 20; Length 15;
 Best Local Similarity 45.5%; Pred. No. 19;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 YAPFHATDLP 14
 ||| : ||| :
 Db 5 yafykdilp 15

RESULT 14

ID W72822 standard; peptide; 15 AA.

AC W72822;

DT 13-JAN-1999 (first entry)

DE HIV-1 gp120 monoclonal antibody BAT085 residue 178 to 192.

KW HIV-1; gp120; epitope; monoclonal antibody; envelope; neutralise;
 KW inhibit; infection; T-cell; inhibit syncytium formation; AIDS.

OS Human immunodeficiency virus type 1.

PN US5834599-A.

PD 10-NOV-1998.

PF 04-MAR-1993; 93US-0026276.

PR 04-MAR-1993; 93US-0026276.

PR 23-MAR-1987; 87US-0057445.

PR 24-DEC-1987; 87US-0137861.

PR 25-APR-1989; 89US-0343540.

PR 05-JUN-1992; 92US-0895197.

PA (TANO-) TANOX BIOSYSTEMS INC.

PI Chang NT, Chang T, Fung SC, Kim YW, Sun BN, Sun CR;

DR WPI; 1999-008810/01.

XX

PT Antibody conjugate comprising monoclonal antibody - which binds to

PT epitope within amino acid residue of gp120 which neutralises HIV-1

PT conjugated with, e.g. cytotoxic agent

PS Example 4; Column 25; 22pp; English.

XX

CC The present invention describes an antibody conjugate comprising an

CC antibody (Ab) which binds to an epitope within amino acid residue

CC 308-322 of gp120 and neutralises HIV-1, conjugated with a cytotoxic

CC agent, an anti-viral agent or an agent which facilitates passage through

CC the blood brain barrier. Also described is an antibody conjugate as

CC above but where the Ab binds to an epitope within amino acid residue

CC 288-312 of gp12 which neutralises HIV-1. The present sequence represents

CC an HIV-1 gp120 monoclonal antibody BAT085 residue 178 to 192 from an

CC example of the present invention. The Ab are monoclonal Ab which bind

CC to the gp120 protein on the envelope of HIV-1. They inhibit the

CC infection of T-cells and also inhibit syncytium formation. The

CC antibodies are group specific and neutralise different strains and

CC isolates of HIV-1. The antibodies have a variety of uses, including the

CC treatment and prevention of AIDS and AIDS related complex. They are

CC especially used to kill infected T-cells.

XX Sequence 15 AA;

Query Match 30.9%; Score 34; DB 20; Length 15;
 Best Local Similarity 45.5%; Pred. No. 19;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 YAPFHATDLP 14
 ||| : ||| :
 Db 5 yafykdilp 15

RESULT 15

ID W76928 standard; peptide; 20 AA.

AC W76928;

DT 25-JAN-1999 (first entry)

DE Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #68.

KW B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;

KW human immune deficiency virus; HIV; tolerance; treatment; therapy;

KW prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;

KW microbial infection; autoimmune disease; antibody; apoptosis;

OS antitviral T cell immunity.

PN Mus sp.

PD 13-FEB-1998; 98WO-US02766.

PF 13-FEB-1998; 98WO-US02766.

PR 13-FEB-1997; 97US-0040581.

PA (AMNA-) AMERICAN NAT RED CROSS.

PI Scott D, Zambidis E;

DR WPI; 1998-506315/43.

XX

PT New fusion immunoglobulin heavy chain including gp120 epitopes and

PT related complete antibodies - DNA, vectors and transformed cells,

PT used to induce tolerance to the epitopes for treatment of human

PT immune deficiency virus infection

PS Disclosure; Page 38; 154pp; English.

XX

CC This sequence is an epitope used in the construction of a novel fusion

CC immunoglobulin heavy chain (IGH) protein with a mammalian, especially

CC human, IGH chain fused in frame at its N-terminus to one or more human

CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or

CC transfected cells are used to tolerate subjects to gp120 epitopes and to

CC maintain this tolerance, particularly for treatment of HIV infection,

CC optionally together with other therapeutic/prophylactic agents such as

CC vaccines, chemotherapeutic agents and immune response modifiers. Such

CC proteins can be used against other diseases where an immune response is

CC deleterious, e.g. microbial infection, tumours or autoimmune disease.

CC Induction of tolerance suppresses production of antibodies against gp120,

CC so prevents or inhibits bystander apoptosis of uninfected T cells that

CC are bound to gp120 protein, maximising induction of protective antiviral

CC T cell immunity.

XX Sequence 20 AA;

Query Match 30.9%; Score 34; DB 19; Length 20;
 Best Local Similarity 45.5%; Pred. No. 27;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 YAPFHATDLP 14

Db 2 yaflykladip 12

RESULT 16
ID Y82873 standard; peptide; 9 AA.

AC Y82873;

DT 19-JUN-2000 (first entry)

DE Teratocarcinoma-derived growth factor (CRIPRO-1) antigenic peptide.

XX Tumour associated antigen peptide; TAA; cancer; carcinoma;
KW treatment; prevention; cure; anti-tumour vaccine; metastases;
KW breast; bladder; prostate; pancreas; ovary; thyroid; colon;
KW stomach; carcinoma; MHC Class I; HLA-A2; human;
KW Major Histocompatibility Complex; uroplakin;
KW prostate specific antigen; prostate specific membrane antigen;
KW prostate acid phosphatase; mucin; lactadherin;
KW teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPRO-1.

XX Homo sapiens.

OS WO200006723-A1.

PN 10-FEB-2000.

XX 29-JUL-1999; 99WO-IL00417.

XX 30-JUL-1998; 98IL-0125608.

XX (YEDA) YEDA RES & DEV CO LTD.

PA (BIOT-) BIO-TECHNOLOGY GEN CORP.

PI Eisenbach L, Carmon L, Tirosh B, Bar-haim E, Paz A, Fridkin M;

XX Fitzer-attas C;

XX WPI: 2000-205463/18.

PT Tumor associated antigen peptides, especially derived from uroplakin,
PT useful as vaccines to prevent or cure cancers including breast,
PT bladder, prostate, pancreas, ovary, thyroid, colon and stomach -

XX Claim 19; Page 106; 113pp; English.

XX Tumor associated antigen peptides (TAA) may be used for the
CC treatment, prevention and cure of cancer or cancer metastases. The
CC cancer may be breast, bladder, prostate, pancreas, ovary, thyroid,
CC colon, stomach, head or neck cancer or a carcinoma. The tumour
CC associated antigens are presentable to the immune system by HLA-A2
CC molecules and are generally between 8 to 10 amino acids in length.
CC The amino acids located at positions 2 and 9 of the tumour associated
CC antigens are the anchor residues which participate in the binding to
CC MHC class I molecules, more specifically HLA-A2. More tumour
CC associated antigens are described in GENBSEQ records Y82806-Y82882.
CC Those tumour associated antigens described in records Y82806-Y82882
CC and Y82853-Y82869 are derived from uroplakin, such as Uroplakin II,
CC Uroplakin Ia, Uroplakin III and Uroplakin Ib. Those described in
CC records Y82825-Y82829 are derived from prostate specific antigen
CC (PSA). Those described in records Y82830-Y82835 are derived from
CC prostate specific membrane antigen (PSMA). Those described in
CC records Y82836-Y82839 are derived from prostate acid phosphatase
CC (PAP). Those described in records Y82840-Y82846 are derived
CC from lactadherin (BA-46). Those described in records Y82847-Y82854
CC are derived from Mucin and those described in records Y82871-Y82882
CC are derived from Teratocarcinoma derived growth factor (CRIPRO-1).

XX Sequence 9 AA;

Query Match 29.1%; Score 32; DB 21; Length 9;

Best Local Similarity 83.3%; Pred. No. 2.1e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 13 LPACDG 18
|||
Db 2 lpgcdg 7

RESULT 17

ID W85260 standard; peptide; 15 AA.

AC W85260;

DT 16-FEB-1999 (first entry)

DE Helper T-cell peptide derived from a POL protein.

XX Helper T-cell peptide; human leucocyte antigen; HLA; DR4W4; DR1; DR7;
KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;
KW acquired immune deficiency syndrome; malaria; cancer;
KW allograft rejection; allergy; Lyme disease; hepatitis;
KW post-streptococcal endocarditis; glomerulonephritis;
KW food hypersensitivity.

XX Synthetic.

OS Hepatitis B virus.

PN W09832456-A1.

XX 30-JUL-1998.

XX 23-JAN-1998; 98WO-US01373.

XX 07-FEB-1997; 97US-0037432.

XX 23-JAN-1997; 97US-0036713.

XX (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S;

XX WPI: 1998-427679/36.

PT Composition containing peptide that induces cytotoxic T lymphocyte
PT response, and helper peptide - can bind to human leucocyte antigen
PT alleles, used to treat or prevent cancers, parasitic infections and
PT autoimmune disease

XX Claim 11; Page 39; 51pp; English.

XX W85138-283 represent helper T-cell peptides, which can bind to the
CC human leucocyte antigens (HLA) DR4W4, DR1 and DR7. The peptides
CC are used in the course of the invention. The specification describes
CC peptides that that induce a cytotoxic T lymphocyte (CTL) response, and
CC T-helper peptides, that are used together to generate a CTL response for
CC the treatment or prevention of viral, fungal, bacterial or parasitic
CC infections (e.g. hepatitis, acquired immune deficiency syndrome or
CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate
CC cancer or condyloma acuminatum). Helper T-cell peptides may be used
CC alone to induce a helper T cell response, e.g. in cases of autoimmune
CC disease, allograft rejection, allergy, Lyme disease, hepatitis,
CC post-streptococcal endocarditis, glomerulonephritis and food
CC hypersensitivity.

XX Sequence 15 AA;

Query Match 29.1%; Score 32; DB 19; Length 15;

Best Local Similarity 50.0%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 LHAATDLAPAC 16
:|:|:|

XX The peptide was synthesised by standard methods and has a sequence
 CC based on residues 45-60 of the ED1 sequence. The peptide was used
 CC to raise antibodies which will immunoreact with ED1 but not with a
 CC plasma fibronectin monomer. The antibodies can be used for detecting
 CC fibronectin contg. variably included Type III repeats in a sample,
 CC thus determining patients destined to develop toxemia, partic.
 CC preeclampsia, prior to the onset of maternal signs and symptoms
 CC of the disease, allowing for early therapeutic intervention.
 CC See also R23837-42.
 CC
 XX
 SO Sequence 19 AA:

Query Match 28.2%; Score 31; DB 13; Length 19;
 Best Local Similarity 66.7%; Pred. No. 80;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 11 DLPAACDE 19
 Db 1 elifadpge 9

RESULT 21
 W96277
 ID W96277 standard; Peptide; 21 AA.

AC W96277;
 XX 14-JUN-1999 (first entry)
 DT
 XX B-cell epitope of testis specific isoform of calpastin.
 DE
 XX Calpastin; isoform; testis; antibodies; vaccine; inhibition;
 KW fertilisation; egg; spermatazoa; sperm; contraceptive;
 KM B-cell epitope; T-cell epitope.
 XX
 OS Homo sapiens.

XX
 PN W09903490-A1.
 XX
 PD 28-JAN-1999.
 XX

PE 21-JUL-1998; 98WO-US15094.

PR 20-JUL-1998; 98US-0119149.
 PR 21-JUL-1997; 97US-0053337.

XX
 PA (NOUN) UNIV NORTHWESTERN.

PI Goldberg E;

XX
 DR WPI; 1999-131861/11.

PT New testis-specific isoforms of calpastatin peptides - used in
 PT vaccines and for the production of antibodies which can inhibit the
 PT fertilisation of an egg by sperm in a mammal

XX
 PS Claim 8; Page 34; 48pp; English.

XX Testis-specific calpastatin and peptides derived from it can be used
 CC for detecting antibodies for assessing infertility in a patient. The
 CC peptides and antibodies raised by them can also be used for
 CC inhibiting fertilisation of an egg by a sperm in a mammal.
 CC Testis specific calpastatin peptides can therefore be used in the
 CC production of a vaccine used to inhibit fertilisation of an egg by
 CC sperm. The vaccine can be used as topical contraceptives in mammals,
 CC including dogs, cats and other domestic animals and humans.

XX
 SQ Sequence 21 AA:

Query Match 28.2%; Score 31; DB 20; Length 21;

Best Local Similarity 100.0%; Pred. No. 90;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 16 CDGER 20
 Db 3 cdger 7

RESULT 22
 W30416
 ID W30416 standard; peptide; 7 AA.

AC W30416;
 XX 22-APR-1998 (first entry)
 DT
 XX HRE-I affinity peptide SEQ ID NO:34.
 DE
 XX Binding site; HRE-I; screening; H-Ras; target gene; plasmid;
 KW inhibition; affinity peptide.
 XX
 OS Synthetic.

XX
 PN W09737030-A1.

PD 09-OCT-1997.

XX 31-MAR-1997; 97WO-JP01105.

XX 03-OCT-1996; 96JP-0263345.

PR 01-APR-1996; 96JP-0101990.

XX (YAWH) NIPPON STEEL CHEM CO.

XX (YAWA) NIPPON STEEL CORP.

PI Kato T;

XX
 DR WPI; 1997-503115/46.

PT Plasmid for screening peptide(s) which bind target genes - for
 PT treatment of conditions associated with H-Ras

XX
 PS Claim 41; Page 69; 127pp; Japanese.

XX A novel plasmid has been developed for screening peptides which bind
 CC target genes. The plasmid comprises a sequence encoding the test
 CC peptide, a promoter comprising the target gene, and a reporter gene
 CC bound to the promoter. The present sequence represents a specifically
 CC claimed peptide with affinity to HRE-I. The plasmids are used for
 CC screening for peptides which bind to target genes. The identified
 CC peptides can be used for the treatment of conditions associated with
 CC the inhibition of the expression the genes, and treatment of conditions
 CC associated with H-Ras.
 CC
 XX

SQ Sequence 7 AA:

Query Match 27.3%; Score 30; DB 16; Length 7;
 Best Local Similarity 71.4%; Pred. No. 2; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 2;

Oy 14 PACDGER 20
 Db 1 pycdker 7

RESULT 23
 R89429
 ID R89429 standard; Protein; 15 AA.

XX
 AC R89429;

DT 13-SEP-1996 (first entry)

XX JP06199894-A.
 PN 19-JUL-1994.
 XX
 PD
 XX
 PF 02-APR-1993; 93JP-0076791.
 XX
 PR 27-AUG-1992; 92JP-0228965.
 PR 10-NOV-1992; 92JP-0299691.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 PA (INOM/) INOMAMARI M.
 XX
 DR WPI; 1994-269451/33.
 XX
 PT T cell epitope present in the core protein region of Hepatitis C
 PT virus (HCV) - used for activation of cellular immunity mechanisms
 XX
 PS Claim 5; Fig 2; 14pp; Japanese.
 XX
 CC A T-cell stimulating peptide is claimed which is ca. 5-20 amino
 CC acids long and part of the core protein of HCV and is recognised by
 CC and stimulates T-cells. A CD8-positive T-cell stimulating peptide
 CC has the sequence given in R56606 (NP-9) or R56616 (9MA). A CD4-
 CC positive T-cell stimulating peptide has the sequence given in R56609
 CC (NP-12) or R56614 (NP-17). Synthetic peptide mixts. (Mix A: NP-1 -
 CC NP-5, Mix B: NP-6 - NP-10, Mix C: NP-11 - NP14, MixD: NP-15 - NP-18)
 CC were used in experiments to evaluate activity.
 CC Peptides 9MA, 9CM and 9CA (R56616-18) are variants of peptide NP-9.
 XX
 SQ Sequence 20 AA;

Query Match 27.3%; Score 30; DB 15; Length 20;
 Best Local Similarity 53.3%; Pred. No. 1.3e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
 OY 2 VNVAFLHATDLPAC 16
 ||| || |||
 Db 2 vny-----atgnlpgc 12

Search completed: February 5, 2001, 10:47:29
 Job time: 623 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:49:26 ; Search time 58.67 Seconds
(without alignments)
23.147 Million cell updates/sec

Title: US-08-981-824-2

Perfect score: 102
Sequence: 1 SNMTAMMIARFKMPPEVK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 5001

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR66:*

1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	24.5	14	2	PI0142
2	25	24.5	25	2	S11383
3	24	23.5	25	2	A34921
4	23	22.5	10	2	A60476
5	23	22.5	13	2	PNO122
6	23	22.5	14	2	PH1614
7	23	22.5	14	2	PH1617
8	23	22.5	17	2	I34269
9	23	22.5	22	2	S63674
10	23	22.5	25	2	S03263
11	22	21.6	15	2	A48372
12	22	21.6	19	2	S03076
13	22	21.6	20	2	A54083
14	22	21.6	20	2	C56894
15	22	21.6	20	2	A56894
16	22	21.6	20	2	B56894
17	22	21.6	9	2	PC7073
18	21	20.6	16	2	T09741
19	21	20.6	17	2	S32587
20	21	20.6	18	2	S14661
21	21	20.6	19	2	S02808
22	21	20.6	20	2	S57286
23	21	20.6	21	2	S51066
24	21	20.6	25	2	A39108
25	21	20.6	25	2	S68642
26	21	20.6	25	2	S68005
27	20.5	20.1	25	2	S17683
28	20	19.6	8	2	A61597
29	20	19.6	13	2	S22689

ALIGNMENTS

30	20	19.6	14	2	S36578	dodecenoyl-CoA del
31	20	19.6	16	2	S65709	major allergen Myr
32	20	19.6	17	2	S78421	ribosomal protein
33	20	19.6	18	2	S29264	ovoheimerlythrin - d
34	20	19.6	21	2	PQ0145	glucan endo-1,3-be
35	20	19.6	21	2	S78416	ribosomal protein
36	20	19.6	22	2	S13977	chlorophyll a/b-b1
37	20	19.6	23	2	D60583	glycoprotein horimo
38	20	19.6	23	4	JE0016	probable 2.9k prot
39	20	19.6	24	2	S38729	probable malate ca
40	20	19.6	24	2	S53793	actin - mouse (fra
41	20	19.6	25	2	S09540	gene 1.5 protein -
42	19.5	19.1	16	2	F44908	chitinase (EC 3.2.
43	19	18.6	11	2	G42762	multicatalytic end
44	19	18.6	12	2	PH1587	Ig H chain V-D-J r
45	19	18.6	14	2	A61308	hemocyanin chain 2

RESULT 1

PI0142
carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - pseudomonas carboxydoflava
C:Species: Pseudomonas carboxydoflava
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C:Accession: PI0142
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydot
A:Reference number: PI0138; MUID:90055678
A:Accession: PI0142
A:Molecule type: Protein
A:Residues: 1-14 <KRA>
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large,
C:Keywords: oxidoreductase

Query Match 24.5%; Score 25; DB 2; Length 14;

Best Local Similarity 71.4%; Pred. No. 4.5e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 MMARPK 12

DB 1 MMIPRF 7

RESULT 2
S11383
uridine phosphorylase (EC 2.4.2.3) - Lactobacillus casei (fragment)

MA:Alternate names: pyrimidine phosphorylase

C:Species: Lactobacillus casei

C:Date: 19-Mar-1997 #sequence_revision 26-Feb-1998 #text_change 26-Feb-1998

C:Accession: S11383

R:Avraham, Y.; Grossowicz, N.; Yashphe, J.
Biochim. Biophys. Acta 1040, 287-293, 1990

A:Title: Purification and characterization of uridine and thymidine phosphorylase fro

A:Reference number: S11383; MUID:90381286

A:Accession: S11383

A:Molecule type: Protein

A:Residues: 1-25 <AVR>

A:Experimental source: strain ATCC 7469

C:Keywords: glycosyltransferase; homotetramer; pentosyltransferase

Query Match 24.5%; Score 25; DB 2; Length 25;

Best Local Similarity 55.6%; Pred. No. 8.1e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 12 KMPEVK 20

DB 4 KVPEPKLK 12

RESULT 3
A34921
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - Flaveria linearis (fragment)
C:Species: Flaveria linearis
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 12-Apr-1995
C:Accession: A34921
R:Hudson, G.S.; Mahon, J.D.; Anderson, P.A.; Gibbs, M.J.; Badger, M.R.; Andrews, T.J.; W
J. Biol. Chem. 265, 808-814, 1990
A:Title: Comparisons of rbcL genes for the large subunit of ribulose-bisphosphate carbox
A:Reference number: A34921; MUID:90110139
A:Accession: A34921
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-25 <HUD>
C:Superfamily: ribulose-bisphosphate carboxylase small chain
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 23.5%; Score 24; DB 2; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 11 FKMPPEVKEK 20
|::|::|
Db 1 FKWMPPLCKK 10

RESULT 4
A60476
S-layer protein - Bacillus thuringiensis (fragment)
C:Species: Bacillus thuringiensis
C:Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 12-Mar-1993
C:Accession: A60476
R:Luckevich, M.D.; Beveridge, T.J.
J. Bacteriol. 171, 6656-6667, 1989
A:Title: Characterization of a dynamic S layer on Bacillus thuringiensis.
A:Reference number: A60476; MUID:90078111
A:Accession: A60476
A:Molecule type: protein
A:Residues: 1-10 <LUC>
C:Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 22.5%; Score 23; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KMPEV 17
|::|::|
Db 3 KTFPDV 8

RESULT 5
PN0122
OIL protein - vaccinia virus (strain L-IVP) (fragment)
C:Species: vaccinia virus
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Jun-2000
C:Accession: PN0122
R:Ryazankina, O.I.; Shchelkunov, S.N.; Muravlev, A.I.; Netesova, N.A.; Mikhrukov, N.N.;
Mol. Biol. (Mosk.) 24, 968-976, 1990
A:Title: The molecular biological study of vaccinia virus genome II: localization and f
A:Reference number: PN0119; MUID:91066899
A:Accession: PN0122
A:Molecule type: DNA
A:Residues: 1-13 <RJ>
C:Superfamily: variola major virus hypothetical protein Q1L

Query Match 22.5%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 13 MPEVKEK 20
|::|::|
Db 3 MYPEFANK 10

RESULT 6
PH1614
Ig H chain V-D-J region (clone B-less 18) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1614
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A:Reference number: PH1580; MUID:93301609
A:Accession: PH1614
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 22.5%; Score 23; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMYAM 6
|::|::|
Db 8 NMYAM 12

RESULT 7
PH1617
Ig H chain V-D-J region (clone B-less 32) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1617
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A:Reference number: PH1580; MUID:93301609
A:Accession: PH1617
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 22.5%; Score 23; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMYAM 6
|::|::|
Db 8 NMYAM 12

RESULT 8
I54269
vitamin D binding protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C:Accession: I54269
R:Braun, A.; Bichlmair, R.; Muller, B.; Cleve, H.
Hum. Genet. 90, 526-532, 1993
A:Title: Molecular evaluation of an Alu repeat including a polymorphic variable poly
A:Reference number: I54269; MUID:93154720
A:Accession: I54269
A>Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:S54074; NID:g264876; PIDN:AAD13872.1; PID:g4261572
C:Superfamily: serum albumin; serum albumin repeat homology

Query Match 22.5%; Score 23; DB 2; Length 17;
 Best Local Similarity 35.7%; Pred. No. 1.2e+03;
 Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 YAMMIAEFKMFPEV 17
 | : : |
 | : : |
 DB 1 YTFELSRRTLPEV 14

RESULT 9

S63674
 28 K secretory protein - rat (fragments)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C:Accession: S63674
 R:Pesheko, I.V.; Novoselov, V.I.; Evdokimov, V.A.; Nikolaev, Y.V.; Shuvaeva, T.M.; Lipyk
 FEBS Lett. 381, 12-14, 1996
 A:Title: Novel 28-kDa secretory protein from rat olfactory epithelium.
 A:Reference number: S63674; MUID:96193902
 A:Accession: S63674
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5,6-11,12-17,18-22 <PES>

Query Match 22.5%; Score 23; DB 2; Length 22;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 KMPEVKE 19
 | : | : |
 | : | : |
 DB 6 KLAPEKFD 13

RESULT 10

S06263
 gastrin-releasing peptide - smaller spotted catshark (tentative sequence) (fragment)
 C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
 C:Date: 31-Mar-1990 #sequence_revision 30-Jan-1998 #text_change 31-Mar-2000
 C:Accession: S06263
 R:Conlon, J.M.; Henderson, I.W.; Thim, L.
 Gen. Comp. Endocrinol. 68, 415-420, 1987
 A:Title: Gastrin-releasing peptide from the intestine of the elasmobranch fish, Scyliorhinus
 A:Reference number: S06263; MUID:88137922
 A:Accession: S06263
 A:Molecule type: protein
 A:Residues: 1-25 <CON>
 A>Note: the sequence from the summary is inconsistent with that from table 1 and table 3
 C:Superfamily: gastrin-releasing peptide
 C:Keywords: neuropeptide

Query Match 22.5%; Score 23; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KMFP 15
 | | | |
 | | | |
 DB 11 KMFP 14

RESULT 11

A48372
 benzoyl-CoA ligase - Methanospirillum hungatei (fragment)
 C:Species: Methanospirillum hungatei
 C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
 C:Accession: A48372
 R:Auburger, G.; Winter, J.
 Appl. Microbiol. Biotechnol. 37, 789-795, 1992
 A:Title: Purification and characterization of benzoyl-CoA ligase from a syntrophic, benz
 A:Reference number: A48372; MUID:93040109

A:Accession: A48372
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <AUB>
 A>Note: sequence extracted from NCBI backbone (NCBIP:118357)

Query Match 21.6%; Score 22; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 KMFE 16
 | : | : |
 | : | : |
 DB 2 KLYPE 6

RESULT 12

S03076
 T-cell receptor gamma chain J region (JPI) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 30-May-1997
 C:Accession: S03076
 R:Huck, S.; Lefranc, M.P.
 FEBS Lett. 224, 291-296, 1987
 A:Title: Rearrangements to the JPI, JP and JP2 segments in the human T-cell rearrangl
 A:Reference number: S03076; MUID:88083552
 A:Accession: S03076
 A:Molecule type: DNA
 A:Residues: 1-19 <HUC>
 A:Cross-references: EMBL:X08084
 C:Keywords: T-cell receptor

Query Match 21.6%; Score 22; DB 2; Length 19;
 Best Local Similarity 66.7%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 FMKPE 16
 | : | : |
 | : | : |
 DB 5 FKFAE 10

RESULT 13

AS4083
 p190/210, fatty acid synthase, p140ex2 strand exchange protein activator - fission y
 C:Species: Schizosaccharomyces pombe
 C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
 C:Accession: AS4083
 R:Kaslan, E.; Heyer, W.D.
 J. Biol. Chem. 269, 14103-14110, 1994
 A:Title: Schizosaccharomyces pombe fatty acid synthase mediates DNA strand exchange 1
 A:Reference number: AS4083; MUID:94245730
 A:Accession: AS4083
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <KAS>
 A>Note: sequence extracted from NCBI backbone (NCBIP:148744)
 C:Superfamily: yeast fatty-acid synthase

Query Match 21.6%; Score 22; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 13 MFPEVKE 20
 | | | | : :
 | | | | : :
 DB 1 MFPEVKE 8

RESULT 14

C56894
 Intracystalline chromoprotein 1 - Neothyris lenticularis (fragment)
 C:Species: Neothyris lenticularis

C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Jun-2000
 C/Accession: C56894
 R/Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.
 Comp. Biochem. Physiol. B 102, 93-95, 1992
 A>Title: An intracrystalline chromoprotein from red brachiopod shells: implications for
 A/Reference number: A56894; MUID:92405551
 A/Contents: Deshayes, red brachiopod shells
 A/Accession: C56894
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <CUS>
 A/Note: sequence extracted from NCBI backbone (NCBIP:114884)
 C/Keywords: Chromoprotein

Query Match 21.6%; Score 22; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.1e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 YAMMIAR 10
 |||:
 Db 7 YATMISK 13

RESULT 15
 A56894
 Intracrystalline chromoprotein I - Terebratella sanguinea (fragment)
 C/Species: Terebratella sanguinea
 C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Jun-2000
 C/Accession: A56894
 R/Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.
 Comp. Biochem. Physiol. B 102, 93-95, 1992
 A>Title: An intracrystalline chromoprotein from red brachiopod shells: implications for
 A/Reference number: A56894; MUID:92405551
 A/Contents: Leach, red brachiopod shells
 A/Accession: A56894
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <CUS>
 A/Note: sequence extracted from NCBI backbone (NCBIP:114882)
 C/Keywords: Chromoprotein

Query Match 21.6%; Score 22; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.1e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 YAMMIAR 10
 |||:
 Db 7 YATMISK 13

RESULT 16
 B56894
 Intracrystalline chromoprotein I - Waltonia inconspicua (fragment)
 C/Species: Waltonia inconspicua
 C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Jun-2000
 C/Accession: B56894
 R/Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.
 Comp. Biochem. Physiol. B 102, 93-95, 1992
 A>Title: An intracrystalline chromoprotein from red brachiopod shells: implications for
 A/Reference number: A56894; MUID:92405551
 A/Contents: Sowerby, red brachiopod shells
 A/Accession: B56894
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <CUS>
 A/Note: sequence extracted from NCBI backbone (NCBIP:114883)
 C/Keywords: Chromoprotein

Query Match 21.6%; Score 22; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.1e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 4 YAMMIAR 10
 |||:
 Db 7 YATMISK 13

RESULT 17
 PC7073
 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C/Accession: PC7073
 R/Isigita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y
 Electrophoresis 21, 1853-1871, 2000
 A>Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles o
 A/Reference number: PC7072
 A/Accession: PC7073
 A/Molecule type: protein
 A/Residues: 1-9 <TSU>
 C/Keywords: brain; core protein; oxidoreductase

Query Match 20.6%; Score 21; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 2e+05;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 12 KMPEVK 18
 |||:
 Db 3 KVAPKVK 9

RESULT 18
 T09741
 photosystem I chain psal - upland cotton chloroplast (fragment)
 C/Species: chloroplast Gossypium hirsutum (upland cotton)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C/Accession: T09741
 R/Small, R.L.; Ryburn, J.A.; Cronm, R.C.; Seelanan, T.; Wendel, J.F.
 Am. J. Bot. 85, 1301-1315, 1998
 A>Title: The tortoise and the hare: choosing between noncoding plastome and nuclear A
 A/Reference number: Z16323
 A/Accession: T09741
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-16 <SMA>
 A/Cross-references: EMBL:AF031581; NID:92623684; PID:93723945
 C/Genetics:
 A/Gene: psal
 A/Genome: psal
 C/Keywords: chloroplast; photosynthesis; photosystem I

Query Match 20.6%; Score 21; DB 2; Length 16;
 Best Local Similarity 42.9%; Pred. No. 2.5e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 11 FKPEPV 17
 |||:
 Db 4 FSSFPST 10

RESULT 19
 S32587
 L-ascorbate peroxidase (EC 1.11.1.11) isozyme II - spinach (fragment)
 C/Species: Spinacia oleracea (spinach)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
 C/Accession: S32587; S15878
 R/Kudo, A.; Saij, H.; Tanaka, K.; Tanaka, K.; Kondo, N.
 Plant Mol. Biol. 18, 691-701, 1992
 A>Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from Arabidop
 A/Reference number: S20866; MUID:92216045
 A/Accession: S32587

A:Molecule type: protein
 A:Residues: 1-17 <RUB>
 A>Note: This is a revision to the sequence from reference S15878
 R:Tanaka, K.; Takeuchi, E.; Kubo, A.; Sakaki, T.; Haraguchi, K.; Kawamura, Y.
 Arch. Biochem. Biophys. 286, 371-375, 1991
 A:Title: Two immunologically different isozymes of ascorbate peroxidase from spinach leaf
 A:Reference number: S15878; MUID:91378325
 A:Accession: S15878
 A:Molecule type: protein
 A:Residues: 1-3-17 <TAN>
 A>Note: this sequence has been revised in reference S20866
 C:Keywords: chloroplast; oxidoreductase

Query Match 20.6%; Score 21; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.6e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 12 KMEPYKE 19
 : : | : | : |
 Db 2 KSYPTVHE 9

RESULT 20

S14661
 photosystem I protein psaA - maize (fragment)
 C:Species: Zea mays (maize)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S14661
 R:Kangasjarvi, J.; Gengenbach, B.G.
 submitted to the EMBL Data Library, March 1991
 A:Description: Nucleotide sequence of maize plastid genome BamHI 14 fragment.
 A:Reference number: S14660
 A:Accession: S14661
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-18 <KAN>
 A:Cross-references: EMBL:X58080; NID:g12429; PIDN:CAA41109.1; PID:g12431
 C:Superfamily: Photosystem I P700 apoprotein

Query Match 20.6%; Score 21; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 PEVK 18
 : : | : | : |
 Db 8 PEVK 11

RESULT 21

S02808
 nucleolin - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
 C:Accession: S02808
 R:Sapp, M.; Richter, A.; Weisshart, K.; Calzergues-Ferrer, M.; Amalric, F.; Wallace, M.C.
 Eur. J. Biochem. 179, 541-548, 1989
 A:Title: Characterization of a 48-kDa nucleic-acid-binding fragment of nucleolin.
 A:Reference number: S02808; MUID:89153087
 A:Accession: S02808
 A:Molecule type: protein
 A:Residues: 1-19 <SAP>

Query Match 20.6%; Score 21; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 2.9e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 8 IARFKMPEVK 18
 : : | : | : |
 Db 3 MAKQKAPPEAK 13

RESULT 22

S57286
 translation elongation factor eEF-1 beta - Sulfolobus solfataricus (fragments)
 C:Species: Sulfolobus solfataricus
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S57286
 R:Arcari, P.; Raimo, G.; Iannicelli, G.; Gallo, M.; Bocchini, V.
 Biochim. Biophys. Acta 1263, 86-88, 1995
 A:Title: The first nucleotide sequence of an archaeal elongation factor 1-beta gene.
 A:Reference number: S57286; MUID:95359209
 A:Accession: S57286
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <ARC>

Query Match 20.6%; Score 21; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KMEPEY 17
 : : | : | : |
 Db 8 KVFPEY 13

RESULT 23

S51066
 ribosomal protein S15 - Thermus aquaticus (fragment)
 C:Species: Thermus aquaticus
 C:Date: 15-Jul-1995 #sequence_revision 01-Nov-1996 #text_change 01-Nov-1996
 C:Accession: S51066
 R:Tsibolli, P.; Herfurth, E.; Choli, T.
 Eur. J. Biochem. 226, 169-177, 1994
 A:Title: Purification and characterization of the 30S ribosomal proteins from the bac
 A:Reference number: S51053; MUID:95045586
 A:Accession: S51066
 A:Molecule type: protein
 A:Residues: 1-21 <TSI>
 A>Note: the source is designated as Thermus thermophilus
 C:Keywords: protein biosynthesis; ribosome

Query Match 20.6%; Score 21; DB 2; Length 21;
 Best Local Similarity 44.4%; Pred. No. 3.2e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 MIARFKMP 15
 : : | : | : |
 Db 10 VIOEFARFP 18

RESULT 24

A39108
 lipoprotein TagA precursor - Vibrio cholerae (fragment)
 C:Species: Vibrio cholerae
 C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 31-Dec-1993
 C:Accession: A39108
 R:Parsons, C.; Taxman, E.; Mekalanos, J.J.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1641-1645, 1991
 A:Title: ToxR regulates the production of lipoproteins and the expression of serum re
 A:Reference number: A39108; MUID:91156664
 A:Accession: A39108
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-25 <PAR>
 A:Cross-references: GB:M6058
 C:Keywords: lipid binding; lipoprotein

Query Match 20.6%; Score 21; DB 2; Length 25;
 Best Local Similarity 27.3%; Pred. No. 3.9e+03;
 Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 7 MIAFKMPEV 17
| : | : : |
Db 1 MVMVYSLSMKV 11

RESULT 25

S68642
nicotinic acetylcholine receptor-binding protein 4 - black-banded coral snake (fragment)
C:Species: Micrurus nigrocinctus (black-banded coral snake)
C:Date: 23-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 17-Mar-1999
C:Accession: S68642
R:Alape-Giron, A.; Sciles, B.; Schmidt, J.; Giron-Cortes, M.; Thelestam, M.; Joernvall,
FEBS Lett. 380, 29-32, 1996
A:Title: Characterization of multiple nicotinic acetylcholine receptor-binding proteins
A:Reference number: S68639; MUID:96181662
A:Accession: S68642
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-25 <ALA>

Query Match 20.6%; Score 21; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 3.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 15 PEVKER 20
| | | : |
Db 14 PEGRDK 19

Search completed: February 5, 2001, 10:49:28
Job time: 741 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:55:56 ; Search time 32.57 Seconds
(without alignments)

19,831 Million cell updates/sec

Title: US-08-981-824-2

Sequence: 102
1 SNMYAMMIAAFKMFPEVKEK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1436

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	28	27.5	15 1 MCRA_METTE	P22948 methanosc
2	25	24.5	14 1 DCMK_PSECF	P19914 pseudomonas
3	23	22.5	10 1 SLAP_BACTG	P49325 bacillus th
4	23	22.5	23 1 UDP_LACCA	P19662 lactobacill
5	23	22.5	24 1 CT31_LITCI	P81851 litorea cit
6	23	22.5	25 1 GRP_SCYCA	P09472 scyllorhinu
7	21	20.6	13 1 PED1_HYDAT	P80578 hydra atten
8	21	20.6	22 1 CR33_LITCE	P56339 litorea cae
9	21	20.6	22 1 CR33_LITCE	P56340 litorea cae
10	21	20.6	24 1 AMAR_BACTR	P37356 bacillus th
11	20	19.6	15 1 MILT_ONCKE	P81037 oncorhynch
12	20	19.6	18 1 HEMH_THETS	P80155 theromyzon
13	20	19.6	18 1 RL23_HALCU	P05975 halobacteri
14	20	19.6	19 1 LPGE_ECOLI	P33336 escherichia
15	20	19.6	19 1 PSRN_SYNVU	P12313 synchococc
16	20	19.6	20 1 AMP_FUSNU	P81207 fusobacteri
17	20	19.6	24 1 PEPI_ASPNG	P55749 aspergillus
18	20	19.6	25 1 Y15_BPT3	P20835 bacterioph
19	19	18.6	9 1 BUK_CLOPA	P81337 clostridium
20	19	18.6	15 1 UBL1_MONDO	P50103 monodelphis
21	19	18.6	19 1 DHAB_COMTE	P80704 commomops t
22	19	18.6	19 1 NS2_MYCTU	P81136 mycobacteri
23	19	18.6	24 1 CH60_ACTICA	P81874 achinetobact
24	19	18.6	24 1 CLPE_HORVU	P48883 hordeum vul
25	19	18.6	25 1 UBL1_BOVIN	P23356 bos taurus
26	18	17.6	8 1 AL18_CARMA	P81821 carclinus ma
27	18	17.6	10 1 URE3_MORMO	P17339 morganella
28	18	17.6	15 1 UC08_MAIZE	P80614 zea mays (m
29	18	17.6	18 1 ALI2_CYPDO	P82153 cydia pomon
30	18	17.6	20 1 CAOS_RAT	P19633 rattus norv
31	18	17.6	20 1 HGL1_FASHE	P80577 fasciola he
32	18	17.6	21 1 PEDB_HYDAT	P80577 hydra atten
33	18	17.6	22 1 AOFM_MOUSE	P06433 mus musculu

34	18	17.6	22	1	CR31_LITSP	P56238	litorea	spl
35	18	17.6	22	1	CR34_LITCE	P56241	litorea	cae
36	18	17.6	24	1	CRTC_CANFA	P28490	canis	famli
37	18	17.6	24	1	IRBP_SHEEP	P12663	ovis	aries
38	18	17.6	25	1	FLB1_TREHY	P80158	treponema	h
39	18	17.6	25	1	IRBP_PIG	P12662	sus	scrofa
40	18	17.6	25	1	PK12_SOLRU	P24744	solanum	tub
41	17.5	17.2	23	1	COXJ_ONCMY	P80333	oncorhynch	
42	17	16.7	8	1	AL12_CARMA	P81815	carclinus	ma
43	17	16.7	9	1	PGLR_DIAAB	P81179	diatrepes	a
44	17	16.7	9	1	SAP_STOVA	P24047	stomopneute	
45	17	16.7	12	1	PA2B_VIPBO	P31859	vipera	beru

ALIGNMENTS

RESULT 1	MCRA_METTE	STANDARD:	PRT:	15 AA.
ID	P22948;			
AC	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	METHYL-COENZYME M METHYLRREDUCTASE ALPHA SUBUNIT (EC 1.8.-.-)			
DE	(FRAGMENT).			
OS	Methanosarcina thermophila.			
OC	Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;			
OC	Methanosarcina.			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN-DSM 1825 / TM-1;			
RX	MEDLINE-91193204; PubMed-2013570;			
RA	Jablonski P.E., Ferry J.G.;			
RT	"Purification and properties of methyl coenzyme M methylreductase from acetate-grown Methanosarcina thermophila.";			
RT	J. Bacteriol. 173:2481-2487(1991).			
RL	J. Bacteriol. 173:2481-2487(1991).			
CC	-1- FUNCTION: THIS ENZYME COMPLEX CATALYZES THE FINAL STEP IN			
CC	METHANOGENESIS, WHICH IS THE TERMINAL STEP OF ANAEROBIC			
CC	DEGRADATION OF BIOMASS.			
CC	-1- CATALYTIC ACTIVITY: REDUCTION OF METHYL-COENZYME M (2-(METHYLTHIO)			
CC	ETHANESULFONIC ACID) WITH 7-MERCAPTOHEPTANOLYLTHREONINE PHOSPHATE			
CC	TO METHANE AND AN HETERODISULFIDE (CH(3)-S-COM + H-S-HTP - CH(4) +			
CC	COM-S-S-HTP).			
CC	-1- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)			
CC	TO ONE MOLECULE OF COENZYME F430. F430 IS A YELLOW NICKEL			
CC	PORPHINOID.			
CC	-1- SUBUNIT: TRIMER OF AN ALPHA, A BETA, AND A GAMMA SUBUNITS.			
CC	-1- MISCELLANEOUS: THE OPTIMAL TEMPERATURE FOR ENZYME ACTIVITY IS 60			
CC	DEGREES CELSIUS.			
CC	-1- MISCELLANEOUS: REDUCED FERREDOXIN COULD REDUCTIVELY REACTIVATE THE			
CC	ENZYME.			
KW	Methanogenesis: Oxidoreductase.			
KW	NON TER			
FT	SEQUENCE 15 AA: 1686 MW: D5D59892FCA5F63C CRC64;			
QY	5 AMMIARFKMFPEVK 18			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0%; Pred. No. 65;			
QY	Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;			
QY	1: 1:11 111			
DB	2 ADIFARFKTSMEVK 15			
QY	1: 1:11 111			
DB	1: 1:11 111			
QY	27.5%; Score 28; DB 1; Length 15;			
DB	Best Local Similarity 50.0			

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DE CARBON MONOXIDE DEHYDROGENASE MEDIUM CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydoflava.
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
CC Hydrogenophaga.
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
  carboxydophilic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
  ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
  SMALL.
DR PIR: P10142; P10142.
KM Oxidoreductase; Molybdenum.
FT NON_TER 14
SQ SEQUENCE 14 AA: 1756 MW; 655836D1FB7C25B CRC64;

Query Match 24.5%; Score 25; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 MIAFEK 12
DB 1 MIAFEK 7

RESULT 3
SLAP_BACTG STANDARD; PRT; 10 AA.
ID SLAP_BACTG
AC P4932;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-LAYER PROTEIN (SURFACE LAYER PROTEIN) (FRAGMENT).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
  Bacillus/staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckevich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
  OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
  CELL WALL; S-LAYER.
KM Cell wall; S-layer.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 22.5%; Score 23; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KMPEV 17
DB 3 KTFPDV 8

RESULT 4
UDP_LACCA STANDARD; PRT; 23 AA.
ID UDP_LACCA
AC P19662;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

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DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE URIDINE PHOSPHORYLASE (EC 2.4.2.3) (UDRPASE) (FRAGMENT).
GN UDP.
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
  Lactobacillus.
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 7469; PubMed=2119230;
RX MEDLINE=90381286; PubMed=2119230;
RA Avraham Y., Grossowicz N., Yashpe J.;
RT "Purification and characterization of uridine and thymidine
  phosphorylase from Lactobacillus casei.";
RL Biochim. Biophys. Acta 1040:287-293(1990).
CC -1- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS
  OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE
  COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES,
  OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.
CC -1- CATALYTIC ACTIVITY: URIDINE + PHOSPHATE -> URACIL + ALPHA-D-RIBOSE
  1-PHOSPHATE.
CC -1- PATHWAY: NUCLEOTIDE AND DEOXYRIBONUCLEOTIDE CATABOLISM.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO THE PNP/UDP FAMILY 1 OF PHOSPHORYLASES.
DR PIR: S11383; S11383.
DR INTERPRO: IPR000845;
DE PROSITE, PS01232; PNP_UDP_1; PARTIAL.
KM Transferase; Glycosyltransferase
FT UNSURE 1
FT UNSURE 7
FT NON_TER 23
SQ SEQUENCE 23 AA: 2630 MW; 918B2E2F32F35A17 CRC64;

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Query Match 22.5%; Score 23; DB 1; Length 23;
Best Local Similarity 57.1%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 RKKPE 16
DB 1 RKKVPE 7

RESULT 5
CT31_LITCI STANDARD; PRT; 24 AA.
ID CT31_LITCI
AC P81851; P81852; P81853;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CITROPIN 3.1.2 (CONTAINS: CITROPIN 3.1.1; CITROPIN 3.1).
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
  OC Litoria.
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowle J.H., Chia B.C.S.,
  RA Wallace J.C., Tyler M.J.;
RT "Hollase defence peptides from the skin glands of the Australian blue
  RT "mountains tree-frog Litoria citropa. Solution structure of the
  RT antibacterial peptide citropin 1.1.";
RL Eur. J. Biochem. 265:627-637(1999).
CC -1- TISSUE SPECIFICITY: DORSAL AND SUBVENTRAL SKIN GLANDS.
FT PEPTIDE 1
FT PEPTIDE 24
FT PEPTIDE 1
FT PEPTIDE 23
FT PEPTIDE 22
FT PEPTIDE 1
SQ SEQUENCE 24 AA: 2614 MW; C9001E295BD0E15D CRC64;

Query Match 22.5%; Score 23; DB 1; Length 24;
Best Local Similarity 50.0%; Pred. No. 7.7e+02;

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Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 13 MEPEVEK 20

DB 2 LEQVIREK 9

RESULT 6

GRP_SCYCA STANDARD; PRT; 25 AA.
ID GRP_SCYCA
AC P09472;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE GASTRIN-RELEASING PEPTIDE (GRP).
OS Scyliorhinus canicula (Spotted dogfish). (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RX MEDLINE-88137922; PubMed-3436516;
RA Conlon J.M., Henderson I.W., Thim L.;
RT "Gastrin-releasing peptide from the intestine of the elasmobranch
fish, Scyliorhinus canicula (common dogfish).";
RL Gen. Comp. Endocrinol. 68:415-420(1987).
CC -1- FUNCTION: GRP STIMULATES GASTRIN RELEASE AS WELL AS OTHER
GASTROINTESTINAL HORMONES.
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
FAMILY.
DR PIR: S06263; S06263.
DR INTERPRO: IPR000874; -.
DR PRAM: P02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD.RES 25 25
SO SEQUENCE 25 AA; 2781 MW; B735F911B89007F8 CRC64;

Query Match 22.5%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 12 KMFP 15
DB 11 KMFP 14

RESULT 7

PEDI_HYDAT STANDARD; PRT; 13 AA.
ID PEDI_HYDAT
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PEDI.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydroidea; Hydra.
RN [1]
RP SEQUENCE.
RX MEDLINE-96232307; PubMed-8674432;
RA Hofmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
peptides from Hydra vulgaris.";
RL Development 122:1941-1948(1996).
CC -1- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
MORPHOGEN.
KW Morpogen.
SO SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 20.6%; Score 21; DB 1; Length 13;

Best Local Similarity 40.0%; Pred. No. 9.1e+02; Mismatches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 REFMPEVEK 19

DB 4 RPEVLDPVSE 13

RESULT 8

CR32_LITCE STANDARD; PRT; 22 AA.
ID CR32_LITCE
AC P56239;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERIN 3.2.
OS Litoria caerulea.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-PAROTOID GLAND;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins from
Litoria caerulea.";
RL J. Chem. Res. 138:910-936(1993).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
GLANDS.
CC -1- MASS SPECTROMETRY: MW-2397; METHOD-FAB.
KW Antibiotic; Amphibian skin; Amidation.
FT MOD.RES 22 22
SO SEQUENCE 22 AA; 2400 MW; 1D440B3829D4367C CRC64;

Query Match 20.6%; Score 21; DB 1; Length 22;
Best Local Similarity 37.5%; Pred. No. 1.5e+03; Mismatches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 13 MEPEVEK 20
DB 2 LMEKIREK 9

RESULT 9

CR33_LITCE STANDARD; PRT; 22 AA.
ID CR33_LITCE
AC P56240;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERIN 3.3.
OS Litoria caerulea.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-PAROTOID GLAND;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins from
Litoria caerulea.";
RL J. Chem. Res. 138:910-936(1993).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
GLANDS.
CC -1- MASS SPECTROMETRY: MW-2424; METHOD-FAB.
KW Antibiotic; Amphibian skin; Amidation.

FT MOD RES 22 22 AMIDATION.
SQ SEQUENCE 22 AA: 2427 MW: 1D440B2200D4367C CRC64;

Query Match 20.6%; Score 21; DB 1; Length 22;
Best Local Similarity 37.5%; Pred. No. 1.5e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 13 MFPEVKE 20
: : : : :
Db 2 LMEKIKER 9

RESULT 10
ID AMMA_BACTR STANDARD; PRT; 24 AA.
AC P37356;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14) (L-AMINOACYLASE)
(FRAGMENT).
OS Bacillus thermoglucosidasius.
OC Bacillus, Firmicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RA Chu H.-Y., Tanizawa K., Tanaka H., Soda K.;
RT "Thermostable aminocyclase from Bacillus thermoglucosidis.
RT Purification and characterization.";
RL Agric. Biol. Chem. 51:2793-2800(1987).
CC -1- CATALYTIC ACTIVITY: A N-ACYL-L-AMINO ACID + H(2)O -> A FATTY ACID
ANION + A L-AMINO ACID.
CC -1- COFACTOR: ACTIVATED BY COBALT (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M40, ALSO KNOWN AS THE
AMA/HIPO/HVC FAMILY OF HYDROLASES.
KM Hydrolyase; Cobalt.
FT NON_TER 24
SQ SEQUENCE 24 AA: 2846 MW: BC954EAD2B0EC64A CRC64;

Query Match 20.6%; Score 21; DB 1; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 KMPEVKE 19
: : : : :
Db 8 RLVDVEKE 15

RESULT 11
ID MILT_ONCKE STANDARD; PRT; 15 AA.
AC P81037;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MULTIPAIN (EC 3.4.22.-) (FRAGMENT).
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RA MEDLINE=97397031; PubMed=9253183;
RA Kawabata C., Ichishima E.;
RT "Mltpain, new cysteine proteinase from the milt of chum salmon,
RT Oncorhynchus keta";
RL Comp. Biochem. Physiol. 117B:445-452(1997).
CC -1- FUNCTION: CYSTEINE PROTEINASE THAT HYDROLYSES BASIC PROTEINS.
CC HYDROLYSE BASIC PROTEINS SUCH AS HISTONE, SALMINE AND CLOUPAINE BUT
CC NOT MILK CASEIN.

CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE WITH BASIC RESIDUES AT
CC P2 AND P1.
CC MEROPS; C01.093; -.
KM Hydrolyase.
DT NON_TER 15
SQ SEQUENCE 15 AA: 1730 MW: 766B7771C0F888E7 CRC64;

Query Match 19.6%; Score 20; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNMYAMI 8
: : : : :
Db 3 SFLYAENV 10

RESULT 12
ID HEMH_THETS STANDARD; PRT; 18 AA.
AC P80155;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE OVOHEMERETHRIN (YP14) (FRAGMENT).
OS Theromyzon tessulatum (leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
RN [1]
RP SEQUENCE.
RC TISSUE=OOCYTE;
RX MEDLINE=93049299; PubMed=1425663;
RA Beert J.-L., Britel M., Sautiere P., Malecha J.;
RT "Ovohemerethrin, a major 14-kDa yolk protein distinct from
RT vitellogenin in leech.";
RL Eur. J. Biochem. 209:563-569(1992).
CC -1- FUNCTION: MAJOR YOLK PROTEIN. THIS IRON PROTEIN MAY PLAY A ROLE
CC IN THE DETOXIFICATION OF FREE IRON AFTER A BLOOD MEAL.
CC -1- SIMILARITY: BELONGS TO THE HEMERYTHRIN FAMILY.
CC PIR; S29264; S29264.
DR HSSP; P02247; ZMR.
DR INTERPRO; IPR002063; -.
DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
KM Oxygen transport; Metal-binding; Iron; Yolk.
FT NON_TER 18
SQ SEQUENCE 18 AA: 2368 MW: 33397EE587C81F1 CRC64;

Query Match 19.6%; Score 20; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 FKMPPE 16
: : : : :
Db 13 FKVEYE 18

RESULT 13
ID RL23_HALCU STANDARD; PRT; 18 AA.
AC P05975;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L23P (HL31) (FRAGMENT).
GN RPL23P.
OS Halobacterium cutirubrum.
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
RN [1]
RP SEQUENCE.
RX MEDLINE=84282108; PubMed=6467081;
RA Matheson A.T., Yaguchi M., Christensen P., Rollin C.F., Hasnain S.;

RT "Purification, properties, and N-terminal amino acid sequence of
 RT certain 50S ribosomal subunit proteins from the archaeobacterium
 RT Halobacterium cutirubrum.";
 RL Can. J. Biochem. Cell Biol. 62:426-433(1984).
 CC -1- FUNCTION: BINDS TO A SPECIFIC REGION ON THE 23S RNA
 CC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
 DR PIR: S08559; S08559.
 DR INTERPRO: IPR001014;
 DR PROSITE: PS00050; RIBOSOMAL_L23; PARTIAL.
 KW Ribosomal protein; RNA-binding.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2041 MW; 3E61DC53F8B4DD4C CRC64;

Query Match 19.6%; Score 20; DB 1; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 14 EPEVKEK 20
 : | | | |
 DB 6 YPLVTEK 12

RESULT 14
 LPEE_ECOLI
 ID LPEE_ECOLI STANDARD; PRT; 19 AA.
 AC P33236;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GEF LEADER PEPTIDE.
 GN GEF.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-92048481; PubMed-1943701;
 RA Poulsen L.R., Refn A., Molin S., Andersson P.;
 RT "The gef gene from Escherichia coli is regulated at the level of
 RT translation";
 RL Mol. Microbiol. 5:1639-1648(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Bernal N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC -----
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 CC EMBL: AE000112; AAC73129.1; ALT_TERM.
 DR PIR: S16473; S16473.
 DR ECOGENE: EGI2074; gefL.
 KW Leader peptide.
 FT NON_TER 18 18
 SQ SEQUENCE 19 AA; 2259 MW; 19B3EDF371EB0BEB CRC64;

Query Match 19.6%; Score 20; DB 1; Length 19;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 16 EYKEK 20
 : | | | |
 DB 13 KYVEK 17

RESULT 15
 PSBN_SYNVU
 ID PSBN_SYNVU STANDARD; PRT; 19 AA.
 AC P12313;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE PHOTOSYSTEM II REACTION CENTER N PROTEIN (FRAGMENT).
 GN PSBN.
 OS Synechococcus vulcanus.
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-89338735; PubMed-2503398;
 RA Ikeuchi M., Koike H., Inoue Y.;
 RT "N-terminal sequencing of low-molecular-mass components in
 RT cyanobacterial photosystem II core complex. Two components correspond
 RT to unidentified open reading frames of plant chloroplast DNA.";
 RL FEBS Lett. 253:178-182(1989).
 CC -1- FUNCTION: NOT KNOWN.
 CC -1- SIMILARITY: BELONGS TO THE PSBN FAMILY.
 DR PIR: S05216; S05216.
 KW Photosystem II; Transmembrane.
 FT MOD_RES 1 1
 FT TRANSMEM 6 1
 FT NON_TER 19 19
 FT POTENTIAL.
 SQ SEQUENCE 19 AA; 2217 MW; A97C99B523106D14 CRC64;

Query Match 19.6%; Score 20; DB 1; Length 19;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 MYAMTARF 11
 : | | | |
 DB 9 IFAXIALF 17

RESULT 16
 AMP_FUSNU
 ID AMP_FUSNU STANDARD; PRT; 20 AA.
 AC P81207;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE AMINOPEPTIDASE (EC 3.4.11.-) (AP) (FRAGMENT).
 OS Fusobacterium nucleatum.
 OC Bacteria; Fusobacteria; Fusobacterium.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-ATCC 10953;
 RX MEDLINE-98361026; PubMed-9695913;
 RA Rogers A.H., Gunadi A., Gully N.J., Zilm P.S.;
 RT "An aminopeptidase nutritionally important to Fusobacterium
 RT nucleatum.";
 RL Microbiology 144:1807-1813(1998).
 CC -1- FUNCTION: CLEAVES A WIDE RANGE OF DIPEPTIDES AND TRIPEPTIDES.
 CC -1- COFACTOR: COBALT.
 CC -1- SUBCELLULAR LOCATION: CELL ENVELOPE-ASSOCIATED.
 KW Hydrolase; Aminopeptidase; Metalloprotease; Cobalt.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2585 MW; 97095B948262C71B CRC64;

Query Match 19.6%; Score 20; DB 1; Length 20;
 Best Local Similarity 33.3%; Pred. No. 2.1e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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OY      12 KMPEVKEK 20
DB      4 KXYDLKER 12

RESULT 17
PEPL_ASPNG STANDARD: PRT: 24 AA.
ID PEPL_ASPNG
AC P55749;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE CARBOXYPEPTIDASE I (EC 3.4.16.-) (CPD-1) (FRAGMENT).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Eurotiales; Trichocomaceae;
OC anamorphic trichocomaceae; Aspergillus.
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE-92344370; PubMed-1637154;
RA Dal Degau F., Ribadeau-Dumas B., Bredem K.;
RT Purification and characterization of two serine carboxypeptidases
RT from Aspergillus niger and their use in C-terminal sequencing of
RT proteins and peptide synthesis.
RL Appl. Environ. Microbiol. 58:2144-2152(1992).
CC -1- FUNCTION: REMOVES ACIDIC, NEUTRAL AND BASIC AMINO ACIDS AS WELL AS
CC PROLINE FROM THE C-TERMINAL POSITION. DIGESTS PREFERENTIALLY
CC PEPTIDES CONTAINING A HYDROPHOBIC RESIDUE IN P1 POSITION, AS WELL
CC AS ARGININE, LYSINE OR PHENYLALANINE IN P1 POSITION OF ESTER
CC SUBSTRATE. OPTIMAL PH IS 4; ENZYME IS UNSTABLE ABOVE PH 8.
CC CATALYZES ALSO PEPTIDE SYNTHESIS.
CC -1- CATALYTIC ACTIVITY: RELEASE OF A C-TERMINAL AMINO ACID WITH A
CC BROAD SPECIFICITY.
CC -1- ENZYME REGULATION: INHIBITED BY DFP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- PTM: CONTAINS BOTH N- AND O-LINKED SUGAR CHAINS. THE N-LINKED
CC OLIGOSACCHARIDES ARE UNIQUE STRUCTURES OF MAN(10)GLCNAc(2) AND
CC MAN(11)GLCNAc(2). DEGLYCOSYLATION DOES NOT AFFECT THE CATALYTIC
CC ACTIVITY, PH OR THERMAL STABILITY, OR RESISTANCE TO PROTEOLYSIS OF
CC THE ENZYME.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S10; ALSO KNOWN AS THE
CC SERINE CARBOXYPEPTIDASE FAMILY.
DR INTERPRO: IPR001563;
DR PROSITE: PS00131; CARBOXYPEPT_SER_SER; PARTIAL.
DR PROSITE: PS00560; CARBOXYPEPT_SER_HIS; PARTIAL.
KW Hydrolase; Carboxypeptidase; Glycoprotein.
FT UNSURE 2
FT UNSURE 11 11 PROBABLE.
FT CARBOHYD 2 2
FT CARBOHYD 11 11 N-LINKED (GLCNAc. . .) (PROBABLE).
FT NON_TER 24 24
SQ SEQUENCE 24 AA; 2623 MW; B7F183DEF6DA6C2 CRC64;

Query Match 19.6%; Score 20; DB 1; Length 24;
Best Local Similarity 29.4%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY      1 SNMTAMTARFKMPEV 17
DB      2 TNKTFARLVNGTSIPEV 18

RESULT 18
ID Y15_BP13 STANDARD: PRT: 25 AA.
AC P20835;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 01-FEB-1991 (Rel. 17, Last annotation update)
DE HYPOTHETICAL GENE 1.5 PROTEIN.
GN 1.5.
OS Bacteriophage T3.

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OC      17-1-like phages.
OC      17-1-like phages.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-LURIA;
RX MEDLINE-87226207; PubMed-3586029;
RA Schmitt M.P., Beck P.J., Kearney C.A., Spence J.L., Digiovanni D.,
RA Condreay J.P., Molinoux I.J.;
RT "Sequence of a conditionally essential region of bacteriophage T3,
RT including the primary origin of DNA replication."
RL J. Mol. Biol. 193:479-495(1987).
CC -----
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CC -----
DR EMBL; X17255; CA35126.1;
DR EMBL; X05031; CAA28701.1;
DR PIR; S09540; S09540.
KW Hypothetical protein.
SQ SEQUENCE 25 AA; 2821 MW; 92B709153A2950A CRC64;

Query Match 19.6%; Score 20; DB 1; Length 25;
Best Local Similarity 27.3%; Pred. No. 2.6e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY      6 MMIRFKMPE 16
DB      14 LMVADNINWPD 24

RESULT 19
ID BURK_CLOPA STANDARD: PRT: 9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BUTYRATE KINASE (EC 2.7.2.7) (BK) (CP 38) (FRAGMENT).
GN BURK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN [1]
RP SEQUENCE.
RX STRAIN-W5;
RX MEDLINE-98291870; PubMed-9629918;
RA Flengruds R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: CATALYZES THE CONVERSION OF BUTYRYL-COA THROUGH BUTYRYL
CC PHOSPHATE TO BUTYRATE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + 2-BUTANOATE = ADP + BUTANOYL PHOSPHATE.
CC -1- PATHWAY: INVOLVED IN THE ACIDOGENIC PHASE OF FERMENTATION.
CC -1- SIMILARITY: BELONGS TO THE ACETOKINASE FAMILY.
DR INTERPRO: IPR000890;
DR PROSITE: PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE: PS01076; ACETATE_KINASE_2; PARTIAL.
KW transferase; Kinase.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 18.6%; Score 19; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 3 MYXMMI 8
11 : : 1
DB 1 MYKLLI 6

RESULT 20

UBLI_MONDO STANDARD: PRT: 15 AA.

AC P50103: 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L1 (EC 3.1.2.15) (UCH-
L1) (UBIQUITIN THIOLESTERASE L1) (PGP 9.5) (FRAGMENT).

OS Monodelphis domestica (short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER; MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowern A.R., Lavender F.L., Whitaker P.A.,
RA Thompson R.J.;

RT Identification of evolutionary conserved regulatory sequences in the
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
hydrolyase (PGP9.5) gene.

J. Neurochem. 66:35-46(1996).

-1- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUITINATED PROTEINS.

THIS ENZYME IS A THIOLESTERASE THAT RECOGNIZE AND HYDROLYZE

A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.

-1- CATALYTIC ACTIVITY: UBIQUITIN C-TERMINAL THIOLESTER + H(2)O =

UBIQUITIN + A THIOLE.

-1- SUBCELLULAR LOCATION: CYTOPLASMIC.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12; ALSO KNOWN AS

FAMILY 1 OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASES.

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CC or send an email to license@isb-sib.ch).

CC EMBL: U32208; AAA89059.1; -

DR INTERPRO: IPR001578; -

DR PROSITE: PS00140; UCH.1; PARTIAL.

KW Ubiquitin conjugation; Hydrolase; Thiol protease; Multigene family.

FT NON_TER 15 13

SQ SEQUENCE 15 AA: 1816 MW: 187336623F6E79 CRC64:

Query Match 18.6% Score 19; DB 1; Length 15;

Best Local Similarity 26.7% Pred. No. 2.3e+03;

Matches 4; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 MMIAEFKMEPEVEK 20

DB 1 MQLKPEINPEMLNK 15

RESULT 21

DHAB_COMTE STANDARD: PRT: 19 AA.

AC P80704; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE ALDEHYDE DEHYDROGENASE, BETA CHAIN (EC 1.2.99.3) (ALDH) (FRAGMENT).

OS *Commonas testosteroni* (*Pseudomonas testosteroni*).

OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.

RP SEQUENCE.

RC STRAIN-ATCC 15667;

RA Luyckx D.M.A.M., Kim S.W., de Vries S., Duine J.A.;

RL Submitted (JUL-1996) to the SWISS-PROT data bank.

CC -1- CATALYTIC ACTIVITY: AN ALDEHYDE + ACCEPTOR + H(2)O = AN ACID +

REDUCED ACCEPTOR.

CC -1- COFACTOR: MOLYBDENUM.

CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA AND A GAMMA

CHAIN.

KW Oxidoreductase; Molybdenum.

FT NON_TER 19 19

SQ SEQUENCE 19 AA: 2096 MW: 89BD67D4D05A212E CRC64:

Query Match 18.6% Score 19; DB 1; Length 19;

Best Local Similarity 33.3% Pred. No. 2.9e+03;

Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 MYXMMIARFKMEPEV 17

DB 1 MYAFSYTPRTIDEV 15

RESULT 22

NS2_MYCTU STANDARD: PRT: 19 AA.

AC P81136; 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 30 KDA NON-SECRETORY PROTEIN 2 (FRAGMENT).

OS *Mycobacterium tuberculosis*.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

RP SEQUENCE.

RC STRAIN-H37RV;

RA Prasad H.K., Annapurna P.S.;

RL Submitted (DEC-1997) to the SWISS-PROT data bank.

CC -1- SIMILARITY: STRONG, TO THE N-TERMINALS OF C.ELEGANS F20A1.4

CC AND H. INFLUENZAE HI0967.

FT NON_TER 19 19

SQ SEQUENCE 19 AA: 2211 MW: A8C1854BF1PFI70 CRC64:

Query Match 18.6% Score 19; DB 1; Length 19;

Best Local Similarity 42.9% Pred. No. 2.9e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 IARFKMF 14

DB 11 VAFFSFF 17

RESULT 23

CH60_ACICA STANDARD: PRT: 24 AA.

AC P81874; 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).

GN MOPR OR GROEL.

OS *Acinetobacter calcoaceticus*.

OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;

OC *Acinetobacter*.

RP SEQUENCE.

RC STRAIN-69-V;

RC MEDLINE-99274045; PubMed-10344248;

RA Bendorf D., Loffhagen N., Babel W.;

*Induction of heat shock proteins in response to primary alcohols in

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RT Acinetobacter calcoaceticus";
RL Electrophoresis 20:781-789(1999).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK AND ETHANOL.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR INTERPRO: IPR001844; -.
DR PROSITE: PS00296; CHAPERONINS_CPN60; PARTIAL.
KM Chaperone; ATP-binding; Heat shock.
FT NON_TER 24
SQ SEQUENCE 24 AA: 2483 MW: 830298188D735688 CRC64;

Query Match 18.6%; Score 19; DB 1; Length 24;
Best Local Similarity 80.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 AMMTA 9
DB 13 SMITA 17

RESULT 24
CLPP_HORVU STANDARD; PRT; 24 AA.
AC P48883;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROBABLE CLPP-LIKE PROTEASE (EC 3.4.21.92) (ENDOPEPTIDASE CLP)
DE (FRAGMENT).
GN CLPP.
OS Hordeum vulgare (Barley).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAISA.
RX MEDLINE=96197402; Pubmed=8616228;
RA Huebschmann T., Hess W., Boerner T.;
RT "Impaired splicing of the rps12 transcript in ribosome-deficient
RT plastids";
RL Plant Mol. Biol. 30:109-123(1996).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS TO SMALL PEPTIDES IN
CC THE PRESENCE OF ATP AND MAGNESIUM. ALPHA-CASEIN IS THE USUAL TEST
CC SUBSTRATE. IN THE ABSENCE OF ATP, ONLY OLIGOPEPTIDES SHORTER THAN
CC FIVE RESIDUES ARE CLEAVED (SUCH AS SUCCINYL-LEU-TYR-|-NHMEC; AND
CC LEU-TYR-|-LEU-|-TYR-TRP, IN WHICH THE CLEAVAGE OF THE -TYR-|-LEU-
CC AND -TYR-|-TRP- BOND ALSO OCCURS).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S14; ALSO KNOWN AS CLPP
CC FAMILY.
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CC -----
CC EMBL: X89562; CA61738.1; -.
CC MENDEL: 2297; HORVU:clpp.1.
DR INTERPRO: IPR001907; -.
DR PROSITE: PS00381; CLP_PROTEASE_SER; PARTIAL.
DR PROSITE: PS00382; CLP_PROTEASE_HIS; PARTIAL.
KM Hydrolyase; Serine protease; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 24 AA: 2941 MW: 715801FE3E073CE CRC64;

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Query Match 18.6%; Score 19; DB 1; Length 24;
Best Local Similarity 75.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 FPEV 17
DB 17 FPEM 20

RESULT 25
UBLI_BOVIN STANDARD; PRT; 25 AA.
AC P23356;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L1 (EC 3.1.2.15) (UCH-
DE L1) (UBIQUITIN THIOLESTERASE L1) (NEURON CYTOPLASMIC PROTEIN 9.5)
DE (PGP 9.5) (FRAGMENT).
GN UCHL1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE=BRAIN;
RX MEDLINE=92008646; Pubmed=1833240;
RA Giampanco I., Bianchi R., Caccarelli P., Pula G., Sorci G.,
RA Antonoli S., Bocchini V., Donato R.;
RT "Neuron-specific" protein gene product 9.5 (PGP 9.5) is also
RT expressed in glioma cell lines and its expression depends on cellular
RT growth state";
RL FEBS Lett. 290:131-134(1991).
CC -1- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
CC THIS ENZYME IS A THIOLESTERASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -1- CATALYTIC ACTIVITY: UBIQUITIN C-TERMINAL THIOLESTER + H(2)O =
CC UBIQUITIN + A THIOLE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: NEURONS AND CELLS OF THE DIFFUSE
CC NEUROENDOCRINE SYSTEM AND THEIR TUMORS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12; ALSO KNOWN AS
CC FAMILY 1 OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASES.
CC PIR: S17561; S17561.
DR MEROPS: C12.001; -.
DR INTERPRO: IPR001578; -.
DR PROSITE: PS00140; UCH_1; PARTIAL.
KM Ubiquitin conjugation; Hydrolyase; Thiol protease; Multigene family.
FT NON_TER 25
SQ SEQUENCE 25 AA: 2812 MW: 26855AD0A754D55 CRC64;

Query Match 18.6%; Score 19; DB 1; Length 25;
Best Local Similarity 26.7%; Pred. No. 3.8e+03;
Matches 4; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 MIAFEMPEVEKER 20
DB 1 MQLKPMIDEMLKNK 15

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Search completed: February 5, 2001, 10:55:58
Job time: 498 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:55:20 ; Search time 93.77 Seconds
(without alignments)
24.999 Million cell updates/sec

Title: US-08-981-824-2

Perfect score: 102
Sequence: 1 SNNYAMAMARFKMEPEVKEK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_undefined:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	29.4	23	2	09R314
2	26	25.5	17	6	09TRH5
3	26	25.5	19	11	09J1A2
4	26	25.5	22	11	09QW14
5	24	23.5	11	11	09QXN6
6	24	23.5	18	2	09RCR1
7	24	23.5	21	8	035556
8	23	22.5	14	11	09J1U5
9	23	22.5	17	12	085673
10	23	22.5	17	12	000340
11	23	22.5	18	2	09R4N5
12	23	22.5	20	2	09R4W0
13	23	22.5	22	2	005279
14	23	22.5	22	2	09S551
15	22	21.6	12	11	062966
16	22	21.6	15	1	09UWM1
17	22	21.6	15	8	035921
18	22	21.6	16	4	09UMJ9
19	22	21.6	20	2	09RLP2

20	22	21.6	20	4	09UK71
21	22	21.6	20	6	029341
22	22	21.6	20	6	09TRC0
23	22	21.6	21	6	09XSL5
24	22	21.6	24	2	09ZB05
25	22	21.6	24	2	09XK2
26	22	21.6	24	2	09R4Y3
27	22	21.6	24	6	097793
28	22	21.6	25	2	09RSD7
29	22	21.6	25	5	076530
30	22	21.6	25	11	09JK04
31	22	21.6	25	12	09TER9
32	21.5	21.1	20	6	09TDX5
33	21.5	21.1	20	6	077646
34	21	20.6	13	2	09RZ4
35	21	20.6	15	2	09RG03
36	21	20.6	15	6	09TR14
37	21	20.6	17	2	052748
38	21	20.6	17	8	09XDN9
39	21	20.6	18	8	019969
40	21	20.6	18	8	019979
41	21	20.6	18	8	019971
42	21	20.6	18	8	019975
43	21	20.6	18	8	019973
44	21	20.6	19	8	019977
45	21	20.6	19	2	09REZ7

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	23 AA.
09R314	09R314			
AC	09R314			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)			
DE	DNA ADENINE METHYLASE HOMOLOG (FRAGMENT).			
GN	M. HPYL.			
OS	Helicobacter pylori (Campylobacter pylori).			
OC	Bacteria: Proteobacteria; epsilon subdivision; Helicobacter group;			
CC	Helicobacter.			
OX	NCBI_TaxID=210;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-219, AND 213;			
RA	Raudoniklene A., Berg D.E.;			
RT	"IceA2 segment from H. pylori (Alaska strain 219)."			
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF008929; AAC64502.1;			
DR	EMBL; AF008928; AAC64500.1;			
KW	Methyltransferase.			
FT	NON_TER			
SO	SEQUENCE	23 AA: 2635 MW: 6D6CC63737422B3 CRC64;		

Query Match 29.4%; Score 30; DB 2; Length 23;
Best Local Similarity 36.4%; Pred. No. 2.5e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY	9	ARFKMEPEVKE 19
DB	6	SKYRLPIRKE 16
QY	2	
09TRH5		
AC	09TRH5	PRELIMINARY:
DT	01-MAY-2000 (TREMBLrel. 13, Created)	PRT: 17 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	

DE ALPHA-SI-CASEIN HOMOLOG (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE-93231344; PubMed-1299613;
 RA Neuhoom B., Giuffrida M.G., Conti A.;
 RT "Isolation of a new ligand-carrying casein fragment from bovine
 RT mammary gland microsomes";
 RT FEBS Lett. 305:189-191(1992).
 SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 25.5%; Score 26; DB 6; Length 17;
 Best Local Similarity 77.8%; Pred. No. 8.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 14 FPEV--KER 20
 ||| ||
 Db 5 FPEVGEK 13

RESULT 3
 ID 09JIA2 PRELIMINARY; PRT; 19 AA.
 AC 09JIA2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE NORPEPHRINE TRANSPORTER (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Padbury J.F., McGonigal B., Tseng Y.;
 RT "Cloning and Sequence Analysis of the Rat Norepinephrine Transporter
 RT Promoter";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF246668; AAF78041.1; -;
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2082 MW; 4AA83339008F55CD CRC64;

Query Match 25.5%; Score 26; DB 11; Length 19;
 Best Local Similarity 46.2%; Pred. No. 9.6e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

OY 6 MMIAFFKPEVK 18
 ||:| | | | |
 Db 1 MLIAKMK--PQVQ 11

RESULT 4
 ID 09QM14 PRELIMINARY; PRT; 22 AA.
 AC 09QM14;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE PROTEIN TYROSINE KINASE JAK1 (FRAGMENT).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10095;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93232338; PubMed-8514334;

RA Harpur A.G., Zimiecki A., Wilks A.F., Falk K., Rotzsche O.,
 RA Rammensee H.G.;
 RT "A prominent natural H-2 Kd ligand is derived from protein tyrosine
 RT kinase JAK1";
 RL Immunol. Lett. 35:235-237(1993).
 SQ SEQUENCE 22 AA; 2681 MW; D0110BD1FC3C084B CRC64;

Query Match 25.5%; Score 26; DB 11; Length 22;
 Best Local Similarity 57.1%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 11 FKMFPEV 17
 ||| |
 Db 6 FSFPEI 12

RESULT 5
 ID 09QXN6 PRELIMINARY; PRT; 11 AA.
 AC 09QXN6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE INTERLEUKIN-2 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-129;
 RA Lyons P.A., Armitage N., Lord C.J., Denny P., Hill N.J., Podolin P.L.,
 RA Peterson L.B., Wicker L.S., Todd J.A.;
 RT "A 780 Kb physical map of proximal mouse chromosome 3 encompassing the
 RT type 1 diabetes locus, Id43";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF195955; AAF22748.1; -;
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1233 MW; AE23EC9CBB736D6 CRC64;

Query Match 23.5%; Score 24; DB 11; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 MYAMMIA 9
 ||:| | |
 Db 1 MYSMOLA 7

RESULT 6
 ID 09RGRL PRELIMINARY; PRT; 18 AA.
 AC 09RGRL;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ADHESIN (FRAGMENT).
 GN FHAB.
 OS Bordetella parapertussis.
 CC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 OC Bordetella.
 NCBI_TaxID=519;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-8234;
 RA Jacob-Dubuisson F., Kehoe B., Willery E., Reveneau N., Loch C.,
 RA Relman D.A.;
 RT "Molecular characterization of the Bordetella bronchiseptica
 RT filamentous hemagglutinin and its secretion machinery";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF111798; AAF21948.1; -;

FT NON_TER 18 18
 SO SEQUENCE 18 AA: 2135 MW: F129A793B031E143 CRC64;

Query Match 23.5%; Score 24; DB 2; Length 18;
 Best Local Similarity 20.0%; Pred. No. 2e+03;
 Matches 3; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 SNMYAMIMARFKMP 15
 :|:|:|:|:|:|
 Db 3 TNLVRLVFSHVGMP 17

RESULT 7

ID Q35556 PRELIMINARY; PRT; 21 AA.
 AC Q35556;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE HYPOTHETICAL 2.5 KDA PROTEIN.
 OS Pythium oligandrum.
 OC Mitochondrion.
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Pythium.
 NCBI_Taxid=41045;
 RN NCBI [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17-1;
 RA Martin F.N.;
 RL Curr. Genet. 27:0-0(0).
 DR EMBL: U28355; AAA70034.1; -
 KW Hypothetical protein; Mitochondrion.
 SO SEQUENCE 21 AA: 2491 MW: 88387AB7A5D4445E CRC64;

Query Match 23.5%; Score 24; DB 8; Length 21;
 Best Local Similarity 36.4%; Pred. No. 2.3e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 7 MIARFKMEPEV 17
 |:|:|:|:|:|:|
 Db 1 MIVFKIYGD I 11

RESULT 8

ID Q9J3U5 PRELIMINARY; PRT; 14 AA.
 AC Q9J3U5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE B-RAF PROTEIN (FRAGMENT).
 GN B-RAF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN NCBI [1]
 RP SEQUENCE FROM N.A.
 RA Barnier J.V., Papin C., Eyche A., Lecoc O., Calothy G.;
 RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-specific expression";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ276308; CAB81556.1; -
 FT NON_TER 14 14
 SO SEQUENCE 14 AA: 1748 MW: D1E0505C4A927F02 CRC64;

Query Match 22.5%; Score 23; DB 11; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 14 FPEVK 18
 |:|:|:|:|:|:|
 Db 4 FPEVE 8

RESULT 9

ID Q85673 PRELIMINARY; PRT; 17 AA.
 AC Q85673;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE REOVIRUS SEROTYPE 3 LI (FRAGMENT).
 OS Reovirus sp.
 OC Viruses; dsRNA viruses; Reoviridae; unclassified Reoviridae.
 NCBI_Taxid=10891;
 RN NCBI [1]
 RP SEQUENCE OF 1-6 FROM N.A.
 RX MEDLINE=82217029; PubMed=7086967;
 RA Kozak M.;
 RT "Sequences of ribosome binding sites from the large size class of reovirus mRNA";
 RL J. Virol. 42:467-473(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83017876; PubMed=6927854;
 RA Antczak J.B., Chmelo R., Pickup D.J., Joklik W.K.;
 RT "Sequence at both terminal of the 10 genes of reovirus serotype 3 (strain Dearling).";
 RL Virology 121:307-319(1982).
 DR EMBL: J02313; AAA47269.1; -
 FT NON_TER 17 17
 SO SEQUENCE 17 AA: 1929 MW: E36B60E136ZBA8F1 CRC64;

Query Match 22.5%; Score 23; DB 12; Length 17;
 Best Local Similarity 35.7%; Pred. No. 2.7e+03;
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 3 MYAMIMARFKMEPE 16
 |:|:|:|:|:|:|
 Db 1 MSMILTFQGPRIE 14

RESULT 10

ID Q00340 PRELIMINARY; PRT; 17 AA.
 AC Q00340;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL PROTEIN IN O2L 3 REGION (FRAGMENT).
 OS Vaccinia virus (strain L-1VP).
 OC Vaccines; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_Taxid=31531;
 RN NCBI [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L-1VP;
 RA Ryzankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,
 RA Mikryukov N.N., Gutovov V.V., Nikulin A.E., Kulichkov V.A.,
 RA Malugin E.G.;
 RT "Localization and determination of the nucleotide sequence of vaccinia virus genes coding for the proteins 36k and 12k";
 RL Dokl. Biochem. 247:780-787(1990).
 DR EMBL: X61166; CAB57393.1; -
 FT NON_TER 17 17
 SO SEQUENCE 17 AA: 2017 MW: 848F2A871E90FBC CRC64;

Query Match 22.5%; Score 23; DB 12; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 13 MPPEVKER 20
 Db 3 MYPEFARK 10

RESULT 11
 O9R4N5 PRELIMINARY; PRT; 18 AA.
 AC O9R4N5; (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE EXTRACETABLE ANTIGEN 1 (FRAGMENT).
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/staphylococcus group; Bacillus.
 OX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95247684; PubMed=7730281;
 RA Farcaus J.W., Ribot W.J., Downs M.B., Ezzell J.W.;
 RT "Purification and characterization of the major surface protein
 from the avirulent Bacillus anthracis Delta Sterne-1.";
 RL J. Bacteriol. 177:2481-2489(1995).
 SQ SEQUENCE 18 AA; 1926 MW; 1DBEBF0A4925EFB6 CRC64;

Query Match 22.5%; Score 23; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.9e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KMPEV 17
 Db 3 KTFPDV 8

RESULT 12
 O9R4W0 PRELIMINARY; PRT; 20 AA.
 AC O9R4W0; (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE 64 KRA HEAT SHOCK AND ALKALINE PH-INDUCED PROTEIN (FRAGMENT).
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 OC Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95012609; PubMed=7927682;
 RA Wu Y.L., Lee L.H., Rollins D.M., Chlung W.M.;
 RT "Heat shock- and alkaline pH-induced proteins of Campylobacter jejuni:
 RT characterization and immunological properties.";
 RL Infect. Immun. 62:4256-4260(1994).
 SQ SEQUENCE 20 AA; 2339 MW; 0DDE08352969DEA7 CRC64;

Query Match 22.5%; Score 23; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 3.2e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 9 ARKMPPEVKE 19
 Db 10 ARNKLYEGVKK 20

RESULT 13
 O05279 PRELIMINARY; PRT; 22 AA.
 AC O05279;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE HYPOTHETICAL 3.0 KDA PROTEIN.
 OS Chloranite-Aster yellow phytoplasma.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Molluscites;
 OC Achromatoplasma; Phytoplasma.
 OX NCBI_TaxID=54389;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carder J.H., Barbara D.J., Davies D.L., Clarke M.F.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U77617; AAB51346.1; -
 KW Hypothetical protein
 SQ SEQUENCE 22 AA; 2995 MW; B14DBEC1453B0F3 CRC64;

Query Match 22.5%; Score 23; DB 2; Length 22;
 Best Local Similarity 33.3%; Pred. No. 3.5e+03;
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 6 MFIARFMPPEV 17
 Db 1 MFIYVNLFPQI 12

RESULT 14
 O9S551 PRELIMINARY; PRT; 22 AA.
 AC O9S551;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE BETA-GALACTOSIDASE (FRAGMENT).
 GN LACZ.
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.
 OX NCBI_TaxID=715;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=4074;
 RC MEDLINE=99392473; PubMed=10463177;
 RA Schaller A., Kuhn R., Kuhnert P., Nicolet J., Anderson T.J.,
 RA MacInnes J.I., Segers R.P.A.M., Frey J.;
 RT "Characterization of aprIVA, a new RTX determinant of Actinobacillus
 RT pleuropneumoniae.";
 RL Microbiology 145:2105-2116(1999).
 DR EMBL: AF021919; AAD01699.1; -
 FT NON_TER
 SQ SEQUENCE 22 AA; 2849 MW; 762A86A651B6D3BB CRC64;

Query Match 22.5%; Score 23; DB 2; Length 22;
 Best Local Similarity 40.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 YAMMIRPKM 13
 Db 1 YRLMESEFKI 10

RESULT 15
 O62966 PRELIMINARY; PRT; 12 AA.
 AC O62966;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE INTERSTITIAL COLLAGENASE (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE-96408720; PubMed-8813727;
RA Rajakumar R.A., Quinn C.O.;
RT "Parathyroid hormone induction of rat interstitial collagenase mRNA in
  osteosarcoma cells is mediated through an AP-1-binding site.";
RL Mol. Endocrinol. 10:867-878(1996).
DR EMBL, U53605; AAB47407.1; -.
FT NON_TER
SQ SEQUENCE 12 AA; 1432 MW; 148A4DFE8AD720 CRC64;

Query Match
Best Local Similarity 21.6%; Score 22; DB 11; Length 12;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 MYAMMARFKMF 14
DB 1 MHSATLAFTEFF 12

RESULT 16
ID Q9UMW1 PRELIMINARY; PRT; 15 AA.
AC Q9UMW1:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
DE BENZOYL-COA LIGASE (FRAGMENT).
OS Methanospirillum hungatei.
OC Archaea; Euryarchaeota; Methanomicrobiales; Methanomicrobiaceae;
  Methanospirillum.
ON NCBL_TaxID-2203;
RN [1]
RP SEQUENCE.
RA Auburger G., Winter J.;
RL Appl. Microbiol. Biotechnol. 37:789-795(1992).
SQ SEQUENCE 15 AA; 1880 MW; D2972EF3B690AC5C CRC64;

Query Match
Best Local Similarity 21.6%; Score 22; DB 1; Length 15;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 12 KMFPE 16
DB 2 KLYPE 6

RESULT 17
ID Q35921 PRELIMINARY; PRT; 15 AA.
AC Q35921:
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
DE MITOCHONDRIAL ATPASE 6 (FRAGMENT).
ON TRENBL.
GN Saimo salar (Atlantic salmon).
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
  Protacanthopterygii; Salmoniformes; Salmonidae; Saimo.
ON NCBL_TaxID-8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE-95093530; PubMed-8000479;
RA Hardman G., Byrnes L., Peden J., Wolff J., Gannon F.;
RT Cloning and sequencing of the Atlantic salmon (Saimo salar)
  cytochrome c oxidase subunit iii gene (coxi3) and analysis of coxi3
  expression during parv-smolt transformation.";

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RL Mol. Mar. Biol. Biotechnol. 3:210-216(1994).
DR EMBL, L04502; AAA62410.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 15 AA; 1784 MW; 6BFA79B9E031C4BD CRC64;

Query Match
Best Local Similarity 21.6%; Score 22; DB 8; Length 15;
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 MYAMMARFKMF 15
DB 1 MIFLVLRMSDEP 13

RESULT 18
ID Q9UMJ9 PRELIMINARY; PRT; 16 AA.
AC Q9UMJ9:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
DE GALACTOSE-1-PHOSPHATE URIDYL TRANSFERASE (FRAGMENT).
GN GALT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBL_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Reichardt J.K.V.;
RT "The molecular genetic basis of galactosemia.";
RL Int. Pediatr. 8:110-113(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-95193790; PubMed-7887416;
RA Elias L.J., Langley S., Steele E., Evinger J., Fridovich-Kell J.L.,
  Brown A., Singh R., Fernhoff P., Hjelm L.N., Dembure P.P.;
RT "Galactosemia: a strategy to identify new biochemical phenotypes and
  molecular genotypes.";
RN Am. J. Hum. Genet. 56:630-639(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Elias L.J., II, Langley S., Paulk E.M., Hjelm L.N., Dembure P.P.;
RT "A molecular approach to galactosemia.";
RL Eur. J. Pediatr. Suppl. 2:21-27(1995).
DR EMBL, L46718; AAB59602.1; -.
KW Transferase.
FT NON_TER
SQ SEQUENCE 16 AA; 1832 MW; 312B633F6A3D8A52 CRC64;

Query Match
Best Local Similarity 21.6%; Score 22; DB 4; Length 16;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 RPKFPEV 17
DB 4 RLRALPEV 11

RESULT 19
ID Q9RLP2 PRELIMINARY; PRT; 20 AA.
AC Q9RLP2:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
DE PUTATIVE CYSTEINYL T-RNA SYNTHETASE (FRAGMENT).
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
ON NCBL_TaxID-485;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WR302;
RA Stein D.C., Gunn J.S.;
RT "Use of a non-selective transformation technique to construct a
RT multiple restriction-modification deficient mutant of Neisseria
RT gonorrhoeae";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U42459; AAD56389.1; -.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2245 MW; 4C893C704879FFD3 CRC64;

Query Match 21.6%; Score 22; DB 2; Length 20;
Best Local Similarity 38.5%; Pred. No. 4.7e+03;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 7 MIAFKMFPEVKE 19
Db 1 MTAIYNTLPKKE 13

RESULT 20
O9UK71 PRELIMINARY; PRT; 20 AA.
ID 09UK71
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE LITHIUM-SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1 (EC 3.1.3.25)
DE (FRAGMENT).
GN IMPA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Parthasarathy L., Parthasarathy R.;
RT "Molecular cloning, genomic organization and promoter analysis of the
RT human brain lithium-sensitive myo-inositol monophosphatase A1
RT isoenzyme";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178754; AAD52997.1; -.
DR HSSP; P29218; 1IMB.
KW Hydrolyase.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2257 MW; 067C2976A73D64A4 CRC64;

Query Match 21.6%; Score 22; DB 4; Length 20;
Best Local Similarity 57.1%; Pred. No. 4.7e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 YAMMIAR 10
Db 11 YAVTIAR 17

RESULT 21
O29341 PRELIMINARY; PRT; 20 AA.
ID 029341
AC 029341
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE NGF-INDUCIBLE PROTEIN TIS21 (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE=SMALL INTESTINE;
RA Minireoe A.K., Fredholm M., Davies W.;
RL Mamm. Genome 7:509-517(1996).
DR EMBL; F14751; CAA23227.1; -.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2058 MW; DEC82EC21D641A0 CRC64;

Query Match 21.6%; Score 22; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 RFKMFPEV 17
Db 3 RFDMLPEI 10

RESULT 22
O9TRCO PRELIMINARY; PRT; 20 AA.
ID 09TRCO
AC 09TRCO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ENTEROTOXIN-BINDING GLYCOPROTEIN P16K (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA MEDLINE=94259890; PubMed=8201051;
RA Shida K., Takamizawa K., Nagaoka M., Kushi A., Osawa T., Tsuji T.;
RT "Enterotoxin-binding glycoproteins in a protease-peptone fraction of
RT heated bovine milk.";
RL J. Dairy Sci. 77:930-939(1994).
DR HSSP; P00711; 1HFZ.
SQ SEQUENCE 20 AA; 2321 MW; C738FD14F55C74C3 CRC64;

Query Match 21.6%; Score 22; DB 6; Length 20;
Best Local Similarity 25.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 8 IAFKMFPEVKE 19
Db 3 LTKXEVFRELKD 14

RESULT 23
O9XSLS PRELIMINARY; PRT; 21 AA.
ID 09XSLS
AC 09XSLS;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ALPHA S2-CASEIN (FRAGMENT).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Velturi C., Pilla F., Lagoniagro R.;
RT "A new allele of goat alpha s2-casein.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ242728; CAB44433.2; -.
FT NON_TER 1
SQ SEQUENCE 21 AA; 21

```


SO SEQUENCE 21 AA: 2591 MW: A608995532CA3098 CRC64;

Query Match 21.6%; Score 22; DB 6; Length 21;

Best Local Similarity 33.3%; Pred. No. 4.9e+03;

Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 8 IAREKMEPEVK 19

DB 10 ISRRKRIWPIFE 21

RESULT 24

O92E05 PRELIMINARY; PRT; 24 AA.

AC O92E05;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DE PORA PROTEIN (FRAGMENT).

GN PORA.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OY NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-19/92;

RA Wedge E., Caugant D.A., Musacchio A., Saunders N.B., Zollinger W.D.;

RT *Specificities of reference monoclonal antibodies and human

RT postvaccination sera with meningococcal P1.19,15 outer membrane

RT proteins.";

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ012727; CA10150.1; -.

FT NON_TER 1 24

FT NON_TER 24

SO SEQUENCE 24 AA: 2743 MW: 260BA0002923D9F6 CRC64;

Query Match 21.6%; Score 22; DB 2; Length 24;

Best Local Similarity 55.6%; Pred. No. 5.6e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 REKMEPEVK 18

DB 10 RSKSQPOVK 18

RESULT 25

O9XBK2 PRELIMINARY; PRT; 24 AA.

AC O9XBK2;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE TRANSLATION ELONGATION FACTOR TS (EF-TS) (FRAGMENT).

GN TSF.

OS Bacillus cereus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OY NCBI_TaxID=1396;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 10987;

RX MEDLINE-99231848; PubMed-10217496;

RT "Genome organization is not conserved between Bacillus cereus and

RT Bacillus subtilis.";

RL Microbiology 145:621-631(1999).

DR EMBL; AJ010135; CAB40592.1; -.

FT NON_TER 24

SO SEQUENCE 24 AA: 2671 MW: F1AB99BFEB5DDABD CRC64;

Query Match 21.6%; Score 22; DB 2; Length 24;

Best Local Similarity 44.4%; Pred. No. 5.6e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 12 KMEPEYKER 20

DB 6 QWVKELREK 14

Search completed: February 5, 2001, 10:55:22
 Job time: 911 sec

PS Claim 11; Page 9; 12pp; German.
 CC W18842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 CC
 CC Sequence 20 AA;
 SO
 Query Match 100.0%; Score 102; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNMYAMTARFKMPEVKEK 20
 DB 1 smymammarfkmpkevkek 20
 RESULT 2
 ID W01794 standard; peptide; 20 AA.
 XX W01794;
 AC
 XX
 AC
 XX
 AC
 XX
 DT 15-OCT-1997 (first entry)
 XX
 DE Human 65 kD glutamine decarboxylase peptide.
 KW Human; glutamine decarboxylase; GAD; diagnosis; predisposition;
 KW tumour; immunological; disease; autoimmune; diabetes; reagent;
 KW determination; T cell; subpopulation; medication; treatment;
 KW prevention; production; antigen; immunogen; tolerogen; isolation;
 KW reinjection; inactivation.
 KW
 XX Homo sapiens.
 OS
 XX
 PN DE19525784-A1.
 XX
 PD 16-JAN-1997.
 XX
 XX 14-JUL-1995; 95DE-1025784.
 XX
 XX 14-JUL-1995; 95DE-1025784.
 XX
 XX 14-JUL-1995; 95DE-1025784.
 XX
 XX (BOE) BOEHRINGER MANNHEIM GMBH.
 PA
 PI Albert W, Boltard C, Endl J, Jung G, Schendel D;
 PI Stahl P, Van Endert P;
 PI
 XX
 XX WPI: 1997-078452/08.
 DR
 XX
 PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of
 PT diabetes, etc.
 PT
 PS Claim 1; Page 12; 15pp; German.
 XX
 CC The present peptide is a fragment of the human 65 kD glutamine
 CC decarboxylase (GAD), which can be used to diagnose, or diagnose a
 CC predisposition to, a tumour or immunological disease, preferably an
 CC autoimmune disease, especially diabetes. It can also be used as a
 CC reagent to determine specific T cell subpopulations, in medicaments
 CC to treat or prevent immunological diseases, preferably autoimmune
 CC diseases, especially diabetes; to produce antigens, especially
 CC immunogens or tolerogens and to isolate specific T cell
 CC subpopulations, which can be used to produce antigens or for
 CC reinjection, optionally after inactivation.

XX
 SO Sequence 20 AA;
 Query Match 100.0%; Score 102; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNMYAMTARFKMPEVKEK 20
 DB 1 smymammarfkmpkevkek 20
 RESULT 3
 ID R72277 standard; Peptide; 20 AA.
 XX R72277;
 AC
 XX R72277;
 AC
 XX
 DT 13-NOV-1995 (first entry)
 XX
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX
 XX Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KW insulin-dependant diabetes mellitus; stiff man disease.
 KW
 XX Homo sapiens.
 OS
 XX
 PN W09507992-A.
 XX
 PD 23-MAR-1995.
 XX
 XX 24-AUG-1994; 94WO-US09478.
 XX
 XX 17-SEP-1993; 93US-0123859.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
 PI
 XX WPI: 1995-131360/17.
 DR
 XX
 PT New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hydridoma(s) etc.
 PT
 PS Claim 1; Page 76; 100pp; English.
 XX
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72296 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependant diabetes mellitus or stiff man disease.
 CC
 CC Sequence 20 AA;
 SO
 Query Match 96.1%; Score 98; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NMVAMTARFKMPEVKEK 20
 DB 1 nmymammarfkmpkevkek 19
 RESULT 4
 ID Y59541 standard; peptide; 20 AA.
 XX Y59541;
 AC Y59541;

```
XX 03-APR-2000 (first entry)
DT GAD65 fragment, peptide #17.
XX
DE GAD65 fragment, peptide #17.
XX
KM GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
XX therapy.
XX
OS Homo sapiens.
XX
PN US9598366-A.
XX
PD 07-DEC-1999.
XX
PF 09-APR-1997; 97US-0827618.
XX
PR 07-JUN-1995; 95US-0485725.
PR 21-SEP-1990; 90US-0586536.
PR 18-JUN-1991; 91US-0716909.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
PI Tobin AJ, Kaufman DL, Erlander MG;
XX
DR WPI; 2000-095930/08.
XX
PT Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders such as insulin dependent diabetes mellitus and Stiff man
PS disease -
XX
PS Claim 1; Column 33; 61pp; English.
XX
CC This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and Stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunosays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.
XX
SQ Sequence 20 AA;

Query Match 96.1%; Score 98; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMYAMMIARFKMPEVKEK 20
DB 1 nmyammiarfkmpfvkex 19

RESULT 5
ID Y59577 standard; peptide; 20 AA.
XX
AC Y59577;
XX
DT 03-APR-2000 (first entry)
XX
DE GAD65 fragment, peptide #17.
XX
KM GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
XX therapy.
XX
OS Homo sapiens.
XX
```

```
PN US9598366-A.
XX
XX 07-DEC-1999.
XX
XX 09-APR-1997; 97US-0827618.
XX
PR 07-JUN-1995; 95US-0485725.
PR 21-SEP-1990; 90US-0586536.
PR 18-JUN-1991; 91US-0716909.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
PI Tobin AJ, Kaufman DL, Erlander MG;
XX
XX WPI; 2000-095930/08.
XX
XX Ameliorating glutamic acid decarboxylase associated autoimmune
XX disorders such as insulin dependent diabetes mellitus and Stiff man
XX disease -
XX
XX Example 11; Column 42; 61pp; English.
XX
XX This sequence represents a fragment of the glutamic acid decarboxylase 65
XX (GAD65) protein. The invention relates to a method of ameliorating GAD
XX associated autoimmune disorders by administering a GAD65 peptide to the
XX patient. The method can be used for ameliorating GAD associated
XX autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
XX and Stiff man disease. GAD65 can also be useful for screening drugs that
XX alter GAD function, for generating monoclonal antibodies and in
XX immunosays. GAD65 is an effective diagnostic tool for predicting IDDM
XX and the diagnosis is quite easy. It is also possible to obtain much
XX larger quantities of polypeptide via recombinant techniques than are
XX available from natural sources.
XX
SQ Sequence 20 AA;

Query Match 96.1%; Score 98; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMYAMMIARFKMPEVKEK 20
DB 1 nmyammiarfkmpfvkex 19

RESULT 6
ID W10300 standard; peptide; 20 AA.
XX
AC W10300;
XX
DT 11-SEP-1997 (first entry)
XX
DE Mammalian GAD 65 peptide.
XX
KM Soluble; fusion; major histocompatibility complex; MHC;
KW heterodimer; complex; GAD 65; antigen; binding groove; tolerance;
KW autoantigen; disease; insulin dependent; diabetes mellitus; IDDM;
KW antagonist; T cell; energy; presenting cell.
XX
OS Mammalian spp.
XX
XX WO9640944-A2.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US10102.
XX
XX 27-OCT-1995; 95US-0005964.
XX
XX 07-JUN-1995; 95US-0480002.
XX
XX 07-JUN-1995; 95US-0482133.
XX
XX 07-JUN-1995; 95US-0483241.
```

XX (ANER-) ANERGEN INC.
 PA (ZIMO) ZYMOGENETICS INC.
 XX Deshpande S, Gross JA, Kindvogel W, Reich EP, Sheppard PO;
 PI WPI; 1997-052337/05.
 DR
 XX Novel fused major histocompatibility complex:antigenic peptide
 PT complex - useful to induce tolerance to an autoantigen-related
 PT disease e.g. insulin-dependent diabetes mellitus
 XX
 PS Claim 10; Page 110; 142pp; English.
 XX
 CC A novel soluble fused major histocompatibility complex (MHC)
 CC heterodimer:peptide complex, comprises DNA encoding 1st and 2nd
 CC MHC domains, linked by DNA encoding a 5-25 residue linker, and a
 CC DNA encoding an antigenic peptide able to associate with a peptide
 CC binding groove of the MHC molecule, e.g. the present peptide,
 CC linked in frame to the DNA encoding the 2nd domain by a DNA
 CC encoding a 5-25 residue linker. The complex can be used to induce
 CC immunological tolerance in adults susceptible to, or suffering from
 CC an autoimmune related disease, e.g. insulin dependent diabetes
 CC mellitus (IDDM), by antagonising the binding of particular T cells
 CC and antigen presenting cells, to induce energy (immunological
 CC non-responsiveness) in the targeted T cell. As the heterodimers and
 CC corresponding antigen are permanently linked into a single chain,
 CC obviating the requirement for complex heterodimer truncation or
 CC formation, the complex eliminates inefficient and non-specific
 CC peptide loading.
 CC
 SO Sequence 20 AA;

Query Match 76.5%; Score 78; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.1e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNMYAMMTARFKMP 15
 ID 6 snmyammtarfkmp 20

RESULT 7
 R76653
 ID R76653 standard; peptide; 14 AA.
 XX
 AC R76653;
 XX
 DT 05-MAR-1996 (first entry)
 XX
 DE Peptide derived from human glutamic acid decarboxylase 12.
 XX
 KW diabetes; T-cell subpopulation; detection; antigen production;
 KW diagnosis; autoimmune disease.
 XX
 OS Homo sapiens.
 XX
 PN DE4418091-A1.
 PD 27-JUL-1995;
 XX
 PE 24-MAY-1994; 94DE-4418091.
 XX
 PR 04-FEB-1994; 94DE-4403522.
 PR 20-JAN-1994; 94DE-4401629.
 XX
 PA (ENDL/) ENDL J.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Albert W, Dormair K, Endl J, Jung G, Meinel E;
 PI Stahl P, Schendel D;
 XX

DR WPI; 1995-264505/35.
 XX
 XX Antigen-specific activated T-lymphocytes and their detection - by
 PT interaction with inventive peptide(s) of peptide-MHC complexes;
 PT useful in diagnosis of e.g. diabetes and autoimmune diseases
 XX
 PS Claim 1; Fig 2; 21pp; German.
 XX
 CC R76642-62 are derived from human glutamic acid decarboxylase and
 CC specifically react with T-cell sub-populations isolated from recently
 CC diagnosed Type-I diabetics. Pharmaceutical compans. contg. these
 CC peptides and those shown in R77571-72, are useful for the diagnosis of
 CC a disease or predispositions of immune system diseases, tumours, and
 CC autoimmune diseases, including diabetes. The peptides are able to detect
 CC specific T-cell subpopulations that are then used for antigen prodn.,
 CC e.g. by reinjection.
 CC
 SO Sequence 14 AA;

Query Match 72.5%; Score 74; DB 16; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMVAMMTARFKMP 15
 ID 1 nmvammtarfkmp 14

RESULT 8
 W18861
 ID W18861 standard; peptide; 14 AA.
 XX
 AC W18861;
 XX
 DT 05-JAN-1998 (first entry)
 XX
 DE 65 kD Glutamic acid decarboxylase peptide fragment 12.
 XX
 KW GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
 KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
 KW predisposition; autoimmune; tumour; rheumatoid arthritis;
 KW multiple sclerosis.
 XX
 OS Synthetic.
 XX
 PN DE19526561-A1.
 PD 23-JAN-1997.
 XX
 PE 20-JUL-1995; 95DE-1026561.
 XX
 PR 20-JUL-1995; 95DE-1026561.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;
 PI Pozzilli P, Stahl P;
 PI WPI; 1997-088254/09.
 DR
 XX
 PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
 PT involving intradermal admin. of auto-reactive substances
 XX
 PS Claim 11; Fig 2; 12pp; German.
 XX
 CC W18842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive

CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 XX

SO Sequence 14 AA:

Query Match 72.5%; Score 74; DB 18; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMYAMMARRKMF 15
 |||||
 Db 1 nmyammarrkmp 14

RESULT 9
 R29627
 ID R29627 standard: peptide; 23 AA.

XX R29627;

DT 05-MAY-1993 (first entry)

XX GAD peptide.

XX Glutamic acid decarboxylase; auto immune disease; insulin dependent;
 KW diabetes mellitus; drug screening; antibody; stiff man syndrome.
 XX

OS Synthetic.

XX Key Location/Qualifiers

FT Msc-difference 15 /label= Thr, Glu

XX EP519469-A.

XX 23-DEC-1992.

XX 17-JUN-1992; 92EP-0110308.

XX 18-JUN-1991; 91US-0716909.

XX (REGC) UNIV CALIFORNIA.

XX Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;

XX WPI; 1992-425701/52.

PT Glutamic acid decarboxylase isolated polypeptide(s) - useful for
 PT diagnosis and treatment of auto-immune diseases, e.g. insulin
 PT dependent diabetes mellitus, drug screening and antibody prodn.

XX Claim 6; Page 20; 35pp; English.

CC The peptide corresponds to a glutamic acid decarboxylase (GAD 65)
 CC sequence and may be used for the detection of autoantibodies to GAD
 CC 65. They can also be used for screening drugs such as those that
 CC alter GAD function and for generation of antibodies which can be
 CC used to detect GAD 65. Such methods can be used in the diagnosis
 CC and therapy of autoimmune diseases such as insulin dependent
 CC diabetes mellitus and "stiff man" syndrome. The polypeptide can be
 CC used to bind or block the continuance of an autoimmune response to
 CC GAD 65. It may also be coupled to therapeutic agents and used
 CC immunotherapeutically. See also R29625-9.

XX Sequence 23 AA:

Query Match 72.5%; Score 74; DB 13; Length 23;
 Best Local Similarity 93.8%; Pred. No. 5.6e-07;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 AMMIARRKMFPEVK 20
 |||||
 Db 1 ammiarrkmpvkvk 16

RESULT 10
 W35531
 ID W35531 standard: peptide; 13 AA.

XX W35531;

DT 22-APR-1998 (first entry)

XX Glutamic acid decarboxylase peptide GAD65 253-265.

XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
 KW scaffold; inhibition; metastasis; wound healing; solid phase.
 XX

OS Unidentified.

XX W09738011-A1.

PD 16-OCT-1997.

PF 03-APR-1997; 97WO-DE00146.

XX 03-APR-1996; 96DK-0000398.

XX (PEPR-) PEPRSEARCH AS.

XX Heegaard PMH, Jakobsen PH;

XX WPI; 1997-512645/47.

XX Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PT derivatives

XX Example 27; Page 150; 262pp; English.

CC A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and
 CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence
 CC represents a peptide used in an example from the present invention. An
 CC (A)-solid phase complex can be used as a scaffold for the production of
 CC chemical derivatives, characterised by covalently attaching molecules at
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for
 CC the incorporation into an immunostimulating Complex (Iscom) resulting an
 CC (A)-Iscom complex which is used for the chemical coupling of antigenic
 CC substances in an aqueous solution by conjugation. (A) derivatised with
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like
 CC binding activities can be used for the promotion of cell-attachment to
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
 CC and for promotion of wound healing. Also a derivatised (A) can be used
 CC for the selection of specifically-binding aptamers or as a diagnostic
 CC agent. Such diagnostic (A) molecules could be used to detect molecules
 CC derived from or indicative of pregnancy or of a disease, such as an
 CC infectious, autoimmune or cancerous disease.

XX Sequence 13 AA:

Query Match 64.7%; Score 66; DB 18; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.5e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 IARRKMFPEVK 20
 |||||
 Db 1 iarrkmpvkvk 13

RESULT 11
R29626
XX R29626 standard; peptide; 24 AA.
AC R29626;
XX
XX 05-MAY-1993 (first entry)
XX
XX GAD peptide.
XX
XX Glutamic acid decarboxylase; auto immune disease; insulin dependent;
XX diabetes mellitus; drug screening; antibody; stiff man syndrome.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 15
XX FT /label= Thr, Glu
XX
XX EP519469-A.
XX
XX 23-DEC-1992.
XX
XX 17-JUN-1992; 92EP-0110308.
XX
XX 18-JUN-1991; 91US-0716909.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Clare-Salzler MJ, Erlender MG, Kaufman DL, Tobin AJ;
XX WPI: 1992-425701/52.
XX
XX Glutamic acid decarboxylase isolated polypeptide(s) - useful for
XX diagnosis and treatment of auto-immune diseases, e.g. insulin
XX dependent diabetes mellitus, drug screening and antibody prodn.
XX
XX Claim 5; Page 20; 35pp; English.
XX
XX The peptide corresponds to a glutamic acid decarboxylase (GAD 65)
XX sequence and may be used for the detection of autoantibodies to GAD
XX 65. They can also be used for screening drugs such as those that
XX alter GAD function and for generation of antibodies which can be
XX used to detect GAD 65. Such methods can be used in the diagnosis
XX and therapy of autoimmune diseases such as insulin dependent
XX diabetes mellitus and "stiff man" syndrome. The polypeptide can be
XX used to bind or block the continuance of an autoimmune response to
XX GAD 65. It may also be coupled to therapeutic agents and used
XX immunotherapeutically. See also R29625-9.
XX
XX Sequence 24 AA:
SQ
Query Match 52.0%; Score 53; DB 13; Length 24;
Best Local Similarity 62.5%; Pred. No. 0.0038;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

XX Proteolipoprotein; PLP; autoantigen; regulatory memory T cell;
XX inhibitory cytokine secretion; inflammatory cytokine secretion;
XX autoimmune disease; multiple sclerosis; juvenile diabetes;
XX rheumatoid arthritis.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "acylated with two n-capric acids, two
XX FT n-caprylic acids or with two n-lauric acids"
XX
XX W09937315-A1.
XX
XX 29-JUL-1999.
XX
XX 27-JAN-1999; 99WO-US01884.
XX
XX 16-OCT-1998; 98US-0104663.
XX 27-JAN-1998; 98US-0072702.
XX 25-JUN-1998; 98US-0090677.
XX
XX (BAIJ/) BAI J P..
XX
XX Bal JP;
XX
XX WPI: 1999-478981/40.
XX
XX New conjugates of autoantigens, fragments or analogs with fatty
XX acids, used for treating autoimmune disease, e.g. juvenile diabetes,
XX multiple sclerosis and rheumatoid arthritis
XX
XX Example 15; Page 42; 68pp; English.
XX
XX The present sequence represents a peptide analogue of glutamic acid
XX decarboxylase (GAD), an autoantigen. The sequence is used in the
XX conjugates of the invention. The specification describes a conjugate,
XX comprising an autoantigen, an immune-reactive peptide fragment of an
XX autoantigen, or their analogues, and at least one fatty acid. The
XX conjugates induce regulatory memory T cells and enhance the secretion of
XX inhibitory cytokines and suppress the secretion of inflammatory
XX cytokines. The conjugates also stimulate in vitro proliferation of
XX mammalian T lymphocytes. The conjugates can be used for ameliorating
XX autoimmune disease, e.g. multiple sclerosis, juvenile diabetes or
XX rheumatoid arthritis. They can be used for treating e.g. colitis,
XX systemic lupus erythematosus, dermatomyositis, Sjogren's syndrome,
XX erythematous, erythema nodosum, Takayasu's arteritis, myasthenia gravis,
XX Addison's disease, sarcoidosis, ulcerative colitis, erythema multiforme,
XX IgA nephropathy, polyarteritis nodosa, ankylosing spondylitis,
XX gonopasture's syndrome, thromboangitis obliterans, Sjogren's syndrome,
XX primary biliary cirrhosis, thyrotoxicosis, scleroderma, myocarditis,
XX chronic active hepatitis, polymyositis/dermatomyositis, polychondritis,
XX pemphigus vulgaris, idiopathic thrombocytopenia, Wegener's
XX granulomatosis, membranous nephropathy, amyotrophic lateral sclerosis,
XX tabes dorsalis, giant cell arteritis/polymyalgia, pernicious anemia,
XX rapidly progressive glomerulonephritis, or fibrosing alveolitis.
XX
XX Sequence 9 AA:
SQ
Query Match 36.3%; Score 37; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
Y30061
XX Y30061 standard; peptide; 9 AA.
XX
XX Y30061;
XX
XX 08-OCT-1999 (first entry)
XX
XX Peptide analogue of glutamic acid decarboxylase (GAD).
XX

RESULT 13
Y99016
XX Y99016 standard; Peptide; 15 AA.
XX

KW Soluble; fusion: major histocompatibility complex: MHC;
 KW heterodimer; complex; GAD 65; antigen; binding groove; tolerance;
 KW autoantigen; disease; insulin dependent; diabetes mellitus; IDDM;
 KW antagonist; T cell; energy; presenting cell.
 OS Mammalian spp.
 XX
 XX WO9640944-A2.
 PN 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96MO-US10102.
 PF
 XX 27-OCT-1995; 95US-0005964.
 PR 07-JUN-1995; 95US-0480002.
 PR 07-JUN-1995; 95US-0482133.
 PR 07-JUN-1995; 95US-0483241.
 XX
 XX (ANER-) ANERGEN INC.
 PA (ZIMO) ZIMOGENETICS INC.
 PI
 XX Deshpande S, Gross JA, Kindsvogel W, Reich EP, Sheppard PO;
 DR WPI; 1997-052337/05.
 XX
 PT Novel fused major histocompatibility complex:antigenic peptide
 PT complex - useful to induce tolerance to an autoantigen-related
 PT disease e.g. insulin-dependent diabetes mellitus
 PS
 XX Claim 10: Page 109; 142pp; English.
 CC A novel soluble fused major histocompatibility complex (MHC)
 CC heterodimer:peptide complex, comprises DNA encoding 1st and 2nd
 CC MHC domains, linked by DNA encoding a 5-25 residue linker, and a
 CC DNA encoding an antigenic peptide able to associate with a peptide
 CC binding groove of the MHC molecule, e.g. the present peptide,
 CC linked in frame to the DNA encoding the 2nd domain by a DNA
 CC encoding a 5-25 residue linker. The complex can be used to induce
 CC immunological tolerance in adults susceptible to, or suffering from
 CC an autoantigen related disease, e.g. insulin dependent diabetes
 CC mellitus (IDDM), by antagonising the binding of particular T cells
 CC and antigen presenting cells, to induce anergy (immunological
 CC non-responsiveness) in the targeted T cell. As the heterodimers and
 CC corresponding antigen are permanently linked into a single chain,
 CC obviating the requirement for complex heterodimer truncation or
 CC formation, the complex eliminates inefficient and non-specific
 CC peptide loading.
 CC
 CC
 CC Sequence 11 AA:
 SO
 XX
 XX
 QY 1 SNMYAM 6
 Db 6 snmyam 11
 DB
 RESULT 16
 R72276
 ID R72276 standard; Peptide; 20 AA.
 XX
 AC R72276;
 XX
 DT 13-NOV-1995 (first entry)
 XX
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX
 KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KW insulin-dependant diabetes mellitus; stiff man disease.
 XX
 PT

OS Homo sapiens.
 XX
 XX WO9507992-A.
 PN 23-MAR-1995.
 PD
 XX 24-AUG-1994; 94MO-US09478.
 PF
 XX 17-SEP-1993; 93US-0123859.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Cläre-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
 PI WPI; 1995-131360/17.
 DR
 XX
 PT New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hydridoma(s) etc.
 PS
 XX Example 11; Page 76; 100pp; English.
 CC
 CC 086481 and 086482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependant diabetes mellitus or stiff man disease.
 CC
 CC
 CC Sequence 20 AA:
 SO
 XX
 QY 1 SNMYAM 6
 Db 15 snmyam 20
 DB
 RESULT 17
 R72278
 ID R72278 standard; Peptide; 20 AA.
 XX
 AC R72278;
 XX
 DT 13-NOV-1995 (first entry)
 XX
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX
 KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KW insulin-dependant diabetes mellitus; stiff man disease.
 XX
 OS Homo sapiens.
 XX
 XX WO9507992-A.
 PN 23-MAR-1995.
 PD
 XX 24-AUG-1994; 94MO-US09478.
 PF
 XX 17-SEP-1993; 93US-0123859.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Cläre-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
 PI WPI; 1995-131360/17.
 DR
 XX
 PT New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT

PT dependent diabetes, also related nucleic acid, vectors,
PT antibodies, hydridoma(s) etc.
XX
PS Example 11; Page 76; 100pp; English.
XX
CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
CC acid decarboxylase (GAD65) respectively, from which the GAD65
CC fragments described in R72261-R72298 were derived. These fragments
CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC and treat GAD-related autoimmune disorders, such as insulin
CC dependant diabetes mellitus or stiff man disease.
XX
SQ Sequence 20 AA:
SO
Query Match 30.4%; Score 31; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 PEVEXK 20
| | | | |
Db 1 pevexk 6
RESULT 18
Y59576
ID Y59576 standard; peptide: 20 AA.
XX
AC Y59576;
XX
DT 03-APR-2000 (first entry)
XX
DE GAD65 fragment, peptide #16.
XX
KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN US5998366-A.
XX
PD 07-DEC-1999.
XX
PF 09-APR-1997; 97US-0827618.
XX
PR 07-JUN-1995; 95US-0485725.
PR 21-SEP-1990; 90US-0586536.
PR 18-JUN-1991; 91US-0716909.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tobin AJ, Kaufman DL, Erlander MG;
XX
DR WPI; 2000-095930/08.
XX
PT Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders such as insulin dependent diabetes mellitus and stiff man
PT disease -
XX
PS Example 11; Column 42; 61pp; English.
XX
CC This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.

XX
SQ Sequence 20 AA;
XX
Query Match 30.4%; Score 31; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNMYAM 6
| | | | |
Db 15 snmyam 20
RESULT 19
Y59578
ID Y59578 standard; peptide: 20 AA.
XX
AC Y59578;
XX
DT 03-APR-2000 (first entry)
XX
DE GAD65 fragment, peptide #18.
XX
KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
PN US5998366-A.
XX
PD 07-DEC-1999.
XX
PF 09-APR-1997; 97US-0827618.
XX
PR 07-JUN-1995; 95US-0485725.
PR 21-SEP-1990; 90US-0586536.
PR 18-JUN-1991; 91US-0716909.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tobin AJ, Kaufman DL, Erlander MG;
XX
DR WPI; 2000-095930/08.
XX
PT Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders such as insulin dependent diabetes mellitus and stiff man
PT disease -
XX
PS Example 11; Column 42; 61pp; English.
XX
CC This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.
XX
SQ Sequence 20 AA;
XX
Query Match 30.4%; Score 31; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 PEVEXK 20
| | | | |
Db 1 pevexk 6

RESULT 20
 Y57065
 ID Y57065 standard; peptide; 20 AA.
 XX
 AC Y57065;
 XX
 DT 28-FEB-2000 (first entry)
 XX
 DE Glutamate decarboxylase peptide GAD p18.
 XX
 KW Neglected target tissue antigen; NTFA; autoimmunity; autoimmune response;
 KW Immunotherapeutic agent; Insulin dependent diabetes mellitus;
 KW Multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
 KW uveoretinitis; inflammatory response.
 XX
 OS Homo sapiens.
 XX
 PN W09956763-A1.
 PD 11-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-US10250.
 XX
 PR 07-MAY-1998; 98US-0084636.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Kaufman DL, Tian J, Olcott A;
 XX
 DR WPI: 2000-052905/04.
 XX
 PT Administration of neglected target tissue antigens to modulate immune
 PT responses
 XX
 PS Disclosure: Page 23; 79pp; English.
 XX
 CC Amino acid sequences Y57063-Y57091 are examples of neglected target
 CC tissue antigens NTFA. NTFA are antigens (whole antigens or fragments)
 CC not involved in autoimmunity. These peptides and proteins are used in the
 CC method of the invention which involves administering an NTFA as an
 CC antigen based immunotherapeutic agent, to a host afflicted with an
 CC autoimmune response associated with an autoimmune disease. The
 CC immunotherapeutic agent is used to treat autoimmune diseases such as
 CC insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
 CC thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal inflammatory
 CC immune responses. The NTFA induces regulatory tolerance by elicitation of
 CC regulatory T cells among T cells recognizing the NTFA but not
 CC participating in the immune response. The NTFA are capable of recognition
 CC by substantial populations of uncommitted T cells which can be primed, or
 CC biased, towards regulatory responses to provide effective treatment. The
 CC NTFA are effective in regulating undesirable immune responses even when
 CC target determinants used as agents promoting tolerance agents have failed
 CC to induce an effective regulatory T cell response. NTFA as agents
 CC promoting tolerance are anticipated to be safer than use of target
 CC determinants.
 CC
 XX
 SQ Sequence 20 AA:
 Query Match: 30.4%; Score 31; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 15 PEVKEK 20
 |||||
 Db 1 pevkek 6
 RESULT 21
 R43871
 ID R43871 standard; Protein; 14 AA.

XX
 AC R43871;
 XX
 DT 23-DEC-1993 (first entry)
 XX
 DE OmpA2-R-7 signal peptide.
 XX
 KW Polypeptide; antibodies; HTLV; AIDS; vaccine.
 XX
 OS Human T-cell lymphotropic virus.
 XX
 PN EP552850-A.
 PD 28-JUL-1993.
 XX
 PF 10-OCT-1985; 85EP-0307260.
 XX
 PR 10-OCT-1984; 84US-0659339.
 PR 23-JAN-1985; 85US-0693866.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Chang NT, Gallo RC, Wong-staal F;
 XX
 DR WPI: 1993-236543/30.
 DR N-PSDB: Q45924.
 XX
 PT Cloning and expression of new HTLV-III DNA - used to obtain
 PT polypeptide(s) and antibodies for diagnosis, prevention and
 PT treatment of HTLV-III infection, partic. AIDS
 XX
 PS Disclosure: Figure 6a; 31pp; English.
 XX
 CC A fragment of DNA approximately 200-500 base pairs in length is
 CC ligated into a recombinant vector (ompA1-R-6; ompA2-R-7 or ompA3-R-3)
 CC and used to transform E.coli. These cells then express a polypeptide
 CC which is immunoreactive with HTLV-III-specific antibody. The
 CC HTLV-III polypeptides can be used for the production
 CC of antibodies, in immunoassays for the detection of HTLV-
 CC III-specific antibodies and in vaccines for the prevention of AIDS.
 CC The antibodies can also be used to detect HTLV-III polypeptides.
 CC
 XX
 SQ Sequence 14 AA:
 Query Match: 29.4%; Score 30; DB 14; Length 14;
 Best Local Similarity 54.5%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 OY 9 ARKKPEVKE 19
 | | | | |
 Db 4 aeftpikvke 14
 RESULT 22
 R96007
 ID R96007 standard; peptide; 15 AA.
 XX
 AC R96007;
 XX
 DT 19-FEB-1997 (first entry)
 XX
 DE Nuclear localisation signal.
 XX
 KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SPI;
 KW TAPA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
 virus.
 XX
 OS Synthetic.
 XX
 PN W09617956-A2.

XX 13-JUN-1996.
 XX
 PD 07-DEC-1995; 95WO-US15944.
 PF
 XX 09-DEC-1994; 94US-0353476.
 PR
 XX (GENE-) GENE POOL INC.
 PA
 XX Weininger AM, Weininger S;
 PI
 XX WPI; 1996-287199/29.
 DR
 XX Probe nucleic acids, target binding assemblies, etc - for detection
 PT and localisation of specific nucleic acid sequences, esp. HIV and
 PT HPV
 PS
 XX Claim 23; Page 114; 172pp; English.
 CC This sequence represents a nuclear localisation sequence of a target
 CC binding assembly (TBA) of the invention. The TBA is recognised by the
 CC target binding region (TBR) of a probe of the invention. The probe of
 CC the invention contains a TBR, a booster binding region (BBR), and an
 CC optional support or attachment (OSA). The TBA contains at least one
 CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an
 CC assembly sequence, an asymmetry sequence, a nuclear localisation signal
 CC sequence, and an OSA. The assembly sequence and asymmetry sequences are
 CC responsible for the folding and association of the NARs. The NARs are
 CC selected from NF-kappa-B, SPI, TARA, human papillomavirus (HPV) E2, HPV
 CC LTR, human immunodeficiency virus (HIV) LTR and Tat binding units. The
 CC linker sequence is an oligopeptide, which does not interfere with NAR
 CC function, but provides stability and control over the spacing of the NAR
 CC from the rest of the TBA. The OSA is an attached support or indicator,
 CC or other means of localisation of the probe. The probe can be used in a
 CC method for detecting or localising a specific target nucleic acid
 CC sequence (TNA). The method is highly sensitive, and has a high degree of
 CC specificity. The method can be used for detecting specific nucleic acid
 CC sequences, including those found in human cells, in HIV, HPV, and other
 CC nucleic acid containing systems, including bacteria and viruses.
 CC
 SQ Sequence 15 AA;
 XX
 XX
 Query Match 29.4%; Score 30; DB 17; Length 15;
 Best Local Similarity 57.1%; Pred. No. 34;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 14 FPEYKER 20
 DB 2 ypeikdk 8
 XX
 RESULT 23
 ID R06363
 XX R06363 standard; protein: 22 AA.
 AC R06363;
 XX
 DT 13-DEC-1990 (first entry)
 XX
 DE C-terminal of fish growth hormone.
 XX
 KW Osteichthyes: flatfish.
 KM
 XX Pleuronectiformes paralicthys.
 OS
 XX JP0217479-A.
 PN
 XX 06-JUL-1990.
 PD
 XX 20-OCT-1988; 88JP-0264928.
 PF
 XX 26-SEP-1988; 88JP-0240265.
 PR

PR 26-AUG-1988; 88JP-0211694.
 XX
 XX (NIOC) NIPPON OIL KK.
 PA
 XX WPI; 1990-250742/33.
 DR
 XX Fish growth hormone - extracted from pituitary gland of
 PT Pleuronectiformes Paralicthys fish.
 PT
 XX Claim 3; Page 1; 6pp; English.
 PS
 XX The protein is extracted from the pituitary gland of P. paralicth-
 CC thys. It can be used to accelerate the growth of the species of
 CC Pleuronectiformes and Salmo oncorhynchus. The protein has a mol.
 CC wt. of 22,000 and an isoelectric pt. of 7.1.
 CC See also R06362, R07480 and R07481.
 CC
 SQ Sequence 22 AA;
 XX
 XX
 Query Match 29.4%; Score 30; DB 11; Length 22;
 Best Local Similarity 36.4%; Pred. No. 51;
 Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 6 MMARFKMPE 16
 DB 7 ltvakrltpe 17
 XX
 RESULT 24
 ID W63838
 XX W63838 standard; Protein: 25 AA.
 AC W63838;
 XX
 DT 01-OCT-1998 (first entry)
 XX
 DE Plasmid PRMP100 M.HpyI protein fragment from H. pylori strain 60190.
 XX
 KW IcaA; immunoassay; detection; ulcerogenic; gastric carcinoma; treatment;
 KW peptic ulcer; immunisation; vaccine; protection.
 KM
 XX Synthetic.
 OS Helicobacter pylori.
 OS
 XX WO9743901-A1.
 PN
 XX 27-NOV-1997.
 PD
 XX 20-MAY-1997; 97WO-US08558.
 PF
 XX 20-MAY-1996; 96US-0650528.
 PR
 XX (UYVA-) UNIV VANDERBILT.
 PA
 XX Blaser MJ, Miller GG, Peek RM, Thompson SA;
 PI
 XX WPI; 1998-286350/25.
 DR
 XX N-PSDB; V43963.
 DR
 XX New Helicobacter pylori proteins - induced by contact with
 PT epithelium and related DNA, are associated with ulcer formation,
 PT useful in diagnosis and immunisation
 XX
 XX Disclosure; Fig 2; 107pp; English.
 PS
 XX This sequence is a M.hpyI protein fragment found in plasmid PRMP100. This
 CC plasmid also contains fragments of proteins CysE and IcaA derived from
 CC Helicobacter pylori strain 60190. This plasmid is used in method which
 CC provides an IcaA protein or fragments of the protein capable of being
 CC used in standard immunoassays to detect H. pylori-specific antibodies,
 CC particularly for diagnosis, especially antibodies characteristic of
 CC IcaA-positive strains which are ulcerogenic. Detecting presence of

CC Icea-positive strains also allows the risk of developing gastric
CC carcinoma to be assessed. Ligands, particularly antibodies, that
CC recognise Icea proteins are used to treat peptic ulcers, while
CC immunisation with Icea-negative H. pylori is used to protect against
CC infection (and its consequences such as ulcers, gastritis and gastric
CC cancer). Immunogenic Icea fragments, or the nucleic acid encoding them,
CC can also be used for vaccination. Antibodies (Ab) raised against Icea can
CC be used therapeutically or to screen other strains for homologous
CC proteins. Expression of Icea is strongly correlated with ulceration, so
CC detecting Icea allows differentiation between ulcerogenic and
CC non-ulcerogenic strains.

XX
SQ Sequence 25 AA:

Query Match 29.4%; Score 30; DB 19; Length 25;
Best Local Similarity 36.4%; Pred. No. 58;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 9 ARFKMPEVKE 19
:::|:|:|
Db 6 skyklipfike 16

RESULT 25
W63841
ID W63841 standard; Protein; 25 AA.
XX
AC W63841;
XX
DT 01-OCT-1998 (first entry)
DE Plasmid pRMP100 M.HpyI protein fragment from H. pylori strain J178.
XX
XX Icea; immunoassay; detection; ulcerogenic; gastric carcinoma; treatment;
KW peptic ulcer; immunisation; vaccine; protection.
XX
OS Synthetic.
OS Helicobacter pylori.
XX
PN WO9743901-A1.
XX
PD 27-NOV-1997.
XX
PF 20-MAY-1997; 97WO-US08558.
XX
PR 20-MAY-1996; 96US-0650528.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Blaser MJ, Miller GG, Peek RM, Thompson SA;
XX
DR WPI; 1998-286350/25.
DR N-PSDB; V44037.
XX
PT New Helicobacter pylori proteins - induced by contact with
PT epithelium and related DNA, are associated with ulcer formation,
PT useful in diagnosis and immunisation
XX
XX Disclosure; Fig 2; 107pp; English.
XX
XX This sequence is a M.hpyI protein fragment found in plasmid pRMP100. This
XX plasmid also contains fragments of proteins CysE and Icea derived from
XX Helicobacter pylori strain J178. This plasmid is used in method which
XX provides an Icea protein or fragments of the protein capable of being
XX used in standard immunoassays to detect H. pylori-specific antibodies,
XX particularly for diagnosis, especially antibodies characteristic of
XX Icea-positive strains which are ulcerogenic. Detecting presence of
XX Icea-positive strains also allows the risk of developing gastric
XX carcinoma to be assessed. Ligands, particularly antibodies, that
XX recognise Icea proteins are used to treat peptic ulcers, while
XX immunisation with Icea-negative H. pylori is used to protect against
XX infection (and its consequences such as ulcers, gastritis and gastric

CC cancer). Immunogenic Icea fragments, or the nucleic acid encoding them,
CC can also be used for vaccination. Antibodies (Ab) raised against Icea can
CC be used therapeutically or to screen other strains for homologous
CC proteins. Expression of Icea is strongly correlated with ulceration, so
CC detecting Icea allows differentiation between ulcerogenic and
CC non-ulcerogenic strains.

XX
SQ Sequence 25 AA:

Query Match 29.4%; Score 30; DB 19; Length 25;
Best Local Similarity 36.4%; Pred. No. 58;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 9 ARFKMPEVKE 19
:::|:|:|
Db 6 skyklipfike 16

Search completed: February 5, 2001, 10:47:30
Job time: 624 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:47:30 ; Search time 68.99 Seconds
(without alignments)
9.913 Million cell updates/sec

Title: US-08-981-824-3

Perfect score: 113
Sequence: 1 NWELADQPNLEILMHCQT 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 141170

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_36:*

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- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
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- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	100.0	20	W18844	65 kD Glutamic ac
2	113	100.0	20	W01795	Human 65 kD glutam
3	86	76.1	22	R72270	Glutamic acid deca
4	86	76.1	22	R72271	GAD65 fragment, pe
5	50	44.2	20	R72271	Glutamic acid deca
6	50	44.2	20	R72271	GAD65 fragment, pe
7	35	31.0	15	W63553	Beta (1 -> 4)-N-ac
8	35	31.0	21	W31018	Mugwort pollen all
9	34	30.1	23	W31051	Chemokine peptide,
10	33	29.2	17	Y14278	Beta-2 integrin pe
11	33	29.2	23	R20273	Human beta2 integr
12	33	29.2	23	W02061	

13	33	29.2	25	17	R99561
14	33	29.2	25	17	R92504
15	33	29.2	25	18	W15702
16	33	29.2	25	18	W24260
17	33	29.2	25	21	Y53906
18	33	28.3	17	20	Y34179
19	32	28.3	20	20	Y42241
20	32	28.3	20	20	Y43409
21	32	28.3	22	20	Y42236
22	32	28.3	22	20	Y42240
23	32	28.3	22	20	Y43404
24	32	28.3	22	20	Y43408
25	32	28.3	23	20	Y42239
26	32	28.3	23	20	Y43407
27	31	27.4	12	20	Y24751
28	31	27.4	20	16	R74066
29	31	27.4	20	20	Y39986
30	31	27.4	20	20	W89562
31	31	27.4	25	20	W97646
32	30	26.5	13	12	R12838
33	30	26.5	18	9	P82907
34	29	25.7	14	16	W21324
35	29	25.7	14	19	Y20370
36	29	25.7	15	16	R93652
37	29	25.7	15	18	W17995
38	29	25.7	16	16	R82544
39	29	25.7	17	20	Y41871
40	29	25.7	18	17	W05200
41	29	25.7	20	18	W16845
42	29	25.7	20	19	W40241
43	29	25.7	22	12	R1415
44	29	25.7	25	17	R85706
45	28.5	25.2	21	18	W16211

ALIGNMENTS

RESULT	1	
W18844	W18844 standard; peptide; 20 AA.	
XX	W18844:	
AC	05-JAN-1998 (first entry)	
XX	XX	
DE	65 kD Glutamic acid decarboxylase peptide fragment III.	
XX	XX	
KW	GAD: 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;	
KW	Insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;	
KW	predisposition; autoimmune; tumour; rheumatoid arthritis;	
KW	multiple sclerosis.	
OS	Synthetic.	
XX	XX	
PN	DE19526561-AA.	
XX	23-JAN-1997.	
PD	20-JUL-1995; 95DE-1026561.	
XX	XX	
PF	20-JUL-1995; 95DE-1026561.	
XX	XX	
PR	20-JUL-1995; 95DE-1026561.	
XX	XX	
PA	(BOEF) BOEHRINGER MANNHEIM GMBH.	
XX	Donle F, Endl J, Ganz M, Jung G, Klentech-engel R;	
PI	Pozzilli P, Stahl P;	
XX	WPI: 1997-088254/09.	
DR	WPI: 1997-088254/09.	
XX	XX	
PT	Skin test for diagnosis of cell-mediated diseases, esp. diabetes -	
XX	Involving intradermal admn. of auto-reactive substances	

Interferon-gamma 1
Interferon gamma p
Internal fragment
Peptide #2 of huma
Fragment derived f
Human pre-propepar
Multivalent ligand
Multivalent ligand
Multivalent ligand
Multivalent ligand
Multivalent ligand
Multivalent ligand
Multivalent ligand
Multivalent ligand
Lactoferrin duodec
Superantigen pepit
FIV ORF(51-71) pep
Recombinant heat-r
Breast-specific BS
HIV protecting vac
Acetylcholinestera
Glucagon precursor
Human microtubule
HIV principal neut
Helicobacter pylor
G. oxydans T100 L-
Rheumatoid arthrit
Helicobacter fam1
Helicobacter pylor
H. pylori Urease A
Human immunodefici
Human cytokeratin
Peptide containing

PS	Claim 11; Page 9; 12pp; German.
XX	
CC	M18842-70 are peptide fragments of the 65 kD human glutamic acid
CC	decarboxylase (GAD). The fragments are autoreactive substances used for
CC	diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
CC	determined by using a claimed method for diagnosis of cell-mediated
CC	diseases or a predisposition to cell-mediated diseases, which is effected
CC	by administering an autoreactive substance intradermally and establishing
CC	the diagnosis on the basis of the occurrence or lack of a positive
CC	reaction at the site of administration. The method is used for diagnosis
CC	of autoimmune and tumour diseases, preferably T-cell-mediated diseases
CC	such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
XX	
SQ	Sequence 20 AA:
Query Match	100.0%; Score 113; DB 18; Length 20;
Best Local Similarity	100.0%; Pred. No. 6.9e-12;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 NWEIADQPONTLEETILMHCOT 20
Dd	1 nweiadqpntleelmhcqt 20
RESULT	2
ID	W01795
AC	W01795 standard; peptide; 20 AA.
XX	
DT	W01795;
XX	
DT	15-OCT-1997 (first entry)
XX	
DE	Human 65 kD glutamine decarboxylase peptide.
XX	
KW	Humans; glutamine decarboxylase; GAD; diagnosis; predisposition;
KW	tumour; immunological; disease; autoimmune; diabetes; reagent;
KW	determination; T cell; subpopulation; medicament; treatment;
KW	prevention; production; antigen; immunogen; tolerogen; isolation;
KW	reinflection; inactivation.
OS	Homo sapiens.
XX	
PX	DEL9525784-A1.
XX	
PD	16-JAN-1997.
XX	
PF	14-JUL-1995; 95DE-1025784.
XX	
PR	14-JUL-1995; 95DE-1025784.
XX	
PA	(BOEF) BOEHRINGER MANNHEIM GMBH.
XX	
PI	Albert W, Boitard C, Endl J, Jung G, Schendel D;
PI	Stahl P, Van Enderst P;
XX	
DR	WP1; 1997-078452/08.
XX	
PT	Glutamine decarboxylase peptide(s) - for diagnosis and therapy of
PT	diabetes, etc.
XX	
PS	Claim 1; Page 12; 15pp; German.
CC	The present peptide is a fragment of the human 65 kD glutamine
CC	decarboxylase (GAD), which can be used to diagnose, or diagnose a
CC	predisposition to, a tumour or immunological disease, preferably an
CC	autoimmune disease, especially diabetes. It can also be used as a
CC	reagent to determine specific T cell subpopulations, in medicaments
CC	to treat or prevent immunologic diseases, preferably autoimmune
CC	diseases, especially diabetes, to produce antigens, especially
CC	immunogens or tolerogens and to isolate specific T cell
CC	subpopulations, which can be used to produce antigens or for
CC	reinflection, optionally after inactivation.

```

XX      XX      Sequence    20 AA;
SQ      SQ      Query Match          100.0%; Score 113; DB 18; Length 20;
                  Best Local Similarity 100.0%; Pred. No. 6,9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      OY      1 NMELADQPONLEETIMHCQT 20
                |||||||
Db       Db     1 nweIadqpnleelImhcqt 20

RESULT      3
R72270 ID R72270 standard; Peptide; 22 AA.
AC AC R72270;
DE DE 13-NOV-1995 (first entry)
KW KW Glutamic acid decarboxylase (GAD65) fragment.
KM KM Insulin-dependent diabetes mellitus; stiff man disease.
OS OS Homo sapiens.
PN PN W09507992-A.
PD PD 23-MAR-1995.
PE PE 24-AUG-1994; 94WO-US09478.
PF PF 17-SEP-1993; 93US-O123859.
PR PR
PS PS (REGC ) UNIV CALIFORNIA.
PT PT
PI PI Claire-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
DR DR MPI; 1995-131360/17.
DX DX
XX XX New polypeptide fragments of glutamic acid decarboxylase - for
PT PT diagnosis and treatment of autoimmune disease, esp. insulin
PT PT dependent diabetes,, also related nucleic acid, vectors,
PT PT antibodies, hybridoma(s) etc.
PS PS Example 11; Page 76; 100pp; English.
PP PP
XX XX Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
CC CC acid decarboxylase (GAD65) respectively, from which the GAD65
CC CC fragments described in R72261-R72298 were derived. These fragments
CC CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC CC CD and treat GAD-related autoimmune disorders, such as insulin
CC CC dependant diabetes mellitus or stiff man disease.
CX CX
SQ SQ Sequence 22 AA;

Query Match          76.1%; Score 86; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      OY      1 NWEIADQPNLEETIM 16
                |||||
Db       Db     7 nweIadqpnleelIm 22

RESULT      4
R72270 ID Y59571 standard; peptide; 22 AA.
AC AC Y59571
DE DE
KW KW
KM KM
OS OS
PN PN
PD PD
PE PE
PF PF
PR PR
PS PS
PT PT
PI PI
DR DR
DX DX
XX XX
YY YY
ZZ ZZ

```

XX 03-APR-2000 (first entry).
 XX GAD65 fragment, peptide #10.
 DE GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 XX insulin dependent diabetes mellitus; stiff man disease; diagnosis;
 KW therapy.
 XX Homo sapiens.
 OS US9598366-A.
 XX 07-DEC-1999.
 XX 09-APR-1997; 97US-0827618.
 XX 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0586536.
 PR 18-JUN-1991; 91US-0716909.
 XX (REGC) UNIV CALIFORNIA.
 XX Tobin AJ, Kaufman DL, Erlander MG;
 DR WPI; 2000-095930/08.
 XX Ameliorating glutamic acid decarboxylase associated autoimmune
 PT disorders such as insulin dependent diabetes mellitus and stiff man
 PT disease -
 XX Example 11; Column 42; 61pp; English.
 PS This sequence represents a fragment of the glutamic acid decarboxylase 65
 XX (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorders by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 CC and stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.
 CC Sequence 22 AA:
 SQ

Query Match 76.1%; Score 86; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NWEIADOPNLEEIIIM 16
 |||||
 DB 7 nweIadqpnlleelim 22

RESULT 5
 R72271
 ID R72271 standard; Peptide; 20 AA.
 AC R72271;
 XX 13-NOV-1995 (first entry)
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KW insulin-dependent diabetes mellitus; stiff man disease.
 OS Homo sapiens.
 XX W09507992-A.
 PN

XX 23-MAR-1995.
 PD 24-AUG-1994; 94WO-US09478.
 XX 17-SEP-1993; 93US-0123859.
 XX (REGC) UNIV CALIFORNIA.
 XX Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
 DR WPI; 1995-131360/17.
 XX New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hybridoma(s) etc.
 XX Claim 1; Page 76; 100pp; English.
 PS O86481 and O86482 encode R7173 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependent diabetes mellitus or stiff man disease.
 XX Sequence 20 AA:
 SQ

Query Match 44.2%; Score 50; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 EEIIMHCOT 20
 |||||
 DB 1 eeiImhCgt 9

RESULT 6
 Y59551
 ID Y59551 standard; peptide; 20 AA.
 AC Y59551;
 XX 03-APR-2000 (first entry)
 DE GAD65 fragment, peptide #11.
 XX GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependent diabetes mellitus; stiff man disease; diagnosis;
 KW therapy.
 XX Homo sapiens.
 OS US9598366-A.
 XX 07-DEC-1999.
 XX 09-APR-1997; 97US-0827618.
 XX 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0586536.
 PR 18-JUN-1991; 91US-0716909.
 XX (REGC) UNIV CALIFORNIA.
 XX Tobin AJ, Kaufman DL, Erlander MG;
 DR WPI; 2000-095930/08.
 XX Ameliorating glutamic acid decarboxylase associated autoimmune
 PT disorders such as insulin dependent diabetes mellitus and stiff man
 PT

PT disease -
 XX Claim 1; Column 42; 61pp; English.
 PS
 XX
 CC This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorders by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 CC and stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.
 CC
 CC Sequence 20 AA:
 SQ
 Query Match 44.2%; Score 50; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 EETLMHCOT 20
 DB 1 eettlmhct 9
 RESULT 7
 W63553
 ID W63553 standard; peptide: 15 AA.
 XX W63553;
 AC
 XX 24-NOV-1998 (first entry)
 DT
 XX Beta (1 -> 4)-N-acetylglucosaminyl-transferase (Gnt-IV) fragment.
 DE
 XX Beta (1 -> 4)-N-acetylglucosaminyl-transferase; Gnt-IV; bovine; human;
 KW enzyme; sugar chain subunit; branched oligosaccharide; polysaccharide;
 KW drug; reagent; food; biopolymer; glycoprotein; erythropoietin.
 XX
 OS Homo sapiens.
 OS Bos sp.
 XX W09826053-A1.
 PN
 XX 18-JUN-1998.
 PD
 XX 10-DEC-1997; 97WO-JP04546.
 PF
 XX 18-JUN-1997; 97JP-0161462.
 PR 12-DEC-1996; 96JP-0332411.
 XX
 XX (KIRI) KIRIN BEER KK.
 PA
 XX Minowa M, Oguri S, Takeuchi M, Taniguchi N, Yoshida A;
 PI WPI: J998-348516/30.
 DR
 XX Recombinant beta(1-4)-N-acetyl:glucosaminyl:transferase - allows
 PT production of difficultly accessible branched poly:saccharides for
 PT food and drug use
 PT
 XX Claim 4; Page 49; 112pp; Japanese.
 PS
 XX Sequences shown in W63543 to W63556 represent fragments of beta (1 -> 4)-
 CC N-acetylglucosaminyl-transferase (Gnt-IV) enzyme. The invention provides
 CC bovine and human Gnt-IV enzymes that can be used for converting sugar
 CC chain subunits having one structure to another structure. Vectors
 CC containing the DNA sequences encoding these enzymes can be used to
 CC transform host cells for the production of the Gnt-IV enzymes. The
 CC enzymes are useful in the production of branched oligosaccharides and

CC polysaccharides which are difficult of access by other methods. They are
 CC also useful in the production of drugs, reagents and foods and in
 CC modifying the properties of biopolymers containing sugar chains. The
 CC enzyme may also be used for the preparation of glycoproteins such as
 CC erythropoietin.
 CC
 CC Sequence 15 AA:
 SQ
 Query Match 31.0%; Score 35; DB 19; Length 15;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 6 DQPNDEETLMH 17
 DB 1 dkpvnvessylfh 12
 RESULT 8
 W31018
 ID W31018 standard; peptide: 21 AA.
 XX W31018;
 AC
 XX 09-JAN-1998 (first entry)
 DT
 XX Mugwort pollen allergen B cell epitope.
 DE
 XX Cofactor-independent phosphoglycerate mutase; PGM-1; E.C. 5.4.21;
 KW Timothy grass; pollen; allergy; plant allergen; panallergen; B cell;
 KW T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
 KW conserved.
 XX
 OS Artemisia vulgaris.
 OS
 XX W09705258-A2.
 PN
 XX 13-FEB-1997.
 PD
 XX 02-AUG-1996; 96WO-AT00141.
 PF
 XX 02-AUG-1995; 95AT-0001320.
 PR
 XX (BIOM-) BIOMAY PRODN & HANDELS GMBH.
 PA
 XX Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
 PI Kraft D, Richter K, Rheinberger H;
 DR WPI: 1997-145695/13.
 XX
 PT New recombinant DNA encoding plant phosphoglycerate mutase or its
 PT antigenic epitope(s) - useful for diagnosis or treatment of
 PT allergies to pollen and plant-derived foods
 PT
 XX Disclosure: Fig 11a; 160pp; German.
 PS
 XX W31018-W31040 are B cell epitopes of mugwort pollen co-factor-
 CC independent phosphoglycerate mutase (PGM-1) isoform Art6. PGM-1 is
 CC a highly conserved plant allergen (panallergen) which can cause
 CC cross-reactivity in patients allergic to pollen and plant-derived
 CC foods. PGM-1 and it's B cell and T cell epitopes can be used for the
 CC in vitro detection of allergy against PGM-1, by measuring serum IgE
 CC or a cellular reaction. They can also be used in immunotherapy and
 CC will not cause an autoimmune response because PGM-1 is significantly
 CC different from the human enzyme, which is co-factor dependent.
 CC
 CC Sequence 21 AA:
 SQ
 Query Match 31.0%; Score 35; DB 18; Length 21;
 Best Local Similarity 55.6%; Pred. No. 28;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 NWELADPOQ 9
 DB 7 swkladphk 15

RESULT 9
 W31051
 ID W31051 standard; peptide: 23 AA.
 AC W31051;
 XX
 DT 09-JAN-1998 (first entry)
 DE Mugwort pollen allergen B cell epitope.
 XX
 XX Cofactor-independent phosphoglycerate mutase; PGM-1; E.C. 5.4.21;
 KM Timothy grass; pollen; allergy; plant allergen; panallergen; B cell;
 KM T cell; epitope; immunotherapy; detection; diagnosis; hay fever;
 KM conserved.
 XX
 XX Artemisia vulgaris.
 OS WO9705258-A2.
 XX
 XX
 XX 13-FEB-1997.
 PD
 XX 02-AUG-1996; 96WO-AT00141.
 PF
 XX 02-AUG-1995; 95AT-0001320.
 PR
 XX (BIOM-) BIOMAX PRODN & HANDELS GMBH.
 PA
 PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
 PI Kraft D, Richter K, Rheinberger H;
 PI
 PI MPI: 1997-145695/13.
 DR
 XX
 XX New recombinant DNA encoding plant phosphoglycerate mutase or its
 PT antigenic epitope(s) - useful for diagnosis or treatment of
 PT allergies to pollen and plant-derived foods
 PS
 PS Disclosure: Fig 11b; 160pp; German.
 XX
 CC W31051-W31072 are B cell epitopes of mugwort pollen co-factor-
 CC independent phosphoglycerate mutase (PGM-1) isoform Art17. PGM-1 is
 CC a highly conserved plant allergen (panallergen) which can cause
 CC cross-reactivity in patients allergic to pollen and plant-derived
 CC foods. PGM-1 and its B cell and T cell epitopes can be used for the
 CC in vitro detection of allergy against PGM-1, by measuring serum IgE
 CC or a cellular reaction. They can also be used in immunotherapy and
 CC will not cause an autoimmune response because PGM-1 is significantly
 CC different from the human enzyme, which is co-factor dependent.
 CC
 CC Sequence 23 AA:
 SQ

Query Match 30.1%; Score 34; DB 18; Length 23;
 Best Local Similarity 62.5%; Pred. No. 45;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 WELADPOQ 9
 DB 10 wkladphk 17

RESULT 10
 ID Y14278 standard; peptide: 17 AA.
 AC Y14278;
 XX
 XX 29-JUL-1999 (first entry)
 DT
 XX

DE Chemokine peptide, CRD CysOCys16peptide(1-15)[SDF].
 XX
 XX Chemokine; immune response; monocyte chemoattractant protein-1; MCP-1;
 KM chemokine-induced activity; inflammatory response; vascular indication;
 KM haematopoietic cell-associated activity; tumour; coronary artery disease;
 KM myocardial infarction; unstable angina pectoris; atherosclerosis; asthma;
 KM vasculitis; lentiviral infection; low bone mineral density; suppressor;
 KM parasitic infection; autoimmune disease; psoriasis; wound healing;
 KM organ transplant rejection; rheumatoid arthritis; allergy; therapy;
 KM arachidonic acid pathway.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX
 XX WO9912968-A2.
 PN
 XX 18-MAR-1999.
 PD
 XX 11-SEP-1998; 98WO-US19052.
 PF
 XX 11-SEP-1997; 97US-0927939.
 PR
 XX (NEOR-) NEORX CORP.
 PA
 PI Gralinger DJ, Kanaly ST, Tatalick LM;
 PI MPI: 1999-347124/29.
 DR
 XX
 XX New chemokine peptides and mimetics
 PT
 PT Disclosure: Fig 14; 208pp; English.
 PS
 XX
 XX This sequence represents a fragment of the chemokine SDF1.
 CC The invention relates to chemokine peptides and mimetics, particularly
 CC derived from monocyte chemoattractant protein-1 (MCP-1). The chemokine
 CC peptides and variants and derivatives can inhibit or reduce or increase,
 CC or enhance chemokine-induced activity. They can be used for increasing or
 CC enhancing an inflammatory response, an immune response or haematopoietic
 CC cell-associated activity at a tumour site. They can also be used for
 CC preventing or inhibiting an indication associated with haematopoietic
 CC cell recruitment or histamine release from basophils or mast cells. They
 CC can also be used to modulate the chemokine-induced activity of
 CC haematopoietic cells at a preselected physiological site, to treat a
 CC vascular indication, e.g. coronary artery disease, myocardial infarction,
 CC unstable angina pectoris, atherosclerosis, or vasculitis, lentiviral
 CC infection or replication (e.g. HIV), low bone mineral density, a
 CC parasitic infection in a vertebrate animal (e.g. malaria), an autoimmune
 CC disease, to suppress tumour growth in a vertebrate animal, to prevent or
 CC treat psoriasis in a mammal, to enhance wound healing, to prevent or
 CC treat asthma, organ transplant rejection, rheumatoid arthritis or
 CC allergy. They can also be used to inhibit a product or intermediate in
 CC the arachidonic acid pathway and where leukotriene, thromboxane and/or
 CC prostaglandin are inhibited and to prevent or inhibit an indication
 CC associated with elevated TNF-alpha.
 CC
 CC Sequence 17 AA:
 SQ

Query Match 29.2%; Score 33; DB 20; Length 17;
 Best Local Similarity 50.0%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 3 ELADPOQNEEILMHC 18
 DB 4 glacnptnl--lklhc 17

RESULT 11
 ID R20273 standard; peptide: 23 AA.
 AC R20273;
 XX
 XX R20273;
 DT
 XX

DT 10-APR-1992 (first entry)

XX Beta-2 integrin peptide derived from CD11b alpha subunit.

DE

XX Immune response; phagocyte-mediated tissue damage; A domain; MM;

KW Inflammation; CD11/CD18 complex; alpha subunit; C83; M01; Mav-1;

KM Complement receptor type 3; heterodimer.

XX

OS Synthetic.

XX

PN W09119511-A.

XX

PD 26-DEC-1991.

XX

PF 18-JUN-1991; 91WO-US04338.

XX

PR 04-JAN-1991; 91US-0637830.

PR 18-JUN-1990; 90US-0539842.

XX

PA (GEHO-) GEN HOSPITAL CORP.

XX

PI Arnaout MA;

XX

DR WPI; 1992-024197/03.

XX

PT Beta-2 integrin peptide CD11b, recombinant hetero-dimer

PT CD11b/CD18 - or MAb against them; useful for inhibiting CD11/CD18

PT mediated immune response in control of phagocyte-mediated tissue

PT damage

XX

PS Claim 8; Page 73; 84pp; English.

XX

CC The peptide (SEQ ID NO: 20) corresponds to residues 112-134 of

CC CD11b alpha subunit of beta 2 integrin. The sequence occurs

CC immediately prior to the A domain which is conserved in the CD11c

CC and CD1a subunits and also in the collagen/heparin/platelet GRI

CC binding regions of the mature von Willebrand factor. The peptide

CC may be synthesised or prepd. by recombinant techniques using the

CC gene, the sequence of which was disclosed by Arnaout et al., J.

CC Cell Biol. 106:2153 (1988). (References are also provided for the

CC DNA sequences of human CD18, CD1c and CD1a). The peptide is cap-

CC able of inhibiting a CD11/CD18 mediated immune response and is

CC useful for treatment of ischaemia reperfusion injury, burns,

CC frostbite, acute arthritis, asthma and adult respiratory distress

CC syndrome. It may also be used to block intra-islet infiltration of

CC macrophages associated with insulin-dependent diabetes mellitus,

CC and for controlling phagocyte-mediated tissue damage to heart

CC muscle during acute cardiac insufficiency.

CC See also R20256-R20299.

CC

XX

SO Sequence 23 AA;

XX

Query Match 29.2%; Score 33; DB 13; Length 23;

Best Local Similarity 46.7%; Pred. NO. 66;

Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

XX

OY 4 LADQPONLEILMHC 18

DB 3 lrgqpkfpealrgc 17

XX

RESULT 12

W02061

ID W02061 standard; peptide; 23 AA.

XX

AC W02061;

XX

DT 09-APR-1997 (first entry)

XX

DE Human beta2 integrin subunit CD11b, residues 112-134.

XX

XX Beta2 integrin; A-domain; metal binding domain; inflammatory response;

KW Immune response; inhibition; phagocyte-mediated tissue injury;

KW Inflammation.

XX

OS Homo sapiens.

XX

PN W09624063-A1.

XX

PD 08-AUG-1996.

XX

PF 30-JAN-1996; 96WO-US01314.

XX

PR 30-JAN-1995; 95US-0380167.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Arnaout MA;

XX

DR WPI; 1996-371576/37.

XX

PT In vitro identification of integrin function antagonists - by

PT measuring binding of A-domain peptide derived from integrin to

PT ligand in presence and absence of candidate antagonist

XX

PS Disclosure; Page 11; 11pp; English.

XX

CC The sequences given in W02037-80 represent peptides derived from

CC beta2 integrin, esp. A-domain and the metal binding domains. These

CC peptides were selected using the method of the invention which

CC screens compounds for their ability to inhibit the binding of a

CC selected integrin to a ligand which naturally binds to it. The

CC method comprises measuring the binding of an A-domain peptide

CC derived from the selected integrin, to the ligand in the presence

CC and absence of the test compound and determining whether the binding

CC is decreased. Identified compounds are capable of interfering with

CC certain cellular immune/inflammatory responses, particularly

CC phagocyte-mediated tissue injury and inflammation. The numbering

CC of the amino acid residues is based on the the deduced amino acid

CC sequence of the open reading frame of human CD11b from Arnaout et al.,

CC J. Cell. Biol. 106:2153 (1988).

CC

XX

SO Sequence 23 AA;

XX

Query Match 29.2%; Score 33; DB 17; Length 23;

Best Local Similarity 46.7%; Pred. NO. 66;

Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

XX

OY 4 LADQPONLEILMHC 18

DB 3 lrgqpkfpealrgc 17

XX

RESULT 13

R99561

ID R99561 standard; Peptide; 25 AA.

XX

AC R99561;

XX

DT 29-SEP-1996 (first entry)

XX

DE Interferon-gamma inducer protein tryptic peptide (aa79-103).

XX

KW Interferon-gamma inducer protein; IFN-gamma; antiviral; virocidic;

KW antitumour; antibacterial; immunoregulator; adoptive immunotherapy;

XX

XX therapy; cancer.

XX

OS Mus sp.

XX

PN EP112931-A2.

XX

PD 22-MAY-1996.

XX

PF 10-NOV-1995; 95EP-0308055.

XX 29-SEP-1995; 95JP-0274988.
 PR 15-NOV-1994; 94JP-0304203.
 PR 23-FEB-1995; 95JP-0058240.
 PR 10-MAR-1995; 95JP-0078357.
 PR 18-SEP-1995; 95JP-0262062.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Fukuda S, Kohno K, Kunikata T, Kurimoto M, Okamura H;
 PI Taniguchi M, Tanimoto T, Torioge K, Ushio S;
 DR WPI: 1996-252837/26.
 XX
 PT DNA encoding interferon-gamma prodn.-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders
 XX
 PS Example A-3-6; Page 37; 48pp; English.
 CC Tryptic peptides (R99561 and R99562) correspond to amino acids
 CC 79-103 and 26-43, respectively, of a novel interferon-gamma
 CC (IFN-gamma) inducer protein identified in mouse liver. The
 CC peptides were used to design PCR primers (T32405-06) that were
 CC utilised in the amplification of mouse liver cDNA, leading to
 CC the isolation of a clone (T32403) coding for mouse IFN-gamma
 CC inducer protein (R99559).
 CC
 XX
 SQ Sequence 25 AA;

Query Match 29.2%; Score 33; DB 17; Length 25;
 Best Local Similarity 35.7%; Pred. No. 72;
 Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NWEIADQPQNLEEI 14
 : : | | : : : : |
 Db 3 steindppendi1 16

RESULT 14
 R92504
 ID R92504 standard; peptide: 25 AA.

XX AC R92504;

XX DT 30-AUG-1996 (first entry)

XX DE Interferon gamma production inducer peptide #1.

XX Interferon gamma; inducer; IFNgamma; immunocompetent cell; antiviral;
 KW antitumour; antiseptic; immunoregulatory; platelet-increasing agent;
 KW therapy; prevention; condyloma acuminatum; renal cancer; brain cancer;
 KW granuloma; mycosis fungoides; rheumatism; allergy; cytotoxicity; AIDS;
 KW killer T-cell; interleukin-2; IL-2; tumour necrosis factor; TNF;
 KW adoptive immunotherapy; monoclonal antibody.
 KW
 XX
 OS Synthetic.

XX EP692536-A2.

XX PD 17-JAN-1996.

XX PF 13-JUL-1995; 95EP-0304906.

XX PR 10-FEB-1995; 95JP-0045057.

XX PR 14-JUL-1994; 94JP-0184162.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Kohno K, Kunikata T, Kurimoto M, Okamura H, Taniguchi M;
 PI Tanimoto T, Torioge K;
 XX

DR WPI: 1996-070177/08.

XX Protein that induces gamma interferon prodn. in immuno:competent
 PT cells - used e.g. as antiviral or antitumour agent, also induces
 PT cytotoxicity of killer cells
 XX

PS Claim 1; Page 21; 30pp; English.

XX R92504 and R92505 represent fragments of the protein of the invention
 CC (see R92506), which induces interferon gamma (IFNgamma) production in
 CC immunocompetent cells. The protein is useful as an antiviral,
 CC antitumour, antiseptic, immunoregulatory and platelet-increasing agent.
 CC It can be used for treating or preventing AIDS, condyloma acuminatum,
 CC renal or brain cancer, granuloma, mycosis fungoides, rheumatism and
 CC allergy. The protein can also be used to induce IFNgamma production in
 CC cultured cells. The IFNgamma inducer strongly induces cytotoxicity of
 CC killer T-cells and when used with interleukin-2 (IL-2) and tumour
 CC necrosis factor (TNF), may improve the effect (or reduce side effects) of
 CC adoptive immunotherapy in tumours. The DNA encoding this protein (see
 CC T16224) can be used to produce the protein, which can then be purified
 CC (or assayed) using monoclonal antibodies.
 CC
 XX

SQ Sequence 25 AA;

Query Match 29.2%; Score 33; DB 17; Length 25;
 Best Local Similarity 35.7%; Pred. No. 72;
 Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NWEIADQPQNLEEI 14
 : : | | : : : : |
 Db 3 steindppendi1 16

RESULT 15
 W15702
 ID W15702 standard; peptide: 25 AA.

XX AC W15702;

XX DT 26-JAN-1998 (first entry)

XX DE Internal fragment of interferon-gamma inducer protein.

XX Interferon-gamma, IFN-gamma; antiviral; antineoplastic; radiotherapy;
 KW immunoregulatory; antitumour agent; chemotherapy; leukopenia;
 KW thrombocytopenia; immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin; killer cell.
 KW
 XX

OS Homo sapiens.

XX EP767178-A1.

XX PD 09-APR-1997.

XX PF 26-SEP-1996; 96EP-0306997.

XX PR 20-SEP-1996; 96JP-0269105.

XX PR 26-SEP-1995; 95JP-0270725.

XX PR 29-FEB-1996; 96JP-0067434.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T;

XX WPI: 1997-205381/19.

XX Human protein that induces interferon-gamma prodn. in
 PT immuno:competent cells - useful for adoptive immuno:therapy of
 PT tumours and as antimicrobial agent etc.
 XX
 PS Disclosure; Page 21; 26pp; English.

CC The present sequence represents an internal fragment of a novel
 CC protein from human cells, which induces interferon-gamma (IFN gamma)
 CC production in immunocompetent cells. This protein enhances cytotoxicity
 CC of killer cells and induces their formation. It is used as an
 CC antitumor agent for antitumor immunotherapy, an antiviral (including
 CC anti-AIDS) or antibacterial agent, and in the treatment of atopic or
 CC immune system diseases, e.g. asthma, hay fever or rheumatism. When
 CC formulated with interleukin-3, it is also used to treat leukopenia and
 CC thrombocytopenia associated with radiotherapy or chemotherapy of
 CC leukemia and other cancers. When used in antitumor immunotherapy,
 CC this novel protein significantly improves the immunotherapeutic
 CC effect of interleukin-2 (IL-2), compared with use of IL-2
 CC alone, either when administered to the patient (before administration of
 CC IL-2) or by addition to the medium in which cells (intended for return to
 CC the patient) are being grown.

SO Sequence 25 AA;

Query Match 29.2%; Score 33; DB 18; Length 25;
 Best Local Similarity 35.7%; Pred. No. 72;
 Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMELADQPONLEEL 14
 : : | | : : : :
 Db 3 steemdpennid1 16

RESULT 16

W24260
 ID W24260 standard; Peptide; 25 AA.

AC W24260;

DT 15-OCT-1997 (first entry)

DE Peptide #2 of human protein for induction of interferon-gamma.

KW Interferon gamma; immunocompetent cell; malignant tumour;

KW viral disease; bacterial infection; immune disease.

OS Homo sapiens.

PN JP09157180-A.

PD 17-JUN-1997.

PF 24-JAN-1996; 96JP-0028722.

PR 04-OCT-1995; 95JP-0279906.

PR 10-MAR-1995; 95JP-0078357.

PR 29-SEP-1995; 95JP-0274988.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX WPI; 1997-369391/34.

PT A drug containing a polypeptide which induces interferon-gamma -
 useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases

PS Disclosure; Page 10; 12pp; Japanese.

CC The sequences given in W24259-61 are peptide fragments of a protein
 CC which induces interferon-gamma production in immunocompetent cells.
 CC This protein may be used as the major component in a drug for the
 CC prevention and treatment of e.g. malignant tumours, viral diseases,
 CC bacterial infections and immune diseases. This peptide corresponds
 CC to residues 80-104 of the human protein.

SO Sequence 25 AA;

Query Match 29.2%; Score 33; DB 18; Length 25;
 Best Local Similarity 35.7%; Pred. No. 72;
 Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMELADQPONLEEL 14
 : : | | : : : :
 Db 3 steemdpennid1 16

RESULT 17

Y53906
 ID Y53906 standard; Peptide; 25 AA.

AC Y53906;

DT 13-MAR-2000 (first entry)

DE Fragment derived from a protein that induces IFN-gamma production.

KW Mouse; interferon gamma production; IFN-gamma; immunocompetent cell;

KW antiviral; immunoregulatory; antigen; mitogen;

KW IFN-gamma susceptible disease; antibacterial; antitumour;

KW blood platelet enhancing agent; hepatitis; herpes syndrome; condyloma;

KW AIDS; bacterial disease; candidiasis; malaria; solid malignant tumour;

KW renal cancer; mycosis fungoides; chronic granulomatous disease;

KW blood cell malignant tumour; adult T cell leukaemia;

KW chronic myelogenous leukaemia; malignant leukaemia; immune disease;

PF 10-NOV-1995; 99EP-0104104.

PR 15-NOV-1994; 94JP-0304203.

PR 23-FEB-1995; 95JP-0058240.

PR 10-MAR-1995; 95JP-0078357.

PR 18-SEP-1995; 95JP-0262062.

PR 29-SEP-1995; 95JP-0274988.

PR 10-NOV-1995; 95EP-0308055.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Ushio S, Torigoe K, Tanimoto T, Okamura H;

XX WPI; 2000-064289/06.

PT Novel polypeptides used in the treatment of interferon-gamma
 susceptible diseases -

PS Example A2; Page 14; 42pp; English.

CC The present sequence represents a fragment derived from a murine
 CC protein that induces interferon (IFN)-gamma production by immunocompetent
 CC cells. IFN-gamma is a protein which has antiviral, antitumor and
 CC immunoregulatory activities, and is produced by immunocompetent cells
 CC stimulated with antigens or mitogens. The present peptide was used to
 CC design probes which were used to isolate the corresponding human protein
 CC from human liver cells. The protein of the invention is used to treat
 CC IFN-gamma susceptible diseases, and also have use as a antiviral agent,
 CC antibacterial agent, antitumor agent, immunoregulatory agent and blood
 CC platelet enhancing agent. Diseases which can be treated with the
 CC protein include viral diseases such as hepatitis, herpes syndrome,
 CC condyloma, and AIDS; bacterial diseases such as candidiasis and malaria;
 CC solid malignant tumours such as renal cancer, mycosis fungoides, and
 CC chronic granulomatous disease; blood cell malignant tumours such as
 CC adult T cell leukaemia, chronic myelogenous leukaemia, and malignant
 CC leukaemia; and immune diseases such as allergy and rheumatism.

SO Sequence 25 AA;


```
QY      2 WELADQPQNLEIL 15
        | | : : | : | :
Db      - 2 wrlshrpkdylslv 15
```

QY 2 WELADQPONTLEIL 15
| | : : | : | :
Db 4 wrishrpkdlyslv 17

Query Match 29.2%; Score 33; DB 21; Length 25;
Best Local Similarity 35.7%; Pred. No. 72;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NMELADQPONLEET 14
: : : : :
Db 3 sfeedmpdeniddl 16

RESULT 18

Y34179, ' standard; peptide; 17 AA.

AC Y34179;
XX
DT 15-NOV-1999 (first entry)

DE Human pre-proheparanase protein sequence fragment #6.

XX Human; pre-proheparanase; platelet; wound healing; angiogenesis blocker;
KM inflammation; psoriasis; diabetic retinopathy; solid tumour; arthritis;
KM heparin degradation; anticoagulant neutralisation; asthma; CNS disease;
KM inflammatory disease; vascular stenosis; atherosclerosis; diagnosis;
KM tumour growth; fibroproliferative disorder; neurodegenerative disease;
KM therapy.

OS Homo sapiens.

PN MO9943830-A2.

PD 02-SEP-1999.

PF 18-FEB-1999; 99MO-US01489.

PR 26-MAR-1998; 98US-0079401.

PR 24-FEB-1998; 98US-0075706.

PA (PHAA) PHARMACIA & UPJOHN CO.

PI Fairbanks MB, Heinrikson RL, Milder AM;

DR WPI; 1999-540598/45.

PT New isolated platelet heparanase polypeptides, used to develop

PS products for, e.g. wound healing and blocking angiogenesis

XX Example 3; Fig 8; 57pp; English.

XX This sequence represents a fragment of the human pre-proheparanase of the
CC invention. The pre-proheparanase sequence was isolated from human
CC platelets. The heparanase can be used for identifying agents which alter
CC heparanase activity. The heparanase can be used for wound healing or for
CC blocking angiogenesis or inflammation. It can be used for treating
CC e.g. psoriasis, diabetic retinopathy or solid tumours, or for the
CC degradation of heparin and the neutralisation of heparin's anticoagulant
CC properties during surgery. Inhibitors of heparanase activity can be used
CC in the treatment of arthritis, asthma, and other inflammatory diseases,
CC vascular stenosis, atherosclerosis, tumour growth and progression,
CC fibroproliferative disorders, and central nervous system (CNS) and
CC neurodegenerative diseases. The products can also be used for detection
CC and diagnosis. The purified heparanase, both recombinantly produced human
CC heparanase and heparanase isolated from human platelet activity, allows
CC for the convenient selection of compounds having anti-heparanase
CC activity, i.e. inhibitors of heparanase activity, by measuring inhibition
CC of heparanase activity. Inhibition of heparanase activity can be measured
CC by blocking heparanase-mediated release of radioactive fragments from in
CC vivo radiolabelled (HSPG)/heparin.

XX Sequence 17 AA;

Query Match 28.3%; Score 32; DB 20; Length 17;
Best Local Similarity 40.0%; Pred. No. 67;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 NMELADQPON 10
: : : : :
Db 5 swelgneps 14

RESULT 19

Y42241 standard; peptide; 20 AA.

XX Y42241;

DT 20-DEC-1999 (first entry)

DE Multivalent ligand Tlp-18.40 peptide derivative.

XX Angiogenic homology region; AHR; thrombospondin 1; TSP-1; angiotatin;
KM endostatin; anticancer; antiangiogenic; cancer; cardiovascular disease;
KM obesity; osteoarthritis; duodenal ulcer; abnormal neovascularisation;
KM wound healing; arteriosclerosis; ischaemia; diabetes mellitus;
KM blood vessel occlusion.

OS Synthetic.

PN MO9948923-A1.

PD 30-SEP-1999.

PF 22-MAR-1999; 99MO-US06246.

PR 24-MAR-1998; 98US-0046985.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.

PI Ben-Sasson SA;

DR WPI; 1999-601204/51.

PT New peptides and derived multivalent ligands based on angiogenic

PS treating tumours - used to inhibit or promote angiogenesis, e.g. for

XX Claim 12; Fig 2; 76pp; English.

XX The present invention specifically describes peptides comprising the
CC angiogenic homology region (AHR) of thrombospondin (TSP) 4, angiotatin,
CC endostatin or TSP-1. Multivalent ligands based on the peptides and
CC related angiogenic peptides may be anti-angiogenic, e.g. for treating
CC tumours, cardiovascular disease (arteriosclerosis, ischaemia), obesity,
CC osteoarthritis, duodenal ulcers, abnormal ocular vascularisation in
CC diabetes, or they are proangiogenic, e.g. for promotion of wound
CC healing and to stimulate neovascularisation around occluded blood
CC vessels (a potential alternative to by-pass surgery or angioplasty).
CC The multivalent ligands may be used in human or veterinary medicine. They
CC may also be used to raise peptide-specific antibodies (used for detecting
CC the peptides) and to identify and isolate compounds that interact with,
CC and modulate activity of, AHR. AHR are relatively small, conserved
CC sequences from different angiogenic peptides that are (largely)
CC responsible for biological activity. They are cheaper to prepare than
CC complete proteins; may be effective at lower doses; have long-lasting
CC in vivo effect and good biodistribution following oral or parenteral
CC administration. The present sequence represents a multivalent ligand
CC peptide derivative given in the present invention.

XX Sequence 20 AA;

Query Match 28.3%; Score 32; DB 20; Length 20;
Best Local Similarity 35.7%; Pred. No. 81.

Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 WELADOPONLEIL 15
| : : : : | : :
DB 2 WLSHPKALYSIV 15

RESULT 20

ID Y43409 standard; peptide: 20 AA.

AC Y43409;

DR 20-DEC-1999 (first entry)

DE Multivalent ligand Tip-18.40 peptide derivative.

KM Angiogenic homology region; AHR; thrombospondin 1; TSP-1; angiotatin;
KM endostatin; anticancer; antiangiogenic; cancer; cardiovascular disease;
KM obesity; osteoarthritis; duodenal ulcer; abnormal neovascularisation;
KM wound healing; arteriosclerosis; ischaemic limb; ischaemic myocardium;
KM diabetes mellitus; blood vessel occlusion.

OS Synthetic.

PN WO9948924-A1.

PD 30-SEP-1999.

PF 23-MAR-1999; 99WO-US06334.

PR 24-MAR-1998; 98US-0046737.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.

PI Ben-Sasson SA.

DR WPI: 1999-591075/50.

PT New angiogenic peptide derivatives, used for treating e.g. cancer,
PT cardiovascular diseases, obesity, osteoarthritis, duodenal ulcers,
PT abnormal neovascularisation and for wound healing

PS Disclosure: Fig 3; 62pp; English.

XX The present invention specifically describes peptide derivatives
XX comprising an angiogenic homology region (AHR) of endostatin. The peptide
XX derivatives can be used for modulating angiogenesis in humans and
XX animals. The peptides can be used to treat a wide variety of disease
XX conditions, including cancer, cardiovascular diseases (e.g.
XX arteriosclerosis, ischaemic limbs and ischaemic myocardium), obesity,
XX osteoarthritis, duodenal ulcers, abnormal ocular neovascularisation
XX associated e.g. with diabetes mellitus, and to promote wound healing or
XX to stimulate the growth of new blood vessels to bypass, e.g. blood vessel
XX occlusions. The peptide derivatives can also be used for the production
XX of antibodies. The multivalent ligands may enable the administration of
XX lower doses in order to achieve therapeutic efficacy, as compared with
XX a univalent peptide chain. In addition, they can have long in vivo
XX lifetimes and good biodistribution when administered orally or
XX parenterally. The present sequence represents a multivalent ligand
XX Tip-18.40 peptide derivative given in the present invention.

CC Sequence 20 AA;

Query Match 28.3%; Score 32; DB 20; Length 20;

Best Local Similarity 35.7%; Pred. No. 81; Mismatches 4; Indels 0; Gaps 0;

OY 2 WELADOPONLEIL 15
| : : : : | : :
DB 2 WLSHPKALYSIV 15

RESULT 21

ID Y42236 standard; peptide: 22 AA.

AC Y42236;

DR 20-DEC-1999 (first entry)

DE Multivalent ligand Tip-15.40 hybrid peptide.

KM Angiogenic homology region; AHR; thrombospondin 1; TSP-1; angiotatin;
KM endostatin; anticancer; antiangiogenic; cancer; cardiovascular disease;
KM obesity; osteoarthritis; duodenal ulcer; abnormal neovascularisation;
KM wound healing; arteriosclerosis; ischaemia; diabetes mellitus;
KM blood vessel occlusion.

OS Synthetic.

PN WO9948923-A1.

PD 30-SEP-1999.

PF 22-MAR-1999; 99WO-US06246.

PR 24-MAR-1998; 98US-0046985.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.

PI Ben-Sasson SA.

DR WPI: 1999-601204/51.

PT New peptides and derived multivalent ligands based on angiogenic
PT homology regions, used to inhibit or promote angiogenesis, e.g. for
PT treating tumours

PS Claim 7; Fig 2; 76pp; English.

XX The present invention specifically describes peptides comprising the
XX angiogenic homology region (AHR) of thrombospondin (TSP) 4, angiotatin,
XX endostatin or TSP-1. Multivalent ligands based on the peptides and
XX related angiogenic peptides may be anti-angiogenic, e.g. for treating
XX tumours, cardiovascular disease (arteriosclerosis, ischaemia), obesity,
XX diabetes, or they are proangiogenic, e.g. for promotion of wound
XX healing and to stimulate neovascularisation around occluded blood
XX vessels (a potential alternative to by-pass surgery or angioplasty).
XX The multivalent ligands may be used in human or veterinary medicine. They
XX may also be used raise peptide-specific antibodies (used for detecting
XX the peptides) and to identify and isolate compounds that interact with,
XX and modulate activity of, AHR. AHR are relatively small, conserved
XX sequences from different angiogenic peptides that are (largely)
XX responsible for biological activity. They are cheaper to prepare than
XX complete proteins, may be effective at lower doses, have long-lasting
XX in vivo effect and good biodistribution following oral or parenteral
XX administration. The present sequence represents a multivalent ligand
XX hybrid peptide given in the present invention.

CC Sequence 22 AA;

Query Match 28.3%; Score 32; DB 20; Length 22;

Best Local Similarity 35.7%; Pred. No. 90; Mismatches 4; Indels 0; Gaps 0;

OY 2 WELADOPONLEIL 15
| : : : : | : :
DB 4 WLSHPKALYSIV 17

RESULT 22
 Y42240
 ID Y42240 standard; peptide; 22 AA.
 AC Y42240;
 XX
 DT 20-DEC-1999 (first entry)
 XX
 DE Multivalent ligand T1p-16.40 peptide derivative.
 XX
 KW Angiogenic homology region; AHR; thrombospondin 1; TSP-1; angiotatin;
 endostatin; anticancer; antiangiogenic; cancer; cardiovascular disease;
 obesity; osteoarthritis; duodenal ulcer; abnormal neovascularisation;
 wound healing; arteriosclerosis; ischaemia; diabetes mellitus;
 blood vessel occlusion.
 XX
 OS Synthetic.
 XX
 PN MO9948923-A1.
 XX
 PD 30-SEP-1999.
 XX
 PE 22-MAR-1999; 99WO-US06246.
 XX
 PR 24-MAR-1998; 98US-0046985.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 XX
 PI Ben-Sasson SA;
 XX
 DR WPI: 1999-601204/51.
 XX
 PT New peptides and derived multivalent ligands based on angiogenic
 PT homology regions, used to inhibit or promote angiogenesis, e.g. for
 PT treating tumours -
 XX
 PS Claim 12; Fig 2; 76pp; English.
 XX
 CC The present invention specifically describes peptides comprising the
 CC angiogenic homology region (AHR) of thrombospondin (TSP) 4, angiotatin,
 CC endostatin or TSP-1. Multivalent ligands based on the peptides and
 CC related angiogenic peptides may be anti-angiogenic, e.g. for treating
 CC tumours, cardiovascular disease (arteriosclerosis, ischaemia), obesity,
 CC osteoarthritis, duodenal ulcers, abnormal ocular vascularisation in
 CC diabetes, or they are proangiogenic, e.g. for promotion of wound
 CC healing and to stimulate neovascularisation around occluded blood
 CC vessels (a potential alternative to by-pass surgery or angioplasty).
 CC The multivalent ligands may be used in human or veterinary medicine. They
 CC may also be used raise peptide-specific antibodies (used for detecting
 CC the peptides) and to identify and isolate compounds that interact with,
 CC and modulate activity of, AHR. AHR are relatively small, conserved
 CC sequences from different angiogenic peptides that are (largely)
 CC responsible for biological activity. They are cheaper to prepare than
 CC complete proteins; may be effective at lower doses; have long-lasting
 CC in vivo effect and good biodistribution following oral or parenteral
 CC administration. The present sequence represents a multivalent ligand
 CC peptide derivative given in the present invention.
 CC
 SO Sequence 22 AA:
 QY Query Match 28.3%; Score 32; DB 20; Length 22;
 Best Local Similarity 35.7%; Pred. No. 90;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 DB 2 WELADQPNLEIL 15
 4 WLSHNPXKLYSLV 17
 RESULT 23
 Y43404

ID Y43404 standard; peptide; 22 AA.
 AC Y43404;
 XX
 DT 20-DEC-1999 (first entry)
 XX
 DE Multivalent ligand T1p-15.40 hybrid peptide.
 XX
 KW Angiogenic homology region; AHR; thrombospondin 1; TSP-1; angiotatin;
 endostatin; anticancer; antiangiogenic; cancer; cardiovascular disease;
 obesity; osteoarthritis; duodenal ulcer; abnormal neovascularisation;
 wound healing; arteriosclerosis; ischaemic limb; ischaemic myocardium;
 diabetes mellitus; blood vessel occlusion.
 XX
 OS Synthetic.
 XX
 PN MO9948924-A1.
 XX
 PD 30-SEP-1999.
 XX
 PE 23-MAR-1999; 99WO-US06334.
 XX
 PR 24-MAR-1998; 98US-0046737.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 XX
 PI Ben-Sasson SA;
 XX
 DR WPI: 1999-591075/50.
 XX
 PT New angiogenic peptide derivatives, used for treating e.g. cancer,
 PT cardiovascular diseases, obesity, osteoarthritis, duodenal ulcers,
 PT abnormal neovascularisation and for wound healing -
 XX
 PS Disclosure; Fig 2; 62pp; English.
 XX
 CC The present invention specifically describes peptide derivatives
 CC comprising an angiogenic homology region (AHR) of endostatin. The peptide
 CC derivatives can be used for modulating angiogenesis in humans and
 CC animals. The peptides can be used to treat a wide variety of disease
 CC conditions, including cancer, cardiovascular diseases (e.g.
 CC arteriosclerosis, ischaemic limbs and ischaemic myocardium), obesity,
 CC osteoarthritis, duodenal ulcers, abnormal ocular neovascularisation
 CC associated e.g. with diabetes mellitus, and to promote wound healing or
 CC to stimulate the growth of new blood vessels to bypass, e.g. blood vessel
 CC occlusions. The peptide derivatives can also be used for the production
 CC of antibodies. The multivalent ligands may enable the administration of
 CC lower doses in order to achieve therapeutic efficacy, as compared with
 CC a univalent peptide chain. In addition, they can have long in vivo
 CC lifetimes and good biodistribution when administered orally or
 CC parenterally. The present sequence represents a multivalent ligand
 CC T1p-15.40 hybrid peptide given in the present invention.
 CC
 SO Sequence 22 AA:
 QY Query Match 28.3%; Score 32; DB 20; Length 22;
 Best Local Similarity 35.7%; Pred. No. 90;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 DB 2 WELADQPNLEIL 15
 4 WLSHNPXKLYSLV 17
 RESULT 24
 Y43408
 ID Y43408 standard; peptide; 22 AA.
 AC Y43408;
 XX
 DT 20-DEC-1999 (first entry)
 XX

XX Multivalent ligand Tip-16.40 peptide derivative.
 DE Angiogenic homology region; AHR; thrombospondin 1; TSP-1; angiotatin;
 XX endostatin; anticancer; antiangiogenic; cancer; cardiovascular disease;
 KM obesity; osteoarthritis; duodenal ulcer; abnormal neovascularisation;
 KM wound healing; arteriosclerosis; ischaemic limb; ischaemic myocardium;
 KM diabetes mellitus; blood vessel occlusion.
 XX Synthetic.
 OS
 XX MO9948924-A1.
 PN
 XX 30-SEP-1999.
 PD
 XX 23-MAR-1999; 99WO-US06334.
 PF
 XX 24-MAR-1998; 98US-0046737.
 PR
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 PI Ben-Sasson SA;
 PI WPI; 1999-591075/50.
 DR New angiogenic peptide derivatives, used for treating e.g. cancer,
 XX cardiovascular diseases, obesity, osteoarthritis, duodenal ulcers,
 PT abnormal neovascularisation and for wound healing
 PT
 XX Disclosure: Fig 3; 62pp; English.
 PS
 XX The present invention specifically describes peptide derivatives
 CC comprising an angiogenic homology region (AHR) of endostatin. The peptide
 CC derivatives can be used for modulating angiogenesis in humans and
 CC animals. The peptides can be used to treat a wide variety of disease
 CC conditions, including cancer, cardiovascular diseases (e.g.
 CC arteriosclerosis, ischaemic limbs and ischaemic myocardium), obesity,
 CC osteoarthritis, duodenal ulcers, abnormal ocular neovascularisation
 CC associated e.g. with diabetes mellitus, and to promote wound healing or
 CC to stimulate the growth of new blood vessels to bypass, e.g. blood vessel
 CC occlusions. The peptide derivatives can also be used for the production
 CC of antibodies. The multivalent ligands may enable the administration of
 CC lower doses in order to achieve therapeutic efficacy, as compared with
 CC a univalent peptide chain. In addition, they can have long in vivo
 CC lifetimes and good biodistribution when administered orally or
 CC parenterally. The present sequence represents a multivalent ligand
 CC Tip-16.40 peptide derivative given in the present invention.
 CC
 SO Sequence 22 AA;
 QY Query Match 28.3%; Score 32; DB 20; Length 22;
 Best Local Similarity 35.7%; Pred. No. 90;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 OY 2 WELADOPONLEIL 15
 DB 4 WLSHPKDLISIV 17
 RESULT 25
 Y42239
 ID Y42239 standard; peptide: 23 AA.
 XX
 AC Y42239;
 XX
 DT 20-DEC-1999 (first entry)
 XX
 DE Multivalent ligand Tip-17.40 peptide derivative.
 XX
 KM Angiogenic homology region; AHR; thrombospondin 1; TSP-1; angiotatin;
 KM endostatin; anticancer; antiangiogenic; cancer; cardiovascular disease;

KM obesity; osteoarthritis; duodenal ulcer; abnormal neovascularisation;
 KM wound healing; arteriosclerosis; ischaemia; diabetes mellitus;
 KM blood vessel occlusion.
 XX Synthetic.
 OS
 XX MO9948923-A1.
 PN
 XX 30-SEP-1999.
 PD
 XX 22-MAR-1999; 99WO-US06246.
 PF
 XX 24-MAR-1998; 98US-0046985.
 PR
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 PI Ben-Sasson SA;
 PI WPI; 1999-601204/51.
 DR New peptides and derived multivalent ligands based on angiogenic
 XX homology regions, used to inhibit or promote angiogenesis, e.g. for
 PT treating tumours
 PT
 XX Claim 12; Fig 2; 76pp; English.
 PS
 XX The present invention specifically describes peptides comprising the
 CC angiogenic homology region (AHR) of thrombospondin (TSP) 4, angiotatin,
 CC endostatin or TSP-1. Multivalent ligands based on the peptides and
 CC related angiogenic peptides may be anti-angiogenic, e.g. for treating
 CC tumors, cardiovascular disease (arteriosclerosis, ischaemia), obesity,
 CC osteoarthritis, duodenal ulcers, abnormal ocular vascularisation in
 CC diabetes, or they are proangiogenic, e.g. for promotion of wound
 CC healing and to stimulate neovascularisation around occluded blood
 CC vessels (a potential alternative to by-pass surgery or angioplasty).
 CC The multivalent ligands may be used in human or veterinary medicine. They
 CC may also be used to raise peptide-specific antibodies (used for detecting
 CC the peptides) and to identify and isolate compounds that interact with,
 CC and modulate activity of, AHR. AHR are relatively small, conserved
 CC sequences from different angiogenic peptides that are (largely)
 CC responsible for biological activity. They are cheaper to prepare than
 CC complete proteins; may be effective at lower doses; have long-lasting
 CC in vivo effect and good biodistribution following oral or parenteral
 CC administration. The present sequence represents a multivalent ligand
 CC peptide derivative given in the present invention.
 CC
 SO Sequence 23 AA;
 QY Query Match 28.3%; Score 32; DB 20; Length 23;
 Best Local Similarity 35.7%; Pred. No. 95;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 OY 2 WELADOPONLEIL 15
 DB 5 WLSHPKDLISIV 18

Search completed: February 5, 2001, 10:47:31
 Job time: 625 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:49:28; Search time 58.67 seconds
(without alignments)
23.147 Million cell updates/sec

Title: US-08-981-824-3

Perfect score: 113
Sequence: 1 NMEIADQPONLEIIMHCQR 20

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 5001

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR66:*\n1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	27.4	17	2	B48943 phage antigenic de
2	28	24.8	18	2	F49215 urease (EC 3.5.1.5
3	27	23.9	18	2	S10452 hypothetical prote
4	27	23.9	24	2	S68391 H+-transporting AT
5	25.5	22.6	25	2	T17886 aminoglycoside pho
6	25	22.1	20	2	UT0410 bombyxin-IV chain
7	25	22.1	25	2	PN0632 biphenyl dioxygena
8	24	21.2	11	2	S21127 precorrin methyltr
9	24	21.2	19	2	PH0793 T-cell receptor al
10	24	21.2	23	2	S13268 heat shock protein
11	24	21.2	24	2	S65047 ATP-dependent clp
12	24	21.2	24	2	B23317 threonine dehydrat
13	24	21.2	25	2	S73887 alpha-2-macroglobu
14	23.5	20.8	17	2	S66198 alcohol dehydrogen
15	23	20.4	9	2	A12872 transaldolase (EC
16	23	20.4	9	2	A11497 transaldolase (EC
17	23	20.4	14	2	F45037 TCR delta chain V-
18	23	20.4	15	2	PA0020 protein QAI0028 -
19	23	20.4	15	2	S51735 T-cell receptor be
20	23	20.4	18	2	PN0149 beta-Gliadin 13 -
21	23	20.4	20	2	D42842 antifungal 2S stor
22	23	20.4	20	2	S15861 estrogen receptor
23	23	20.4	21	2	D48516 PEB1 5'-region hyp
24	23	20.4	22	2	S52357 hypothetical prote
25	23	20.4	24	2	T42258 Ser/Thr protein ph
26	23	20.4	24	2	PN0655 alkaline trypsin-1
27	23	20.4	25	2	S10850 alpha-amylase inh1
28	23	20.4	25	2	S52124 alpha-gliadin S11
29	23	20.4	25	2	B36934 ORF3' of mada -

30	22	19.5	6	2	B31263 dihydrofolate redu
31	22	19.5	15	2	A26228 spot 42 protein -
32	22	19.5	15	2	T46625 hypothetical prote
33	22	19.5	15	2	JN0263 antigen (clone PV1
34	22	19.5	20	2	S00493 hemocyanin chain I
35	22	19.5	20	2	S11416 ribosomal protein
36	22	19.5	21	2	I65270 collagen alpha 1(I
37	22	19.5	21	2	A60684 L-ascorbate peroxi
38	22	19.5	21	2	S61306 probable nitrate r
39	22	19.5	22	2	S55308 glutathione transf
40	22	19.5	24	2	A45336 cystic fibrosis tr
41	22	19.5	25	2	PC2204 interferon-alpha L
42	22	19.5	25	2	S22228 vitronectin - dog
43	22	19.5	25	3	P00716 Glutelin 7.3/31K -
44	21.5	19.0	23	2	B29175 clostripain (EC 3.
45	21	18.6	10	2	S63696 DNA polymerase - y

ALIGNMENTS

RESULT 1
B48943
phage antigenic determinant (clone pOA79) - phage phi-197 (fragment)
C:Species: phage phi-197
C:Date: 13-Aug-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C:Accession: B48943
R:Schouler, C.; Bouet, C.; Ritzenthaler, P.; Drouet, X.; Mata, M.
Appl. Environ. Microbiol. 58, 2479-2484, 1992
A:Title: Characterization of Lactococcus lactis phage antigens.
A:Reference number: A48943; MUID:92384563
A:Contents: Lactococcus lactis
A:Accession: B48943
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <SCH>
A>Note: sequence modified after extraction from NCBI backbone
A>Note: sequence extracted from NCBI backbone (NCBIN:114551)

Query Match 27.4%; Score 31; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 NMEIIMH 17
DB 6 NMEIIMH 13
RESULT 2
F49215
urease (EC 3.5.1.5) small chain Urea - Helicobacter mustelae (ATCC 43772) (fragment)
C:Species: Helicobacter mustelae
C:Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 30-May-1997
C:Accession: F49215
R:Ruprecht, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A:Title: Purification and characterization of the urease enzymes of Helicobacter spec
A:Reference number: A49215; MUID:93084378
A:Accession: F49215
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <TR>
A>Note: sequence extracted from NCBI backbone (NCBIP:119487)
C:Superfamily: urease 26K chain; urease 11K chain homology; urease 12K chain homology
C:Keywords: hydrolase

Query Match 24.8%; Score 28; DB 2; Length 18;
Best Local Similarity 30.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 8 POMEIIMH 17

Db 3 PKELDKMLH 12

RESULT 3

hypothetical protein (bpha 5' region) - *Aspergillus niger*

C:Species: *Aspergillus niger*

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997

C:Accession: S10452

R:van Gorm, R.F.M.; Boschloo, J.G.; Kuyjnenhoven, A.; Lange, J.; Bos, C.J.; van Balken submitted to the EMBL Data Library, March 1990

A:Reference number: S10452

A:Accession: S10452

A:Molecule type: DNA

A:Residues: 1-18 <VAN>

A:Cross-references: EMBL:X52521; NID:g2336; PID:g2337

Query Match

Best Local Similarity 41.7%; Score 27; DB 2; Length 18; Pred. No. 5.2e+02;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 LADQPONLEIL 15

Db 1 MTDOPLSRQETL 12

RESULT 4

H+-transporting ATP synthase (EC 3.6.1.34) delta chain, chloroplast - *Chlamydomonas reinhardtii*

N:Alternate names: ATP synthase delta chain

C:Species: *Chlamydomonas reinhardtii*

C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999

C:Accession: S68391

R:Riedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.

FEBS Lett. 377, 163-166, 1995

A:Title: Isolation of CF(0)CF(1) from *Chlamydomonas reinhardtii* cw15 and the N-terminal

A:Reference number: S68388; MUID:96128220

A:Accession: S68391

A:Molecule type: protein

A:Residues: 1-24 <FTE>

A:Experimental source: strain CW15

C:Genetics:

C:Superfamily: H+-transporting ATP synthase delta chain

C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thylakoid

Query Match 23.9%; Score 27; DB 2; Length 24;

Best Local Similarity 60.0%; Pred. No. 7.1e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 ELADQPONLEIL 12

Db 15 ELADKQKLE 24

RESULT 5

aminoglycoside phosphotransferase - *Bacillus circulans* (fragment)

C:Species: *Bacillus circulans*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000

C:Accession: T17886

R:Aubert-Pivert, E.; Davies, J.

Gene 147, 1-11, 1994

A:Title: Biosynthesis of butirosin in *Bacillus circulans* NRRL B3312: identification by

A:Reference number: Z18808; MUID:94374689

A:Accession: T17886

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-25 <AVB>

A:Cross-references: EMBL:L20421; NID:g304142; PID:g688437; PIDN:AAA62589.1

C:Genetics:

A:Gene: *aphA4/DutA*

C:Function:

A:Pathway: butirosin biosynthesis

C:Superfamily: kanamycin kinase

Query Match

Best Local Similarity 22.6%; Score 25.5; DB 2; Length 25; Pred. No. 1.3e+03;

Matches 6; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

OY 1 NWEADQPONLEIL 15

Db 7 NW----PEELEIL 16

RESULT 6

bombyxin-IV chain A - silkworm

C:Species: *Bombyx mori* (silkworm)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Mar-1998

C:Accession: JT0410

R:Muryama, K.; Hietter, H.; Nagasawa, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishiz

Agri. Biol. Chem. 52, 3035-3041, 1988

A:Title: Isolation and primary structure of bombyxin-IV, a novel molecular species of

A:Reference number: JT0410

A:Accession: JT0410

A:Molecule type: protein

A:Residues: 1-20 <MAR>

C:Superfamily: Insulin

F:6-11/Disulfide bonds: #status predicted

F:7/Disulfide bonds: Interchain (to chain B-10) #status predicted

F:20/Disulfide bonds: Interchain (to chain B-22) #status predicted

Query Match 22.1%; Score 25; DB 2; Length 20;

Best Local Similarity 31.2%; Pred. No. 1.2e+03;

Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 3 ELADQPONLEILMHC 18

Db 5 ECCIQPCTLDVATVC 20

RESULT 7

biphenyl dioxygenase (EC 1.13.-.-) A4 - *Pseudomonas* sp. (strain LB400) (fragment)

C:Species: *Pseudomonas* sp.

C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 12-Apr-1995

C:Accession: PN0632

R:Hofer, B.; Ellis, L.D.; Dowling, D.N.; Timms, K.N.

Gene 10, 47-55, 1993

A:Title: Genetic analysis of a *Pseudomonas* locus encoding a pathway for biphenyl/poly

A:Reference number: PN0632; MUID:93345822

A:Accession: PN0632

A:Molecule type: DNA

A:Residues: 1-25 <HOF>

A:Cross-references: GB:X66122

C:Genetics:

A:Gene: *bphA4*

C:Superfamily: toluene dioxygenase ferredoxin reductase component

C:Keywords: oxidoreductase; PCB biodegradation

Query Match 22.1%; Score 25; DB 2; Length 25;

Best Local Similarity 38.5%; Pred. No. 1.5e+03;

Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 3 ELADQPONLEIL 15

Db 8 QLODVGSNLRDL 20

RESULT 8
S21127
precocin methyltransferase - Salmonella typhimurium
C:Species: Salmonella typhimurium
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S21127
R:Recessner, C.A.; Warren, M.J.; Santander, P.J.; Atshaves, B.P.; Ozaki, S.; Stojowich, N.
FEBS Lett. 301, 73-78, 1992
A:Title: Expression of 9 Salmonella typhimurium enzymes for cobinamide synthesis. Ident
A:Reference number: S21127; MUID:93083628
A:Accession: S21127
A:Status: Preliminary
A:Molecule type: Protein
A:Residues: 1-11 <PRO>

Query Match 21.2% Score 24; DB 2; Length 11;
Best Local Similarity 66.7% Pred. No. 8.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 QPOMLE 12
| | | | |
Db 6 QPOTIE 11

RESULT 9
PH0793
T-cell receptor alpha chain (H2 V-alpha-7.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0793
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846
A:Accession: PH0793
A:Molecule type: mRNA
A:Residues: 1-19 <CAS>
A:Cross-references: EMBL:X60898
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 21.2% Score 24; DB 2; Length 19;
Best Local Similarity 100.0% Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WELA 5
| | | | |
Db 4 WELA 7

RESULT 10
S13268
heat shock protein, 90K - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 21-Nov-1998
C:Accession: S13268
R:Ichih, H.; Toyoshima, I.; Mizunuma, H.; Kobayashi, R.; Tashima, Y.
Arch. Biochem. Biophys. 282, 290-296, 1990
A:Title: Three-step purification method and characterization of the bovine brain 90-kDa
A:Reference number: S13268; MUID:91053144
A:Accession: S13268
A:Molecule type: Protein
A:Residues: 1-23 <ITC>
A:Experimental source: brain
C:Superfamily: heat shock protein 90
C:Keywords: cytosol; estrogen-induced protein; heat shock; homodimer; phosphoprotein; st

Query Match 21.2% Score 24; DB 2; Length 23;
Best Local Similarity 62.5% Pred. No. 2e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 6 DOPOMLEE 13
| | | | |
Db 15 DQTEYLEE 22

RESULT 11
S65047
ATP-dependent clp proteinase (EC 3.4.21.-) chain P - barley chloroplast (fragment)
C:Species: chloroplast Hordeum vulgare (barley)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C:Accession: S65047; S57946
R:Huebschmann, T.; Hess, W.R.; Boerner, T.
Plant Mol. Biol. 30, 109-123, 1996
A:Title: Impaired splicing of the rps12 transcript in ribosome-deficient plastids.
A:Reference number: S65047; MUID:96197402
A:Accession: S65047
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-24 <HUE>
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
C:Genetics:
A:Gene: clpP
A:Genome: chloroplast
A:Function:
A:Description: ATP-driven cleavage of proteins to small peptides
A:Note: magnesium required
C:Superfamily: ATP-dependent Clp proteinase chain P
C:Keywords: ATP; chloroplast; hydrolase; serine proteinase

Query Match 21.2% Score 24; DB 2; Length 24;
Best Local Similarity 55.6% Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 EEILMHCOT 20
| | | | |
Db 4 EMIDKHCDT 12

RESULT 12
B22317
threonine dehydratase (EC 4.2.1.16) - Salmonella typhimurium (fragment)
C:Species: Salmonella typhimurium
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 22-Nov-1996
C:Accession: B22317
R:Kim, S.S.; Datta, P.
Biochim. Biophys. Acta 706, 27-35, 1982
A:Title: Chemical characterization of biodegradative threonine dehydratases from two
A:Reference number: A90645; MUID:83023208
A:Accession: B22317
A:Molecule type: Protein
A:Residues: 1-24 <KIM>
C:Superfamily: threonine dehydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase; threonine catabolism

Query Match 21.2% Score 24; DB 2; Length 24;
Best Local Similarity 50.0% Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 DOPOMLEEIL 15
| | | | |
Db 6 DLPVAIEDIL 15

RESULT 13
S71387
alpha-2-macroglobulin - Atlantic horseshoe crab (fragments)
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999

C:Accession: S71387
 R:Dolmer, K.; Husted, L.B.; Armstrong, P.B.; Sottrup-Jensen, L.
 FEBS Lett. 393, 37-40, 1996
 A:Title: Localisation of the major reactive lysine residue involved in the self-crosslink
 A:Reference number: S71387; MUID:96397525
 A:Accession: S71387
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13;14-25 <DOL>
 C:Keywords: dimer; disulfide bond; proteinase inhibitor

Query Match 21.2%; Score 24; DB 2; Length 25;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 NMEADOP 8
 DB 2 NMEADGP 9

RESULT 14

S66198
 alcohol dehydrogenase (EC 1.1.1.1) class III - garden pea (fragment)
 C:Species: Pisum sativum (garden pea)
 C:Date: 14-Feb-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
 C:Accession: S66198
 R:Hjeltny, L.; Hackett, M.; Shafat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;
 FEBS Lett. 367, 237-240, 1995
 A:Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M
 nzyme.
 A:Reference number: S66191; MUID:95331382
 A:Accession: S66198
 A:Molecule type: protein
 A:Residues: 1-17 <HJE>
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 20.8%; Score 23.5; DB 2; Length 17;
 Best Local Similarity 30.8%; Pred. No. 1.7e+03;
 Matches 4; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

OY 2 WELADOPNLEI 14
 DB 5 WE-PNKPRTIEDV 16

RESULT 15

transaldolase (EC 2.2.1.2) I - yeast (Pichia jadinii) (fragment)
 A12872
 C:Species: Pichia jadinii, Candida utilis
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Sep-1993
 C:Accession: A12872
 R:Sun, S.C.; Joris, L.; Tsolas, O.
 Arch. Biochem. Biophys. 178, 69-78, 1977
 A:Title: Purification and crystallization of transaldolase isozyme I and evidence for di
 A:Reference number: A12872; MUID:77110646
 A:Accession: A12872
 A:Molecule type: protein
 A:Residues: 1-9 <SUN>
 C:Keywords: transferase

Query Match 20.4%; Score 23; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 16 MHCOT 20
 DB 3 IHCBT 7

RESULT 16
 A11497
 transaldolase (EC 2.2.1.2) III - yeast (Pichia jadinii) (fragment)

C:Species: Pichia jadinii, Candida utilis
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 30-Sep-1993
 C:Accession: A11497
 R:Tsolas, O.; Sun, S.C.
 Arch. Biochem. Biophys. 167, 525-533, 1975
 A:Title: Isolation of a peptide containing a histidyl-cysteinyl sequence from the a
 A:Reference number: A11497; MUID:75145197
 A:Accession: A11497
 A:Molecule type: protein
 A:Residues: 1-9 <TSO>
 C:Keywords: transferase

Query Match 20.4%; Score 23; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 16 MHCOT 20
 DB 3 IHCBT 7

RESULT 17

FA9037
 TCR delta chain V-D-J region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: FA9037
 R:Bezguerra, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E
 Eur. J. Immunol. 22, 491-498, 1992
 A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of th
 A:Reference number: FA9037; MUID:92164730
 A:Accession: FA9037
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-14 <EQ>
 A:Cross-references: GB:S90654; NID:g246298; PIDN:AB21552.1; PID:g246299
 A:Experimental source: dendritic epidermal T-cell lines
 A:Note: sequence extracted from NCBI backbone (NCBI:90654, NCBI:90666)

Query Match 20.4%; Score 23; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 WELAD 6
 DB 4 WELSE 8

RESULT 18

protein OA100028 - Arabidopsis thaliana (fragment)
 PA0020
 C:Species: Arabidopsis thaliana (mouse ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0020
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JRPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
 A:Reference number: PA0001
 A:Accession: PA0020
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: callus

Query Match 20.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 QPONEE 13
 Db 4 QPARMEE 10

RESULT 19

S51735
 T-cell receptor beta-chain joining region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
 C:Accession: S51735
 R:Dimitrov-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.
 submitted to the EMBL data library, November 1993
 A:Reference number: S51732
 A:Accession: S51735
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15 <DUP>
 A:Cross-references: EMBL:Z28344; NID:9607122; PIDN:CAA82198.1; PID:9607123
 C:Keywords: T-cell receptor

Query Match 20.4%; Score 23; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.8e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 LADOPON 10
 Db 8 LGNOPH 14

RESULT 20

PN0149
 beta-gliadin 13 - Aegilops longissima (fragment)
 C:Species: Aegilops longissima
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PN0149
 R:Odintsova, T.I.; Egorov, T.A.
 Biokhimiia 55, 509-516, 1990
 A:Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of
 A:Reference number: PN0146; MUID:90283493
 A:Accession: PN0149
 A:Molecule type: protein
 A:Residues: 1-18 <CD1>
 A:Experimental source: strain K-202
 C:Superfamily: gliadin

Query Match 20.4%; Score 23; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 OPON 10
 Db 9 QPON 12

RESULT 21

D42842
 antifungal 2S storage albumin large chain - radish (fragment)
 C:Species: Raphanus sativus (radish)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
 C:Accession: D42842
 R:Terras, F.R.; Schoofs, H.M.; De Bolle, M.F.; Van Leuven, F.; Rees, S.B.; Vanderleyden, J.
 Biol. Chem. 267, 15301-15309, 1992
 A:Title: Analysis of two novel classes of plant antifungal proteins from radish (Raphanus)
 A:Reference number: A42842; MUID:92348373
 A:Accession: D42842
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <TER>
 A:Experimental source: seed
 A:Note: sequence extracted from NCBI backbone (NCBI:109925)

C:Superfamily: wheat alpha-amylase inhibitor

Query Match 20.4%; Score 23; DB 2; Length 20;
 Best Local Similarity 36.4%; Pred. No. 2.5e+03;
 Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 8 PONEILMHC 18
 Db 4 PQRPPLQOC 14

RESULT 22

S15861
 estrogen receptor - pig (fragments)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 30-May-1997
 C:Accession: S15861
 R:Thole, H.H.; Jungblut, P.W.; Jakob, F.
 Biochem. J. 276, 709-714, 1991
 A:Title: The proton-driven dissociation of oestradiol-receptor dimers as a preparative
 A:Reference number: S15861; MUID:91291128
 A:Accession: S15861
 A:Molecule type: protein
 A:Residues: 1-20 <BIO>
 C:Keywords: steroid hormone receptor

Query Match 20.4%; Score 23; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.5e+03;
 Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 NWEIADOPON 10
 Db 7 NWAUKHAPT 16

RESULT 23

D48518
 PEB1 5'-region hypothetical protein A - Campylobacter jejuni (fragment)
 C:Species: Campylobacter jejuni
 C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 19-May-1995
 C:Accession: D48518
 R:Pei, Z.; Blaser, M.J.
 J. Biol. Chem. 268, 18717-18725, 1993
 A:Title: PEB1, the major cell-binding factor of Campylobacter jejuni, is a homolog of
 A:Reference number: A48518; MUID:93366784
 A:Accession: D48518
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-21 <PE1>
 A:Cross-references: GB:L13662

Query Match 20.4%; Score 23; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 2.6e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 7 OPONEEI 14
 Db 3 KPMILKEI 10

RESULT 24

S52357
 hypothetical protein - human
 C:Species: Homo sapiens (man)
 C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
 C:Accession: S52357
 R:Agriokastiris, A.; Leversha, M.A.; Ferguson-Smith, M.; Moschonas, M.K.
 submitted to the EMBL data library, March 1993
 A:Description: A cosmid clone mapped to human chromosome 11p15 detects a Tag I restr

A:Reference number: S52355
A:Accession: S52357
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <AGR>
A:Cross-references: EMBL:X72881; NID:g667002; PIDN:CAA51393.1; PID:g667004

Query Match
Best Local Similarity 20.4%; Score 23; DB 2; Length 22;
Matches 5; Conservativity 50.0%; Pred. No. 2.7e+03;
Matches 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 LADQPNLEE 13
| : | | |
Db 12 LGEORANTEE 21

RESULT 25

T42258
Ser/Thr protein phosphatase homolog - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T42258
R:Zeke, T.; Gergely, P.; Dombradi, V.
submitted to the EMBL Data Library, July 1996
A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis
A:Reference number: 222131
A:Accession: T42258
A>Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: DNA
A:Residues: 1-24 <ZEK>
A:Cross-references: EMBL:277734; PIDN:CAB01293.1
C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein

Query Match
Best Local Similarity 20.4%; Score 23; DB 2; Length 24;
Matches 6; Conservativity 50.0%; Pred. No. 3e+03;
Matches 6; Mismatches 1; Indels 0; Gaps 0;

OY 7 OPONEEILMHC 18
| : | | | |
Db 1 QSIHLRLIMTC 12

Search completed: February 5, 2001, 10:49:29
Job time: 742 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:55:58 ; Search time 32.57 Seconds
(without alignments)
19.831 Million cell updates/sec

Title: US-08-981-824-3

Perfect score: 113
Sequence: 1 NMEIADQPONLEILMHCQT 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1436

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	22.1	23	1	UDP_LACCA
2	24	21.2	24	1	CLPP_HORVU
3	24	21.2	24	1	THD2_SALT
4	23	20.4	9	1	TAL1_PICJA
5	23	20.4	9	1	TAL3_PICJA
6	23	20.4	9	1	OXLA_AGRH
7	22	19.5	19	1	DHAB_COMTE
8	21	18.6	10	1	GON2_CHEPR
9	21	18.6	10	1	MOSQ_CICXA
10	21	18.6	16	1	MMPX_SOLTU
11	21	18.6	21	1	RL5_HALME
12	21	18.6	22	1	RL5_HALVO
13	21	18.6	23	1	IAPP_LIEPU
14	21	18.6	23	1	RL5_HALHA
15	20	17.7	15	1	FKB7_PINPS
16	20	17.7	15	1	GLN2_PINPS
17	20	17.7	15	1	VORA_METTM
18	20	17.7	16	1	LEO5_BIOGL
19	20	17.7	17	1	EEG_THENO
20	20	17.7	19	1	DCAM_AACCA
21	20	17.7	19	1	ETFA_CLOPA
22	20	17.7	19	1	OXLA_OPHHA
23	20	17.7	20	1	DETS_RAT
24	20	17.7	20	1	PSAL_SYNVU
25	20	17.7	24	1	RAN_XENLA
26	19.5	17.3	18	1	NPA_BOVIN
27	19	16.8	10	1	GON1_ALIMI
28	19	16.8	15	1	RBS_PHYRA
29	19	16.8	17	1	BOL2_MESPE
30	19	16.8	17	1	BOLA_MESPE
31	19	16.8	17	1	GSXK_PINPS
32	19	16.8	20	1	COXF_ONCMY
33	19	16.8	20	1	CPXX_RHQRH

34	19	16.8	21	1	YFLA_METVO
35	19	16.8	24	1	IRBP_SHEEP
36	19	16.8	25	1	UBLI_BOVIN
37	18	15.9	14	1	KARA_BROPL
38	18	15.9	14	1	MAST_PARID
39	18	15.9	14	1	MAST_VESXA
40	18	15.9	15	1	ITRB_ALBUJ
41	18	15.9	16	1	AHL_PRUSE
42	18	15.9	16	1	CAT9_FASHE
43	18	15.9	17	1	BOLA_MESPE
44	18	15.9	17	1	TPIS_PINPS
45	18	15.9	18	1	MCRB_METTE

ALIGNMENTS

RESULT 1	UDP_LACCA	STANDARD:	PRT:	23 AA.
ID	UDP_LACCA			
AC	P19662;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	URIDINE PHOSPHORYLASE (EC 2.4.2.3) (UDRPHASE) (FRAGMENT).			
GN	UDP.			
OS	Lactobacillus casei.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;			
NC	Lactobacillus.			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN-ATCC 7469;			
RC	MEDLINE-90381286; PubMed-2119230;			
RA	Avraham Y., Groszowicz N., Yashphe J.;			
RT	Purification and characterization of uridine and thymidine phosphorylase from Lactobacillus casei.			
RL	Biochim. Biophys. Acta 1040:287-293 (1990).			
CC	- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES.			
CC	OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.			
CC	- CATALYTIC ACTIVITY: URIDINE + PHOSPHATE -> URACIL + ALPHA-D-RIBOSE 1-PHOSPHATE.			
CC	- PATHWAY: NUCLEOTIDE AND DEOXYRIBONUCLEOTIDE CATABOLISM.			
CC	- SUBUNIT: HOMOTETRAMER.			
CC	- SIMILARITY: BELONGS TO THE PNP/UDP FAMILY 1 OF PHOSPHORYLASES.			
DR	PIR: S11383; S11383.			
DR	INTERPRO: IPR000845; .			
DR	PROSITE: PS01232; PNP-UDP-1; PARTIAL.			
KW	Transferase; Glycosyltransferase.			
FT	UNSURE 1			
FT	UNSURE 7			
FT	NON TER 23			
SQ	SEQUENCE 23 AA; 2630 MM; 918B2E2F32F35A17 CRC64;			

Query Match 22.1%; Score 25; DB 1; Length 23;

Best Local Similarity 27.3%; Pred. No. 5.6e+02; Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 8 PONEEILMHC 18
| : : : : |
DB 6 PERLDKVLVC 16

RESULT 2	CLPP_HORVU	STANDARD:	PRT:	24 AA.
ID	CLPP_HORVU			
AC	P48863;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	PROBABLE CLPP-LIKE PROTEINASE (EC 3.4.21.92) (ENDOPEPTIDASE CLP)			

```

DE (FRAGMENT).
GN CLPP.
OS Hordeum vulgare (Barley).
OG Chloroplast.
CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. HAISA;
RX MEDLINE=96197402; PubMed=8616228;
RA Hubschmann T.; Hess W.; Boerner T.;
RT "Impaired splicing of the rps12 transcript in ribosome-deficient
RL plants." Biol. 30:109-123(1996).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS TO SMALL PEPTIDES IN
CC THE PRESENCE OF ATP AND MAGNESIUM. ALPHA-CASEIN IS THE USUAL TEST
CC SUBSTRATE. IN THE ABSENCE OF ATP, ONLY OLIGOPEPTIDES SHORTER THAN
CC FIVE RESIDUES ARE CLEAVED (SUCH AS SUCCINY-L-LEU-TYR-L-NHMEC, AND
CC L-LEU-TYR-L-LEU-TYR-TYR, IN WHICH THE CLEAVAGE OF THE -TYR-L-LEU-
CC AND -TYR-L-TYR- BOND ALSO OCCURS).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S14; ALSO KNOWN AS CLPP
CC FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL: X89562; CA61738.1;
CC MENDEL: 2297; HORVU:CLPP.1;
CC INTERPRO: IPR001907;
CC PROSITE: PS00381; CLP_PROTEASE_SER; PARTIAL.
CC PROSITE: PS00382; CLP_PROTEASE_HIS; PARTIAL.
CC HYDROLASE; Serine protease; Chloroplast.
CC NON_TER 1
CC SEQUENCE 24 AA: 2941 MW: 715EB01FE3E073CE CRC64;
SQ

```

Query Match 21.2%; Score 24; DB 1; Length 24;
 Best Local Similarity 55.6%; Pred. No. 8.5e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY 12 EELMHQOT 20
DB 4 EMDKHCOT 12

```

RESULT 3

```

THD2_SALT STANDARD; PRT; 24 AA.
AC P11954;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1993 (Rel. 31, Last annotation update)
DE THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE)
DE (FRAGMENT).
GN TDCB.
OS Salmonella typhimurium.
CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Salmonella.
RN [1]
RP SEQUENCE.
RX MEDLINE=83023208; PubMed=6751404;
RA Kim S.S.; Datta P.;
RT "Chemical characterization of biodegradative threonine dehydratases
RT from two enteric bacteria."
RL Biochim. Biophys. Acta 706:27-35(1982).
CC -1- CATALYTIC ACTIVITY: L-THREONINE + H(2)O -> 2-OXOBUTANOATE + NH(3)
CC + H(2)O.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.

```

```

CC -1- ENZYME REGULATION: EACH PROTEIN MOLECULE CAN BIND UP TO FOUR
CC MOLECULES OF AMP, WHICH ACTS AS AN ALLOSTERIC ACTIVATOR TO THE
CC ENZYME. THE ENZYME IS ALSO INHIBITED BY ALPHA-KETO ACIDS AND OTHER
CC CATABOLITES. IT IS ALLOSTERICALLY INHIBITED BY ISOLEUCINE
CC AND ALLOSTERICALLY ACTIVATED BY VALINE.
CC -1- PATHWAY: THREONINE CATABOLISM.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: TO THREONINE DEHYDRATASE BIOSYNTHETIC AND SERINE
CC DEHYDRATASE.
CC PIR: B22317; B22317.
CC STGENE: SG10390; TDCB.
CC INTERPRO: IPR000634;
CC PROSITE: PS00165; DEHYDRATASE_SER_THR; PARTIAL.
CC Lysase; Pyridoxal phosphate; Allosteric enzyme.
CC NON_TER 24
CC SEQUENCE 24 AA: 2710 MW: 57BE403BF2C72AF3 CRC64;
SQ

```

Query Match 21.2%; Score 24; DB 1; Length 24;
 Best Local Similarity 50.0%; Pred. No. 8.5e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

OY 6 DOPONLEIL 15
DB 6 DLPVAIEDIL 15

```

RESULT 4

```

TAL3_PICJA STANDARD; PRT; 9 AA.
AC P17440;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE TRANSALDOLASE I (EC 2.2.1.2) (FRAGMENT).
OS Pichia jadinii (Yeast) (Candida utilis).
CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
CC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE.
RX MEDLINE=77110646; PubMed=556924;
RA Sun S.C.; Joris L.; Teolae O.;
RT "Purification of crystallization of transaldolase isozyme I and
RT evidence for different genetic origin of isozymes I and III in
RT Candida utilis."
RL Arch. Biochem. Biophys. 178:69-78(1977).
CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
CC 3-PHOSPHATE -> D-ERYTHROSE 4-PHOSPHATE + D-FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: NONOXIDATIVE PART OF THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
CC PIR: A12872; A12872.
CC INTERPRO: IPR001585;
CC PROSITE: PS00958; TRANSALDOLASE_2; PARTIAL.
CC PROSITE: PS01054; TRANSALDOLASE_1; PARTIAL.
CC TRANSFERASE; Pentose shunt.
CC NON_TER 1
CC SEQUENCE 9 AA: 1008 MW: 274E31AF0EB1E058 CRC64;
SQ

```

Query Match 20.4%; Score 23; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 8.9e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 16 MHCOT 20
DB 3 IHCRT 7

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RESULT 5

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TAL3_PICJA

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ID TAL2_PICJA STANDARD; PRT; 9 AA.
 AC P1741;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE TRANSALDOLASE III (EC 2.2.1.2) (FRAGMENT).
 OS Pichia jadinii (Yeast) (Candida utilis).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-75145197; PubMed-1092268;
 RA Tsoias O., Sun S.C.;
 RT "Isolation of a peptide containing a histidyl-cysteinyl sequence
 from the active center of transaldolase.";
 RL Arch. Biochem. Biophys. 167:525-533(1975).
 CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
 METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
 CC -1- CATALYTIC ACTIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE
 3-PHOSPHATE -> D-ERYTHROSE 4-PHOSPHATE + D-FRUCTOSE 6-PHOSPHATE.
 CC -1- PATHWAY: NONOXIDATIVE PART OF THE PENTOSE-PHOSPHATE PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
 DR INTERPRO: IPR001585;
 DR PROSITE: PS00588; TRANSALDOLASE_2; PARTIAL.
 DR PROSITE: PS01054; TRANSALDOLASE_1; PARTIAL.
 KW TRANSFERASE; Pentose shunt.
 FT NON_TER 1 1
 FT SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;
 SQ
 Query Match 20.4%; Score 23; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 8.9e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 16 MHQT 20
 DB 3 INCHT 7
 RESULT 6
 OXLA_AGRH STANDARD; PRT; 20 AA.
 AC P81382;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE L-AMINO ACID OXIDASE (EC 1.4.3.2) (LAO) (LAOD) (FRAGMENT).
 OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Sclerosauria; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Calloselasma.
 RN [1]
 RP SEQUENCE.
 RX TISSUE-VENOM;
 RX MEDLINE-94361525; PubMed-8080286;
 RA Ponnudurai G., Chung M.C.M., Tan N.-H.;
 RT "Purification and properties of the L-amino acid oxidase from Malayan
 pit viper (Calloselasma rhodostoma) venom.";
 RL Arch. Biochem. Biophys. 313:373-378(1994).
 CC -1- FUNCTION: HAS CYTOTOXIC ACTIVITY. THIS PROTEIN HAS A PH OPTIMUM
 OF 9.0. A DETERMINED PI OF 4.4 AND IS TEMPERATURE STABLE.
 CC -1- CATALYTIC ACTIVITY: A L-AMINO ACID + H(2)O + O(2) -> A 2-OXO ACID +
 NH(3) + H(2)O(2).
 CC -1- COFACTOR: FAD.
 CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
 CC STRONG, TO MOUSE FIG-1.
 KW Oxidoreductase; Flavoprotein; FAD; Venom.
 FT NON_TER 20 20
 FT SEQUENCE 20 AA; 2443 MW; 96260598D7F7D07 CRC64;
 DR

Query Match 20.4%; Score 23; DB 1; Length 20;
 Best Local Similarity 55.6%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7 OPONLEET 15
 DB 12 QENITEEL 20
 RESULT 7
 DHAB_COMTE STANDARD; PRT; 19 AA.
 AC P80704;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ALDEHYDE DEHYDROGENASE, BETA CHAIN (EC 1.2.99.3) (ALDH) (FRAGMENT).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; Beta subdivision; Comamonadaceae; Comamonas.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-ATCC 15667;
 RA Luykx D.M.A.M., Kim S.W., de Vries S., Duine J.A.;
 RL Submitted (JUL-1996) to the SWISS-PROT data bank.
 CC -1- CATALYTIC ACTIVITY: AN ALDEHYDE + ACCEPTOR + H(2)O -> AN ACID +
 REDUCED ACCEPTOR.
 CC -1- COFACTOR: MOLYBDENUM.
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA AND A GAMMA
 CHAIN.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 19 19
 FT SEQUENCE 19 AA; 2096 MW; 89BD67DAD05A212E CRC64;
 SQ

Query Match 19.5%; Score 22; DB 1; Length 19;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 8 PONTLEET 14
 DB 9 PRTIDEV 15
 RESULT 8
 GON2_CHEPR STANDARD; PRT; 10 AA.
 AC P80678;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GONADOLIBERIN II (GONADOTROPIN-RELEASING HORMONE II) (GNRH-II)
 DE (LUTIBERIN II).
 OS Chelysoma productum.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
 OC Corellidae; Chelyosoma.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-96413669; PubMed-8816823;
 RA Powell J.F.F., Reeska-Skinner S.M., Prakash M.O., Fischer W.H.,
 RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
 RT "Two new forms of gonadotropin-releasing hormone in a protochordate
 and the evolutionary implications.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
 FOLLICLE-STIMULATING HORMONES.
 CC -1- SUBUNIT: HOMODIMER, LINKED BY DISULFIDE BRIDGE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: GNRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
 THE GONADUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
 THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
 CC -1- MASS SPECTROMETRY: MW-1117.52; METHOD-MALDI.
 CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
 DR INTERPRO: IPR002012; -

DR PROSITE; PS00473; GNRH; 1.
 KW Hormone; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 6 6 INTERCHAIN.
 FT MOD_RES 10 10 AMIDATION (BY SIMILARITY).
 SO SEQUENCE 10 AA: 1135 MW: 284538DLSEB735A3 CRC64;

Query Match 18.6%; Score 21; DB 1; Length 10;
 Best Local Similarity 37.5%; Pred. No. 9.6e+02;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 NWEIADOP 8
 : : : :
 Db 2 HWSLCHAP 9

RESULT 9
 MOSQ_CLYXA STANDARD; PRT; 10 AA.
 ID P19962;
 AC P19962;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE [Gln-6]-MOSACT.
 OS Clypeaster japonicus (Sand dollar).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
 CN Clypeasteridae; Clypeaster.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-EGG JELLY;
 RC Suzuki N., Kurita M., Yoshino K., Kajitara H., Nomura K., Yamaguchi M.;
 RA "Purification and structure of mosact and its derivatives from the
 RT egg jelly of the sea urchin Clypeaster japonicus";
 RL Zool. Sci. 4:649-656(1987).
 CC -1- FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.
 DR PIR: JN0025; JN0025. 9AFB032456DC5BA CRC64;
 SO SEQUENCE 10 AA: 1019 MW: 9AFB032456DC5BA CRC64;

Query Match 18.6%; Score 21; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 9.6e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 ADQOPNL 11
 : : : : :
 Db 2 SDSAONL 8

RESULT 10
 MPX_SOLTU STANDARD; PRT; 16 AA.
 ID P80501;
 AC P80501;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE UNIDENTIFIED MITOCHONDRIAL MATRIX PROTEIN (FRAGMENT).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Solanum.

RN [1]
 RP SEQUENCE.
 RC TISSUE-TUBER;
 RX MEDLINE-97077345; PubMed-8919912;
 RA Jansch L., Kruff V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 of the protein complexes of plant mitochondria";
 RL Plant J. 9:357-368(1996).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 KW Mitochondrion.
 FT NON_TER 16 16

SO SEQUENCE 16 AA: 1768 MW: C58D4DB48A18B8D CRC64;

Query Match 18.6%; Score 21; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 ELADQPN 10
 : : : : :
 Db 7 ELVEKGN 14

RESULT 11
 RL5_HALME STANDARD; PRT; 21 AA.
 ID P50557;
 AC P50557;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L5P (HME15) (FRAGMENT).
 GN RPL5P.
 OS Halobacterium mediterranei (Haloflex mediterranei).
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloflex.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-DSM 1411;
 RC MEDLINE-94229075; PubMed-8174557;
 RX McDougall J., Wittmann-Liebold B.;
 RA "Comparative analysis of the protein components from 5S rRNA-protein
 RT complexes of halophilic archaeobacteria";
 RL Eur. J. Biochem. 221:779-785(1994).
 CC -1- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS.
 DR INTERPRO: IPR002132; -;
 DR PIR: G33084; G33084.
 DR PIR: PF00281; RIBOSOMAL_L5; PARTIAL.
 DR PROSITE; PS00358; RIBOSOMAL_L5; PARTIAL.
 KW Ribosomal protein.
 FT NON_TER 21
 SO SEQUENCE 21 AA: 2497 MW: 56EB7371B2A13F71 CRC64;

Query Match 18.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 28.6%; Pred. No. 2.2e+03;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 11 LEETLMH 17
 : : : : :
 Db 13 IEKVYVH 19

RESULT 12
 RL5_HALVO STANDARD; PRT; 22 AA.
 ID P50559;
 AC P50559;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L5P (HVO15) (FRAGMENT).
 GN RPL5P.
 OS Halobacterium volcanii (Haloflex volcanii).
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloflex.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-DSM 3757;
 RX MEDLINE-94229075; PubMed-8174557;
 RA McDougall J., Wittmann-Liebold B.;
 RT "Comparative analysis of the protein components from 5S rRNA-protein
 RT complexes of halophilic archaeobacteria";
 RL Eur. J. Biochem. 221:779-785(1994).
 CC -1- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS.
 DR INTERPRO: IPR002132; -;
 DR PIR: H33084; H33084.
 DR PIR: PF00281; RIBOSOMAL_L5; 1.

DR PROSITE: PS00358; RIBOSOMAL_L5; PARTIAL.
 KW RIBOSOMAL protein.
 FT NON_TER 22
 SQ SEQUENCE 22 AA; 2582 MW; 3246EAA801B2A13F CRC64;

Query Match 18.6%; Score 21; DB 1; Length 22;
 Best Local Similarity 28.6%; Pred. No. 2.3e+03;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Oy 11 LEEILMH 17
 Db 13 IEKVYVH 19

RESULT 13
 IAPP_LEPEU STANDARD; PRT; 23 AA.
 AC 007333;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ISLET AMYLOID POLYPEPTIDE (AMYLIN) (FRAGMENT).
 GN IAPP.
 OS Lepus europaeus (European hare).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PANCREAS;
 RX MEDLINE-93215963; PubMed-8462765;
 RA Christmanon L., Betsholtz C., Leckstroem A., Engstroem U.,
 Cortie C., Johnson K.H., Adrian T.E., Westermarck P.,
 "Islet amyloid polypeptide in the rabbit and European hare: studies
 on its relationship to amyloidogenesis.";
 RL Diabetologia 36:183-188(1993)
 RT -1- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE
 UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING
 ADIPOCYTE GLUCOSE METABOLISM.
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
 CC -----
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 CC -----
 CC EMBL: S57802; AAB26083.1; -
 DR Hormone; Amyloid.
 KW NON_TER 1
 FT PEPTIDE <1 >23 ISLET AMYLOID POLYPEPTIDE.
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2546 MW; A5EE561D52B353DD CRC64;

Query Match 18.6%; Score 21; DB 1; Length 23;
 Best Local Similarity 44.4%; Pred. No. 2.4e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 9 QNLEILMH 17
 Db 2 QRLANFLIH 10

RESULT 14
 RLS_HALHA STANDARD; PRT; 23 AA.
 ID RLS_HALHA
 AC P50356;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 50S RIBOSOMAL PROTEIN L5P (HHA15) (FRAGMENT).
 GN RPL5P.
 OS Halobacterium halobium.
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 OC Halobacterium.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-DSM 670;
 RX MEDLINE-94229075; PubMed-8174557;
 RA McDougall J., Wittmann-Liebold B.,
 "Comparative analysis of the protein components from 5S rRNA, protein
 complexes of halophilic archaeobacteria.";
 RL Eur. J. Biochem. 221:779-785(1994).
 CC -1- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS.
 CC PIR: C33084; C33084.
 DR INTERPRO: IPR002132;
 DR PFAM: PF00281; RIBOSOMAL_L5; 1.
 DR PROSITE: PS00358; RIBOSOMAL_L5; PARTIAL.
 KW RIBOSOMAL protein.
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2773 MW; 19B318355A19B298 CRC64;

Query Match 18.6%; Score 21; DB 1; Length 23;
 Best Local Similarity 28.6%; Pred. No. 2.4e+03;
 Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 Oy 11 LEEILMH 17
 Db 16 IEKVYVH 22

RESULT 15
 FKX7_PINPS STANDARD; PRT; 15 AA.
 ID FKX7_PINPS
 AC P81104;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 70 KDA PEPTIDYLPROLYL ISOMERASE (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS
 ISOMERASE) (CYCLOPHILIN) (PIPIASE) (S1205-06) (FRAGMENT).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferales; Coniferales; Pinaceae; Pinus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-NEEDLE;
 RA Plomion C., Costa P., Bahman N., Frigerio J.-M.,
 "Genetic analysis of needle proteins in maritime pine. 1. Mapping
 dominant and codominant protein markers assayed on diploid tissue, in
 a haploid-based genetic map.";
 RT Silvae Genetica 46:161-165(1997).
 RN [2]
 RP SEQUENCE.
 RC TISSUE-NEEDLE;
 RX MEDLINE-99274088; PubMed-10344291;
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
 Frigerio J.-M., Plomion C.,
 "Separation and characterization of needle and xylem maritime pine
 proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- FUNCTION: PPIASE THAT BINDS CALMODULIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: PEPTIDYLPROLYL (OMEGA-180) -
 PEPTIDYLPROLYL (OMEGA-0).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 5.3. ITS MW IS: 72 KDA.
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
 DR INTERPRO: IPR001179;
 DR PROSITE: PS00453; FKBP_PPIASE_1; PARTIAL.
 DR PROSITE: PS00454; FKBP_PPIASE_2; PARTIAL.
 DR PROSITE: PS00059; FKBP_PPIASE_3; PARTIAL.
 KW Isomerase; Rotamase; Repeat; Calmodulin-binding.
 FT NON_TER 1

FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1675 MW: 2B53999722277E3F CRC64;

Query Match 17.7%: Score 20; DB 1; Length 15;
Best Local Similarity 25.0%: Pred. No. 2.2e+03;
Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 NMELADOPONLE 12
: 11 : : 1
Db 4 SWETPETGEVE 15

RESULT 16
GLN2_PINPS STANDARD: PRT: 15 AA.
ID GLN2_PINPS
AC P81107;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROBABLE GLUTAMINE SYNTHETASE LEAF ISOZYME (EC 6.3.1.2) (GLUTAMATE--
DE AMMONIA LIGASE) (S2205/S2287) (N47/N48) (FRAGMENT).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RA Plomion C., Costa P., Bahman N., Frigerio J.-M.;
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map."
RL Silvae Genetica 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RA MEDLINE=99274088; PubMed=10344291;
RX Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins."
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: THE LIGHT-MODULATED CHLOROPLAST ENZYME, ENCODED BY A
CC NUCLEAR GENE AND EXPRESSED PRIMARILY IN LEAVES, IS RESPONSIBLE FOR
CC THE REASSIMILATION OF THE AMMONIA GENERATED BY PHOTORESPIRATION
CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.
CC -1- SUBUNIT: HOMOCYMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 5.7, ITS MW IS: 42 KDA.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
DR INTERPRO: IPR001691;
DR PROSITE: PS00180; GMA_1; PARTIAL.
DR PROSITE: PS00181; GMA_ATP; PARTIAL.
KW Ligase; Chloroplast.
FT NON_TER 15 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1614 MW: 24A2420BEPD60D27 CRC64;

Query Match 17.7%: Score 20; DB 1; Length 15;
Best Local Similarity 75.0%: Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NMEL 4
: 11 : : 1
Db 3 NMPL 6

RESULT 17
VORA_METTM

ID VORA_METTM STANDARD: PRT: 15 AA.

AC P80907;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KETOISOVALLERATE OXIDOREDUCTASE SUBUNIT VORA (EC 1.-.-.-) (VOR) (2-
DE OXISOVALLERATE OXIDOREDUCTASE ALPHA CHAIN) (2-OXISOVALLERATE-
DE FERREDOXIN OXIDOREDUCTASE ALPHA SUBUNIT) (FRAGMENT).
GN VORA.

OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.

RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum."
RL Eur. J. Biochem. 244:862-868(1997).
CC -1- SUBUNIT: HETEROTRIMER OF THE VORA, VOR3 AND VORC SUBUNITS.
CC -1- MISCELLANEOUS: THE PH OPTIMUM IS PH 9.7 AND THE OPTIMAL
CC TEMPERATURE IS 75 DEGREES CELSIUS.
KW Oxidoreductase.

FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1779 MW: 3137086531CA528F CRC64;

Query Match 17.7%: Score 20; DB 1; Length 15;
Best Local Similarity 37.5%: Pred. No. 2.2e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 7 OPONLEI 14
: 11 : : 1
Db 7 KPDSLEXV 14

RESULT 18
LE05_BIOGL STANDARD: PRT: 16 AA.
ID LE05_BIOGL
AC P80744;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HEMOLYMPH 65 KDA LECTIN B605 (FRAGMENT).
GN B605.
OS Blomphalaria glabrata (Bloodfluke planorb).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Planorbidae; Blomphalaria.
RN [1]
RP SEQUENCE.
RX STRAIN=M-LINE; TISSUE=HEMOLYMPH;
RX MEDLINE=97385165; PubMed=9238039;
RA Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;
RT "A family of fibrinogen-related proteins that precipitates parasite-
RT derived molecules is produced by an invertebrate after infection."
RL Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696(1997).
CC -1- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE
CC ECHINOSTOMA PARASENSI.
CC -1- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.
CC -1- INDUCTION: BY INFECTION.
KW Lectin.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA: 1790 MW: 57489A8F2EDDA94 CRC64;

Query Match 17.7%: Score 20; DB 1; Length 16;
Best Local Similarity 33.3%: Pred. No. 2.3e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 ELADOPONLEI 14
: 11 : : 1
Db 2 EADLAQYVDL 13

OY 2 WELADQ 7
1 1 1
DB 11 WVFADQ 16

RESULT 22

OXLA_OPHHA STANDARD; PRT; 19 AA.
AC P81383;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE L-AMINO ACID OXIDASE (EC 1.4.3.2) (LMO) (FRAGMENT).
OS Ophiophagus hannah (King cobra) (Naja hannah).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubridae;
OC Elapidae; Elapinae; Ophiophagus.
RN [1]

SEQUENCE.

RP TISSUE-VENOM;
RX MEDLINE=94361525; PubMed=8080286;
RA Pennudurai G., Chung M.C.M., Tan N.-H.;
RT "Purification and properties of the L-amino acid oxidase from Malayan
pit viper (Calloselasma rhodostoma) venom.";
RL Arch. Biochem. Biophys. 313:373-378(1994).
RN [2]

SEQUENCE OF 1-15.

RP TISSUE-VENOM;
RX MEDLINE=97449790; PubMed=9304806;
RA Ahn M.Y., Lee B.M., Kim Y.S.;
RT "Characterization and cytotoxicity of L-amino acid oxidase from the
venom of King cobra (Ophiophagus hannah).";
RL Int. J. Biochem. Cell Biol. 29:911-919(1997).
CC -1- FUNCTION: HAS CYTOTOXIC ACTIVITY (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: A L-AMINO ACID + H(2)O + O(2) -> A 2-OKO ACID +
NH(3) + H(2)O(2).
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- PTM: GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOXAMINE OXIDASE FAMILY.
CC STRONG, TO MOUSE FIG-1.
KM Oxidoreductase; Flavoprotein; FAD; Glycoprotein; Venom.
FT CONFLICT 1 1 H -> S (IN REF. 2).
FT NON_TER 19 19
SQ SEQUENCE 19 AA: 2298 MW; DD911A5B414F1427 CRC64;

Query Match 17.7%; Score 20; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 NLEE 13
1 1 1 1 1

DB 4 NLEE 7

RESULT 23

DFTS_RAT STANDARD; PRT; 20 AA.
AC P07448;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE DENTINAL FLUID TRANSPORT-STIMULATING PEPTIDE (DFT-STIMULATING
PEPTIDE).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP TISSUE-PAROTID GLAND;
RX MEDLINE=87131231; PubMed=3815601;
RA Yamamoto T., Kobayashi M., Kobayashi M., Yamamoto M., Nomura M.,

RA Aonuma S.;
RT "Isolation and amino acid sequence of dentinal fluid transport-
stimulating peptide from rat parotid glands.";
RL Chem. Pharm. Bull. 34:3803-3811(1986).
RN [2]

CHARACTERIZATION.

RX MEDLINE=67131708; PubMed=5297832;
RA Steinman R.R.;
RT "The movement of acriflavine hydrochloride through molars of rats on
a cariogenic and non-cariogenic diet.";
RL J. South. Calif. Dent. Assoc. 35:151-157(1967).
CC -1- FUNCTION: THIS PEPTIDE STIMULATES THE TRANSPORT OF DENTINAL FLUID,
WHICH IS IMPORTANT FOR THE PREVENTION OF DENTAL CARIES.
DR PIR; J00001; DIRT.
KM Dental caries; Parotid gland; Hormone.
SQ SEQUENCE 20 AA: 2165 MW; FA164F2B6AF80D5A CRC64;

Query Match 17.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 WEL 4
1 1 1
DB 5 WEL 7

RESULT 24

PSAL_SYNVU STANDARD; PRT; 20 AA.
ID PSAL_SYNVU
AC P25937;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI (FRAGMENT).
GN PSAL.
OS Synechococcus vulcanus.
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
RN [1]
RP SEQUENCE.
RX MEDLINE=89338747; PubMed=2503399;
RA Kojima H., Ikeuchi M., Hayama T., Inoue Y.;
RT "Identification of photosystem I components from the cyanobacterium,
Synechococcus vulcanus by N-terminal sequencing.";
RL FEBS Lett. 253:257-263(1989).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE PSAL FAMILY.
CC PIR; S05220; S05220.
KM Photosystem I; Photosynthesis; Transmembrane.
FT NON_TER 20 20
SQ SEQUENCE 20 AA: 2170 MW; 730FECDD2EA02A2C CRC64;

Query Match 17.7%; Score 20; DB 1; Length 20;
Best Local Similarity 28.6%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 7 QPONEEILMHQOT 20
1 1 1 1 1 1 1

DB 6 KPYNGDPFVGHLS 19

RESULT 25

RAN_XENLA STANDARD; PRT; 24 AA.
ID RAN_XENLA
AC P52301;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE GTP-BINDING NUCLEAR PROTEIN RAN (TC4) (FRAGMENTS).
GN RAN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia: Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-OVARY;
 RX MEDLINE-94019818; PubMed-8413630;
 RA Moore M.S., Blobel G.;
 RT "The GTP-binding protein Ran/TCA is required for protein import into
 the nucleus.";
 RL Nature 365:661-663(1993).
 CC -!- FUNCTION: GTP-BINDING PROTEIN INVOLVED IN NUCLEOCYTOPLASMIC
 TRANSPORT. REQUIRED FOR THE IMPORT OF PROTEIN INTO THE NUCLEUS AND
 ALSO FOR RNA EXPORT. INVOLVED IN CHROMATIN CONDENSATION AND
 CONTROL OF CELL CYCLE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- SIMILARITY: BELONGS TO THE RAN FAMILY IN THE RAS SUPERFAMILY.
 DR HSSP: P28746; 1A2K.
 DR INTERPRO: IPR002041;
 DR PROSITE: PS01115; RAN; PARTIAL.
 KW GTP-binding; Nuclear protein; Protein transport.
 FT NON_TER 1 1
 FT NON_CONS 13 14 GTP (BY SIMILARITY).
 FT NP_BIND 18 22
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2657 MW; B69F83236247A250 CRC64;

Query Match

17.7%; Score 20; DB 1; Length 24;

Best local Similarity 50.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 WELADQ 7
 Db 17 WDTAGQ 22

Search completed: February 5, 2001, 10:56:00
 Job time: 500 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:55:22; Search time 93.77 Seconds

(without alignments)
24.999 Million cell updates/sec

Title: US-08-981-824-3

Perfect score: 113

Sequence: 1 NMEIADQPQNLLEIIMHCQT 20

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: SP-ARCHAEA:
2: SP-BACTERIA:
3: SP-FUNGI:
4: SP-HUMAN:
5: SP-INVERTEBRATE:
6: SP-MAMMAL:
7: SP-MHC:
8: SP-ORGANELLE:
9: SP-PHAGE:
10: SP-PLANT:
11: SP-RODENT:
12: SP-VIRUS:
13: SP-VERTEBRATE:
14: SP-UNCLASSIFIED:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	29.2	18	12	078376 human immun
2	33	29.2	23	8	09MG67 pinus ponde
3	29	25.7	17	5	09TWB9 acanthamoeb
4	29	25.7	20	2	09R4W5 helicobacte
5	29	25.7	20	3	09URC7 saccharomyc
6	29	25.7	22	12	084254 bovine papil
7	28	24.8	18	2	09R5F6 helicobacte
8	27	23.9	18	2	047137 escherichia
9	27	23.9	24	10	09S883 chlamydomon
10	26	23.0	18	6	09TMC0 acanthamoeb
11	26	23.0	20	13	09PS25 rana catesb
12	26	23.0	23	2	09R313 chlamydia t
13	25	23.0	16	6	09TRB4 bos taurus
14	25	22.1	19	2	09R4U6 lactobacilli
15	25	22.1	24	12	09PXB7 hog cholera
16	25	22.1	25	4	09UOB1 human saplen
17	24	21.2	14	11	09R1G8 rattus norv
18	24	21.2	14	12	010234 human immun
19	24	21.2	14	12	010234 human immun

20	24	21.2	17	7	030218 homo saplen
21	24	21.2	21	4	09UCH7
22	24	21.2	23	11	P97918
23	24	21.2	25	4	016308 mus musculu
24	23.5	20.8	24	4	09UCG1 homo saplen
25	23.5	20.8	24	6	09RUP6 sus scrofa
26	23	20.4	15	10	P82331
27	23	20.4	19	2	09R4X0
28	23	20.4	20	10	09S8Y7
29	23	20.4	21	4	09UC16
30	23	20.4	22	2	052009
31	23	20.4	22	2	09R660
32	23	20.4	24	4	016476
33	23	20.4	24	5	094373
34	23	20.4	24	10	09S8H6
35	22	19.5	15	2	046963
36	22	19.5	15	5	026159
37	22	19.5	17	5	09RFC3
38	22	19.5	20	2	P97160
39	22	19.5	21	1	09UMH2
40	22	19.5	21	2	056354
41	22	19.5	21	4	09UC33
42	22	19.5	21	5	09RWM1
43	22	19.5	21	11	063076
44	22	19.5	23	2	09R899
45	22	19.5	2	2	055238

ALIGNMENTS

RESULT 1
ID 078376 PRELIMINARY; PRT; 18 AA.
AC 078376;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE VIRAL SAMPLE FLPR41 (FLORIDA PATIENT B), PARTIAL ENV CDS, V4 REGION (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid-11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.O., Leigh-Brown A.J.;
RA Submitted (Apr-1992) to the EMBL/Genbank/DBJ databases.
RN [2]
RX MEDLINE-92271245; PubMed-1589796;
RA Ou C.Y., Ciesielski C.A., Myers G., Banda C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Satten G.A., MacInnes K.A.,
RA Curran J.W., Jaffe H.W.;
RT "Molecular epidemiology of HIV transmission in a dental practice";
RL Science 256:1165-1171(1992).
DR EMBL; M92122; AAA44492.1;
FT NON_TER 1
FT 1
SQ SEQUENCE 18 AA; 2000 MW; 0BIE4794679E050A CRC64;

Query Match 29.2%; Score 33; DB 12; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 PONTLEITHMCQ 19
DB 7 PNTLEITHLPCK 18

RESULT 2
Q9MG67

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ID 09MG67 PRELIMINARY; PRT; 23 AA.
AC 09MG67;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE NAH DEHYDROGENASE SUBUNIT 1 (FRAGMENT).
GN NAD1.
OS Pinus ponderosa.
OC Mitochondrion.
CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=55062;
RN [1]
RP SEQUENCE FROM N.A.
RA Kreiser B.R., Milton J.B., Rehfeldt G.E.;
RT "Primers designed to amplify a mitochondrial NAD1 intron in ponderosa
RT pine (Pinus ponderosa), limber pine (P. flexilis), and Scots pine (P.
RT sylvestris).";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF231325; AAF78900.1;
KW Mitochondrion.
FT NON_TER 1 1
SO SEQUENCE 23 AA; 2614 MW; 52FAB49CF962C2DC CRC64;

Query Match 29.2%; Score 33; DB 8; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 PONEEILM 16
Db 7 PNLSEIIV 15

RESULT 3
O9TMB9 PRELIMINARY; PRT; 17 AA.
AC 09TMB9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE PROFILIN-BINDING CORTICAL COMPLEX-18 KDA POLYPEPTIDE.
OS Acanthamoeba castellanii (Amoeba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]
RP SEQUENCE.
RX MEDLINE=95014701; PubMed=7929556;
RA Machesky L.M., Atkinson S.J., Ampe C., Vandekerckhove J.,
RA Pollard T.D.;
RT "Purification of a cortical complex containing two unconventional
RT actins from Acanthamoeba by affinity chromatography on profilin-
RT agarose.";
RL J Cell Biol. 127:107-115(1994).
SO SEQUENCE 17 AA; 1875 MW; 7260445CDF5AE78B CRC64;

Query Match 25.7%; Score 29; DB 5; Length 17;
Best Local Similarity 45.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 ADOPONEEIL 15
Db 5 ADOPIDEAI 15

RESULT 4
O9R4W5 PRELIMINARY; PRT; 20 AA.
AC 09R4W5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

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DT 01-JUN-2000 (TREMBLrel. 14, last annotation update)
DE 30 KDA MAJOR HEAT SHOCK PROTEIN (FRAGMENT).
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE.
RX MEDLINE=95020803; PubMed=7935068;
RA Yokota K., Hirai Y., Hague M., Hayashi S., Isogai H., Sugiyama T.,
RA Nagamachi E., Tsukada Y., Fujii N., Oguma K.;
RT "Heat shock protein produced by Helicobacter pylori.";
RL Microbiol. Immunol. 38:405-405(1994).
DR INTERPRO; IPR002026;
DR PFM; PF00547; urease-gamma; 1.
SO SEQUENCE 20 AA; 2302 MW; 29C9DFBFD6D21805 CRC64;

Query Match 25.7%; Score 29; DB 2; Length 20;
Best Local Similarity 30.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 8 PONEEILM 17
Db 5 PKEIDKMLH 14

RESULT 5
O9URC7 PRELIMINARY; PRT; 20 AA.
AC 09URC7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
DE LIPID-BINDING PROTEIN.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91353077; PubMed=1882548;
RA Creutz C.E., Snyder S.L., Kambouris N.G.;
RT "Calcium-dependent secretory vesicle-binding and lipid-binding
RT proteins of Saccharomyces cerevisiae.";
RL Yeast 7:229-244(1991).
SO SEQUENCE 20 AA; 2388 MW; 594377C8C3E72B0D CRC64;

Query Match 25.7%; Score 29; DB 3; Length 20;
Best Local Similarity 42.9%; Pred. No. 5.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

OY 2 WELADOPONEEIL 15
Db 5 WD--DDEINDEL 16

RESULT 6
O84254 PRELIMINARY; PRT; 22 AA.
AC 084254;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
DE X PROTEIN (FRAGMENT).
OS Bovine papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX NCBI_TaxID=10571;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89067912; PubMed=2848926;
RA Stamps A.C., Campo M.S.;

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RT "Mapping of two novel transcripts of bovine papillomavirus type 4.";
 RL J. Gen. Virol. 69:3033-3045(1988).

DR EMBL; M35264; AAA46926.1;
 FT NON_TER 1 1
 FT NON_TER 22 22
 SQ SEQUENCE 22 AA: 2273 MW: 2801BC23480C9CF9 CRC64;

Query Match 25.7%; Score 29; DB 12; Length 22;
 Best Local Similarity 45.5%; Pred. No. 6e+02;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 ELADOPONLE 13
 DB 12 DVADRPDLPE 22

RESULT 7

O9RSF6 PRELIMINARY; PRT; 18 AA.

AC O9RSF6; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE UREASE SMALL SUBUNIT (FRAGMENT).

OS Helicobacter mustelae.

OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;

OX NCBI_Taxid=217;

RN [1]

RP MEDLINE-93084378; PubMed-1452359;

RA Turbett G.R., Hoj P.B., Horne R., Mee B.J.;

RT "Purification and characterization of the urease enzymes of

RL Helicobacter species from humans and animals."

SO SEQUENCE 18 AA: 2060 MW: 29C8E6AB7E21805 CRC64;

Query Match 24.8%; Score 28; DB 2; Length 18;
 Best Local Similarity 30.0%; Pred. No. 7.1e+02;
 Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 8 PONEELIMH 17
 DB 3 PKELDKMLH 12

RESULT 8

O47137 PRELIMINARY; PRT; 18 AA.

AC O47137; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OX NCBI_Taxid=562;

RN [1]

RP SEQUENCE FROM N.A.
 Bouche J.P.;

RA Submitted (Apr-1988) to the EMBL/GenBank/DBJ databases.

RT "Identification and sequence of gene dicB: translation of the division

RL Nucleic Acids Res. 16:6327-6338(1988).

SO SEQUENCE FROM N.A.

RX MEDLINE-88232418; PubMed-2836697;
 RA Bejar S., Bouche F., Bouche J.P.;

RT "Cell division inhibition gene dicB is regulated by a locus similar to

RL lambdaoid bacteriophage immunity loci."

SO SEQUENCE 24 AA: 2707 MW: 5CCAE3310F50FB44 CRC64;

Query Match 23.9%; Score 27; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 MHCQ 19
 DB 1 MHCQ 4

RESULT 9

O9S883 PRELIMINARY; PRT; 24 AA.

AC O9S883; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE ATP SYNTHASE DELTA SUBUNIT (FRAGMENT).

OS Chlamydomonas reinhardtii.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OX NCBI_Taxid=3055;

RN [1]

RP MEDLINE-96128220; PubMed-8543042;

RA Fiedler H.R., Schmid R., Liu S., Shavit N., Strothmann H.;

RT "Isolation of CF0CFL from Chlamydomonas reinhardtii cw15 and the N-

SO SEQUENCE 24 AA: 2707 MW: 5CCAE3310F50FB44 CRC64;

Query Match 23.9%; Score 27; DB 10; Length 24;
 Best Local Similarity 60.0%; Pred. No. 1.4e+03;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 ELADOPONLE 12
 DB 15 ELADKMKLE 24

```

RESULT 10
Q9TWC0 ID Q9TWC0 PRELIMINARY: PRT: 16 AA.
AC Q9TWC0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ACTIN (FRAGMENT).
OS Acanthamoeba castellanii (Amoebea).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_Taxid=5755;
RN [1]
RP SEQUENCE.
RX MEDLINE=95014701; PubMed=7929556;
RA Machesky L.M., Atkinson S.J., Ampe C., Vandekerckhove J.,
RA Pollard T.D.;
RT "Purification of a cortical complex containing two unconventional
RT actins from Acanthamoeba by affinity chromatography on profilin-
RT agarose."
RL J. Cell Biol. 127:107-115(1994).
SQ SEQUENCE 16 AA; 2115 MW; A64E24880BA06C4 CRC64;

Query Match 23.0%; Score 26; DB 5; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NWELADOPON 10
Db 1 NWELADOPON 10

RESULT 11
Q9TR02 ID Q9TR02 PRELIMINARY: PRT: 18 AA.
AC Q9TR02;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE P68 KINASE INHIBITOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92332534; PubMed=1378438;
RA Lee T.G., Tomita J., Hovanessian A.G., Katze M.G.;
RT "Characterization and regulation of the 58,000-dalton cellular
RT inhibitor of the interferon-induced, dsRNA-activated protein kinase."
RL J. Biol. Chem. 267:14238-14243(1992).
SQ SEQUENCE 18 AA; 2206 MW; 91778DDEB834082D CRC64;

Query Match 23.0%; Score 26; DB 6; Length 18;
Best Local Similarity 38.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 WELADOPONLEI 14
Db 6 WELADOPONLEI 18

RESULT 12
Q9PS25 ID Q9PS25 PRELIMINARY: PRT: 20 AA.
AC Q9PS25;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

```

```

DE MONOMERIC ALPHA-MACROGLOBULIN PROTEINASE INHIBITOR (FRAGMENT).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE.
RX MEDLINE=93176138; PubMed=7679897;
RA Rubenstein D.S., Thogersen I.B., Pizzo S.V., Englund J.J.;
RT "Identification of monomeric alpha-macroglobulin proteinase inhibitors
RT in birds, reptiles, amphibians and mammals, and purification and
RT characterization of a monomeric alpha-macroglobulin proteinase
RT inhibitor from the American bullfrog Rana catesbeiana."
RL Biochem. J. 290:85-93(1993).
SQ SEQUENCE 20 AA; 2332 MW; 7CE78C52053F74D7 CRC64;

Query Match 23.0%; Score 26; DB 13; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PONTLEE 13
Db 10 PONTLEE 15

RESULT 13
Q9R313 ID Q9R313 PRELIMINARY: PRT: 23 AA.
AC Q9R313;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE VIRULENCE PROTEIN PG3-D (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
RT sequencing."
RL Submitted (MUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF087345; AAD04118.1;
DR EMBL: AF087324; AAD04099.1;
KW Hypothetical protein.
FT NON TER 1 23
FT NON TER 1 23
SQ SEQUENCE 23 AA; 2475 MW; BCB818F08862FE8B CRC64;

Query Match 23.0%; Score 26; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 PONTLEE 15
Db 9 PONTLEE 16

RESULT 14
Q9TRB4 ID Q9TRB4 PRELIMINARY: PRT: 16 AA.
AC Q9TRB4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE ATP-DEPENDENT 20 S PROTEASOME ACTIVATOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

```

OX NCBI_TaxID-9913;
 RN [1]
 RP SEQUENCE:
 RX MEDLINE-94342244; PubMed-8063704;
 RA Demattio G.N., Moomaw C.R., Zagnitko O.P., Proske R.J., Chu-Ping M.,
 AFendis S.J., Swaffield J.C., Slaughter C.A.:
 RT "PA700, an ATP-dependent activator of the 20 S proteasome, is an
 RT ATPase containing multiple members of a nucleotide-binding protein
 RT family."
 RL J. Biol. Chem. 269:20878-20884(1994).
 SO SEQUENCE 16 AA; 1878 MW; F70F74211E26EDE CRC64;

Query Match 22.1%; Score 25; DB 6; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OY 1 NWEADOP 8
 Db 7 NFOULDNP 14

RESULT 15
 O9R4U6 PRELIMINARY; PRT; 19 AA.
 AC O9R4U6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE BACTERIOCIN LACTACIN B INDUCER (FRAGMENT).
 OS Lactobacillus acidophilus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID-1579;
 RN [1]
 RP SEQUENCE:
 RX MEDLINE-95077353; PubMed-7986029;
 RA Barefoot S.F., Chen Y.R., Hughes T.A., Bodine A.B., Shearer M.Y.,
 RA Hughes M.D.:
 RT "Identification and purification of a protein that induces production
 RT of the Lactobacillus acidophilus bacteriocin lactacin B."
 RL Appl. Environ. Microbiol. 60:3522-3528(1994).
 SO SEQUENCE 19 AA; 2171 MW; 3221F0603F19E32F CRC64;

Query Match 22.1%; Score 25; DB 2; Length 19;
 Best Local Similarity 44.4%; Pred. No. 2.2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 NWEADOP 9
 Db 9 NWKLNMPK 17
 RESULT 16
 O9PXB7 PRELIMINARY; PRT; 24 AA.
 ID O9PXB7;
 AC O9PXB7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE GLYCOPROTEIN E0 (FRAGMENT).
 OS Glyc Choleira virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Pestivirus.
 OX NCBI_TaxID-11096;
 RN [1]
 RP SEQUENCE:
 RX MEDLINE-93267778; PubMed-8388499;
 RA Rumenapf T., Unger G., Strauss J.H., Thiel H.J.:
 RT "Processing of the envelope glycoproteins of pestiviruses."
 RL J. Virol. 67:3288-3294(1993).
 SO SEQUENCE 24 AA; 2752 MW; A48D322C89550658 CRC64;

Query Match 22.1%; Score 25; DB 12; Length 24;
 Best Local Similarity 44.4%; Pred. No. 2.8e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 OY 2 WELADOPON 10
 Db 6 WNLSDNGTN 14

RESULT 17
 O9UOB1 PRELIMINARY; PRT; 25 AA.
 ID O9UOB1;
 AC O9UOB1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE CD22 PROTEIN (FRAGMENT).
 GN CD22.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hattia Y., Tsuchiya N., Matsushita M., Shiota M., Hagiwara K.,
 RA Tokunaga K.:
 RT "Identification of the gene variations in human CD22."
 RL Immunogenetics 49:280-286(1999).
 DR EMBL: AB013005; BAA36574.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 25 AA; 2969 MW; 354944648D268289 CRC64;

Query Match 22.1%; Score 25; DB 4; Length 25;
 Best Local Similarity 33.3%; Pred. No. 3e+03;
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 WELADOPONLEE 13
 Db 1 WKRTOSQGLQF 12
 RESULT 18
 O9RIG8 PRELIMINARY; PRT; 14 AA.
 ID O9RIG8;
 AC O9RIG8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE INSULIN RECEPTOR PRECURSOR (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Liu Y., Tam J.W.O.:
 RT "Partial sequence of rat insulin receptor gene."
 RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF110222; AAD40897.1; -.
 DR EMBL: AF110221; AAD40897.1; JOINED.
 KM Receptor.
 FT NON_TER 1
 FT NON_TER 14
 SO SEQUENCE 14 AA; 1826 MW; 51C2994579D01697 CRC64;

Query Match 21.2%; Score 24; DB 11; Length 14;
 Best Local Similarity 27.3%; Pred. No. 2.4e+03;

Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 8 PONTLEIIMHC 18
1 PERLTDLIMRC 11

RESULT 19
010234 PRELIMINARY; PRT: 14 AA.

AC 010234;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98216723; PubMed=9557645;
RA Salvi R., Garbuglia A.R., Di Caro A., Pulciari S., Montella F.,
Benedetto A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
virus type 1 seropositive long-term nonprogressor."
RL J. Virol. 72:3646-3657(1998).
DR EMBL: U89854; AAC26093.1; -.
DR INTERPRO: IPR000328; -.
DR PFIAM: PF00517; GP41; 1.
KV Envelope protein.
FT NON-TER 1
SQ SEQUENCE 14 AA; 173 MW; D5E74A99D45D0566 CRC64;

Query Match 21.2%; Score 24; DB 12; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 9 ONLEIIM 16
1 1 1 1
DB 7 OGIERILL 14

RESULT 20
030218 PRELIMINARY; PRT: 17 AA.

AC 030218;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE FCER2 PROTEIN (FRAGMENT).
GN FCER2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96124133; PubMed=8552454;
RA Forster H.H., Masch R., Kreschmar T., Mischke D.,
Uchanska-Ziegler B., Ziegler A., Schmitt M., Mann H.U.;
RT "Genetic markers on chromosome 19p and prenatal diagnosis of HLA class
II-deficient combined immunodeficiency."
RL Pediatr. Res. 38:812-816(1995).
DR EMBL: S81114; AAB35925.1; -.
KV MHC.
FT NON-TER 1
SQ SEQUENCE 17 AA; 2076 MW; 53F5D4E75F1E5F47 CRC64;

Query Match 21.2%; Score 24; DB 7; Length 17;
Best Local Similarity 33.3%; Pred. No. 2.9e+03;

Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 WEIADOPONLEE 13
1 WDTQSLKOLEE 12

RESULT 21
09UCH7 PRELIMINARY; PRT: 21 AA.

AC 09UCH7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TN GLYCOPHORIN A-TN ANTIGEN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211988; PubMed=7681597;
RA Nakada H., Inoue M., Numata Y., Tanaka N., Funakoshi I., Fukui S.,
Mellors A., Yamashina I.;
RT "Epitopic structure of Tn glycophorin A for an anti-Tn antibody (MLS
128)."
RL Proc. Natl. Acad. Sci. U.S.A. 90:2495-2499(1993).
SQ SEQUENCE 21 AA; 2230 MW; 29F2DD83C77FCE2 CRC64;

Query Match 21.2%; Score 24; DB 4; Length 21;
Best Local Similarity 50.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 13 EIMHCOT 20
1 1 1 1
DB 5 EVAMHTST 12

RESULT 22
P97918 PRELIMINARY; PRT: 23 AA.

AC P97918;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE FC GAMMA RECEPTOR (FRAGMENT).
GN FCGR2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 226-248 FROM N.A.
RX MEDLINE=8631694; PubMed=2944118;
RA Hibbs M.L., Walker I.D., Kirschaum L., Peltersz G.A., Deacon N.J.,
Chambers G.W., McKenzie I.F.C., Hogarth P.M.;
RT "The murine Fc receptor for immunoglobulin purification, partial
amino acid sequence, and isolation of cDNA clones."
RL Proc. Natl. Acad. Sci. U.S.A. 83:6980-6984(1986).
DR EMBL: M14277; AAA37606.1; -.
DR MGD: MGI:95499; Fcgr2b.
FT NON-TER 1
SQ SEQUENCE 23 AA; 2670 MW; 13303A118B855AA6 CRC64;

Query Match 21.2%; Score 24; DB 11; Length 23;
Best Local Similarity 31.2%; Pred. No. 3.9e+03;
Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 2 WEIADOPONLEIIMH 17
1 1 1 1 1

Db 8 YSLKHPALDEETEH 23

RESULT 23

ID 016308 PRELIMINARY; PRT; 25 AA.

AC 016308;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE GLYCOPHORIN A (FRAGMENT).

GN GYPA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95282423; PubMed=7762218;

RA Dupont B.R., Grant S.G., Oto S.H., Bigbee W.L., Jensen R.H.,

RA Langlois R.G.;

RT "Molecular characterization of glycophorin A transcripts in human

RT erythroid cells using RT-PCR, allele-specific restriction, and

RT sequencing";

RL Vox Sang. 68:121-129(1995).

DR EMBL; S77082; AAB34408.1; -.

FT NON_TER

SQ SEQUENCE 25 AA; 2494 MW; 0DA5D769A868BEC3 CRC64;

Query Match 21.28; Score 24; DB 4; Length 25;

Best Local Similarity 50.0%; Pred. No. 4.3e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 13 EILMHQOT 20

Db 15 EVAMHTST 22

RESULT 24

ID 09UCG1

AC 09UCG1; PRELIMINARY; PRT; 24 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE PEPTIDYL-ALPHA-HYDROXYGLYCINE ALPHA-AMIDATING LYSASE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RA Husten E.J., Tausk F.A., Keutmann H.T., Elipper B.A.;

RL J. Biol. Chem. 268:9709-9717(1993).

SQ SEQUENCE 24 AA; 2830 MW; 85463403B13A147 CRC64;

Query Match 20.88; Score 23.5; DB 4; Length 24;

Best Local Similarity 53.8%; Pred. No. 4.9e+03;

Matches 7; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 4 LADOPONLEEL 15

Db 3 LMOQPKGEEVL 15

RESULT 25

ID 09TUP6

AC 09TUP6; PRELIMINARY; PRT; 24 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE HEART FATY ACID BINDING PROTEIN (FRAGMENT).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PIETRAIN; TISSUE-BLOOD;

RA Necheleberger D., Mueller S., Mueller M.;

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF164968; AAD47821.1; -.

DR HSSP; P05413; 1HMT.

DR INTERPRO; IPR000463; -.

DR INTERPRO; IPR000566; -.

DR PFAM; PF00061; 1lipocalin; 1.

DR PROSITE; PS00214; FABP; 1.

FT NON_TER

SQ SEQUENCE 24 AA; 2782 MW; C7533989DDC2043 CRC64;

Query Match

20.88; Score 23.5; DB 6; Length 24;

Best Local Similarity 28.6%; Pred. No. 4.9e+03;

Matches 4; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 2 WELADOPONLEEL 15

Db 9 WKLVDK-KNFDDVM 21

Search completed: February 5, 2001, 10:55:24

Job time: 913 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:49:29 ; Search time 58.67 Seconds
(without alignments)
23.147 Million cell updates/sec

Title: US-08-981-824-4

Perfect score: 108

Sequence: 1 TLKVAIKTGHPRYFNQLSTG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 5001

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR,66:*

1: Piri:*

2: Piri:*

3: Piri:*

4: Piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	27.8	25	2 H64710	Hypothetical prote
2	29	26.9	24	2 A54548	penicillin-binding
3	28	25.9	13	2 PT0256	Ig heavy chain CRD
4	28	25.9	20	2 P00215	metalloendopeptida
5	28	25.9	25	2 I64828	gene HEXA protein
6	28	25.9	25	2 B54348	penicillin-binding
7	27	25.0	23	2 S48156	alpha-amylase inh
8	26	24.1	23	2 PH1728	Ig heavy chain V r
9	25	23.1	16	2 S10807	protein kinase C 1
10	25	23.1	17	2 B44923	carboxypeptidase 3
11	25	23.1	25	2 PH1733	Ig heavy chain V r
12	24	22.2	11	2 PT0302	Ig heavy chain CRD
13	24	22.2	12	2 I64829	gene HEXA protein
14	24	22.2	12	2 PH1464	T-cell receptor be
15	24	22.2	13	2 H56046	urinary tract ston
16	24	22.2	15	2 B41868	hypothetical prote
17	24	22.2	15	2 A61612	allatostatin - tob
18	24	22.2	19	2 PH1304	Ig heavy chain DJ
19	24	22.2	20	2 S58382	Hypothetical prote
20	24	22.2	21	2 S47198	T-cell receptor J-
21	24	22.2	21	2 S47212	T-cell receptor J-
22	24	22.2	22	2 S04228	N4-(beta-N-acetyl
23	24	22.2	25	2 PH1907	T-cell receptor al
24	23	21.3	11	2 S42587	celf protein - Esc
25	23	21.3	13	2 S47365	T-cell antigen rec
26	23	21.3	13	2 S47372	T-cell antigen rec
27	23	21.3	16	2 E49255	T-cell receptor be
28	23	21.3	17	2 PT0234	Ig heavy chain CRD
29	23	21.3	20	2 S78759	ribosomal protein

30 23 21.3 21 2 I49414
31 23 21.3 21 2 B60119
32 23 21.3 24 2 A41037
33 22 20.4 12 2 S34447
34 22 20.4 13 2 S47389
35 22 20.4 13 2 PH1479
36 22 20.4 15 2 A26212
37 22 20.4 15 2 PH1342
38 22 20.4 16 2 A45133
39 22 20.4 16 2 I37452
40 22 20.4 19 2 PH1307
41 22 20.4 19 2 S63485
42 22 20.4 20 2 S03954
43 22 20.4 24 2 T07991
44 22 20.4 25 2 I56978
45 21 19.4 4 2 PL0140

ALIGNMENTS

RESULT 1

H64710

hypothetical protein HPI528 - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: H64710

R:Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; Mcke

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:97394467

A:Accession: H64710

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-25 <TOM>

A:Cross-references: GB:AE000651; GB:AE000511; NID:g2314708; PIDN:AAD08577.1; PID:g231

Query Match 27.8%; Score 30; DB 2; Length 25;
Best Local Similarity 37.5%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKVAIKTGHPRYFNQL 17

Db 10 LDYSLKKGVLKVINRL 25

RESULT 2

A54548

penicillin-binding protein 4 - Enterococcus hirae (fragment)

C:Species: Enterococcus hirae

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994

C:Accession: A54548

R:Jacques, P.; el Kharroubi, A.; Van Beeumen, J.; Piras, G.; Coyette, J.; Ghuyssen, J.

FEMS Microbiol. Lett. 66, 119-123, 1991

A:Title: Mode of membrane insertion and sequence of a 32-amino acid peptide stretch o

A:Reference number: A54548; MUID:92038914

A:Accession: A54548

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-24 <JAC>

A:Note: sequence extracted from NCBI backbone (NCBIP:63855)

Query Match 26.9%; Score 29; DB 2; Length 24;

Best Local Similarity 40.0%; Pred. No. 2.8e+02;

Matches 8; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 TLKVAIKTGHPRYFNQLSTG 20

|| | | | | | | | | | | | | | | | |

```
Db 2 TLTLTQTSXPRGMVYDNTG 21

RESULT 3
PF0256
Ig heavy chain CRD3 region (clone 2-115C) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PF0256
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PF0222; M0ID:91108357
A:Accession: PF0256
A:Molecule type: DNA
A:Residues: 1-13 <YAM>
A:Experimental source: B lymphocyte
A:Keywords: heterotetramer; immunoglobulin

Query Match 25.9%; Score 28; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLKYAIKTCHPR 12
||| : ||| :
Db 1 TLYYDMLTGYSR 12

RESULT 4
PF0215
metalloendopeptidase (EC 3.4.24.-) - Streptomyces griseus (fragment)
C:Species: Streptomyces griseus
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 28-May-1993
C:Accession: PF0215
R:Tsuayuki, H.; Kajiwara, K.; Fujita, A.; Kumazaki, T.; Ishii, S.
J. Biochem. 110, 339-344, 1991
A:Title: Purification and characterization of Streptomyces griseus metalloendopeptidases
A:Reference number: PF0215; M0ID:92121147
A:Accession: PF0215
A:Molecule type: protein
A:Residues: 1-20 <TSU>
C:Keywords: hydrolase; metalloproteinase

Query Match 25.9%; Score 28; DB 2; Length 20;
Best Local Similarity 38.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 8 TGHPRYFNQLSTG 20
||| : ||| :
Db 2 TGNTOYNGQVTLG 14

RESULT 5
I64828
gene HEXA protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I64828
R:Boles, D.J.; Proia, R.L.
Am. J. Hum. Genet. 56, 716-724, 1995
A:Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs
A:Reference number: I51882; M0ID:95193801
A:Accession: I64828
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-25 <RES>
A:Cross-references: GB:S76982; NID:9912780; PIDN:AAD14242.1; PID:g4261942
C:Genetics:
A:Gene: GDB:HEXA
A:Cross-references: GDB:I20040; OMIM:272800
A:Map position: 15q23-15q24

C:Superfamily: beta-hexosaminidase

Query Match 25.9%; Score 28; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 PRYFNQLSTG 20
||| : ||| :
Db 1 PWYLNRIISYG 10

RESULT 6
B54548
penicillin-binding protein 4 - Enterococcus hirae (fragment)
C:Species: Enterococcus hirae
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994
C:Accession: B54548
R:Jacques, P.; el Kharroubi, A.; Van Beeumen, J.; Piras, G.; Coyette, J.; Ghuyssen, J.
FEMS Microbiol. Lett. 66, 119-123, 1991
A:Title: Mode of membrane insertion and sequence of a 32-amino acid peptide stretch o
A:Reference number: A54548; M0ID:92038914
A:Accession: B54548
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-25 <JAC>
A:Note: sequence extracted from NCBI backbone (NCBIP:63854)

Query Match 25.9%; Score 28; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TLKYAIKTCHPR 12
||| : ||| :
Db 10 TLTLTQTSXPR 21

RESULT 7
S48156
alpha-amylase inhibitor - rye
C:Species: Secale cereale (rye)
C>Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C:Accession: S48156
R:Garcia-Casado, G.; Sanchez-Monge, R.; Lopez-Otin, C.; Salcedo, G.
Eur. J. Biochem. 224, 525-531, 1994
A:Title: Rye inhibitors of animal alpha-amylases show different specificities, aggregat
A:Reference number: S48156; M0ID:95010030
A:Accession: S48156
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <GAR>
C:Superfamily: wheat alpha-amylase inhibitor
C:Keywords: alpha-amylase inhibitor

Query Match 25.0%; Score 27; DB 2; Length 23;
Best Local Similarity 80.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GHPRY 13
||| :
Db 11 GHPMY 15

RESULT 8
PH1728
Ig heavy chain V region (clone GCC-8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1728
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
```


A>Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607

A:Accession: PH1728

A:Molecule type: mRNA

A:Residues: 1-23 <MCH>

A:Experimental source: B cell

A>Note: the authors translated the codon TTA for residue 11 as Phe and ATA for residue 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 24.1%; Score 26; DB 2; Length 23;

Best Local Similarity 33.3%; Pred. No. 8.2e+02;

Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TLKYAIKTHPRYFN 15

I : : : : I : :

Db 8 TKSLEIRGNYPYVFD 22

RESULT 9

S10807

protein kinase C inhibitor KCIP-1 isoform d - sheep (fragment)

N:Alternate names: probable lipocortin

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 13-Sep-1998

C:Accession: S10807

R:Tokar, A.; Ellis, C.A.; Sellers, L.A.; Aitken, A.

Eur. J. Biochem. 191, 421-429, 1990

A>Title: Protein kinase C inhibitor proteins. Purification from sheep brain and sequence
A:Reference number: S10804; MUID:90345949

A:Accession: S10807

A:Molecule type: protein

A:Residues: 1-16 <TK>

A:Experimental source: brain

C:Superfamily: 14-3-3 protein

Query Match 23.1%; Score 25; DB 2; Length 16;

Best Local Similarity 35.7%; Pred. No. 8.1e+02;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 7 KTCHPRYFNOLSTG 20

I : : : : I : :

Db 1 KGDYRYLAEFATG 14

RESULT 10

B44923

carboxypeptidase 3 - Rhizomucor circinelloides f. lusitanicus (fragment)

C:Species: Rhizomucor circinelloides f. lusitanicus

C>Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994

C:Accession: B44923

R:DiSanto, M.E.; Li, Q.H.; Logan, D.A.

J. Bacteriol. 174, 447-455, 1992

A>Title: Purification and characterization of a developmentally regulated carboxypeptidase
A:Reference number: A44923; MUID:92105011

A:Accession: B44923

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <DIS>

A>Note: sequence extracted from NCBI backbone (NCBIP:75616)

Query Match 23.1%; Score 25; DB 2; Length 17;

Best Local Similarity 50.0%; Pred. No. 8.6e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 TGHPRYFN 15

I : : : I

Db 9 TGHPEFSN 16

RESULT 11

PH1733

Ig heavy chain V region (clone GCC-13) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1733

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A>Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607

A:Accession: PH1733

A:Molecule type: mRNA

A:Residues: 1-25 <MCH>

A:Experimental source: B cell

A>Note: the authors translated the codon ACA for residue 13 as Ala

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match 23.1%; Score 25; DB 2; Length 25;

Best Local Similarity 30.0%; Pred. No. 1.3e+03;

Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 AIKTHPRYF 14

: : : : I :

Db 10 SVETRYPYV 19

RESULT 12

PT0302

Ig heavy chain CRD3 region (clone 5-112) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0302

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337

A:Accession: PT0302

A:Molecule type: DNA

A:Residues: 1-11 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotrimer; immunoglobulin

Query Match 22.2%; Score 24; DB 2; Length 11;

Best Local Similarity 66.7%; Pred. No. 7.9e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 TGHPRY 13

: : : : I

Db 1 SGGPRY 6

RESULT 13

I64829

gene HEXA protein - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I64829

R:Boles, D.J.; Proia, R.L.

Am. J. Hum. Genet. 56, 716-724, 1995

A>Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sa

A:Reference number: I51882; MUID:95193801

A:Accession: I64829

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-12 <RES>

A:Cross-references: GB:S76984; NID:9912781; PIDN:AA014243.1; PID:94261943

C:Genetics:

A:Gene: GDB:HEXA

A:Cross-references: GDB:120040; OMIM:272800

A:Map position: 15q23-15q24

C:Superfamily: beta-hexosaminidase

Query Match 22.2%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 11 PRYFNQLS 18

I I I I I

Db 1 PWYLNRI 8

RESULT 14

PH1464

T-cell receptor beta chain (clone A3/63) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995

C:Accession: PH1464

R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko

J.; Exp. Med. 177, 811-820, 1993

A:Title: T cell receptor selection by and recognition of two class I major histocompatib

A:Reference number: PH1430; MUID:93171821

A:Accession: PH1464

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Experimental source: cytolytic T-lymphocyte

C:Superfamily: immunoglobulin homology

C:Keywords: receptor; T-cell

Query Match 22.2%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.7e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 AIKTGHPRYF 14

I I I I I

Db 2 ASSTGNTLYF 11

RESULT 15

H56046

urinary tract stone matrix protein 10, 42K - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995

C:Accession: H56046

R:Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995

A:Description: Isolation, characterization and sequence of stone proteins.

A:Reference number: A56046

A:Accession: H56046

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BIN>

Query Match 22.2%; Score 24; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 YFNQLS 18

I I I I I

Db 4 YFNDLA 9

RESULT 16

B41868

hypothetical protein (traE1 3' region) - Enterococcus faecalis plasmid pAD1

C:Species: Enterococcus faecalis

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999

C:Accession: B41868; B37391

R:Pontius, L.T.; Clewell, D.B.

J. Bacteriol. 174, 3152-3160, 1992

A:Title: Conjugative transfer of Enterococcus faecalis plasmid pAD1: nucleotide sequence

A:Reference number: A41868; MUID:92250408

A:Contents: plasmid pAD1

A:Accession: B41868

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <PON>

A:Note: sequence extracted from NCBI backbone (NCBIN:99901, NCBIP:99906)

R:Clewell, D.B.; Pontius, L.T.; An, F.Y.; Ike, Y.; Suzuki, A.; Nakayama, J.

plasmid 24, 156-161, 1990

A:Title: Nucleotide sequence of the sex pheromone inhibitor (iAD1) determinant of Ent

A:Reference number: A37391; MUID:91261999

A:Accession: B37391

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <CLE>

A:Cross-references: GB:M62888; NID:g141853; PIDN:AAA98040.1; PID:g141855

C:Genetics:

A:Genome: plasmid

Query Match 22.2%; Score 24; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 YAIKTGHPRYF 14

I I I I I

Db 2 YTVHVYIPREF 12

RESULT 17

A61612

allotostatin - tobacco hornworm

C:Species: Manduca sexta (tobacco hornworm)

C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jul-1997

C:Accession: A61612

R:Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carne

Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991

A:Title: Identification of an allotostatin from the tobacco hornworm Manduca sexta.

A:Reference number: A61612; MUID:92052112

A:Accession: A61612

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <KRA>

C:Keywords: neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 22.2%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 YFNQLS 18

I I I I I

Db 8 YFNPI 13

RESULT 18

PH1304

Ig heavy chain DJ region (clone C439-111) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1304

R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor ly

A:Reference number: PH1302; MUID:93094761

A:Accession: PH1304

A:Molecule type: DNA

A:Residues: 1-19 <WAS>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 22.2%; Score 24; DB 2; Length 19;
Best Local Similarity 42.8%; Pred. No. 1.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 TGHPRYF 14
| | | |
Db 1 SGYPYY 7

RESULT 19
S58382
hypothetical protein 1 - human
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C:Accession: S58382
R:Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
Nucleic Acids Res. 23, 2815-2822, 1995
A:Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis intron
A:Reference number: S58382; MUID:95388493
A:Accession: S58382
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-20 <DIR>
A:Cross-references: EMBL:X83705; NID:g951023; PIDN:CAA58678.1; PID:g951024

Query Match 22.2%; Score 24; DB 2; Length 20;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 LKVAIKTGHPRYF 14
| | | | | |
Db 5 LSWASGTFFPRSF 17

RESULT 20
S47198
T-cell receptor J-alpha wIII.2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C:Accession: S47198
R:Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40133
A:Accession: S47198
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-21 <PLA>
A:Cross-references: EMBL:X71041; NID:g507005; PIDN:CAA50358.1; PID:g510655
C:Keywords: T-cell receptor

Query Match 22.2%; Score 24; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLKYAIKGTG 9
| | | |
Db 6 TYKYIFGTG 14

RESULT 21
S47212
T-cell receptor J-alpha wIII.3 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C:Accession: S47212
R:Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40133
A:Accession: S47212
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-21 <PLA>
A:Cross-references: EMBL:X71043; NID:g506512; PIDN:CAA50360.1; PID:g510316
C:Keywords: T-cell receptor

Query Match 22.2%; Score 24; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLKYAIKGTG 9
| | | |
Db 6 TYKYIFGTG 14

RESULT 22
S04228
N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 20K chain - rat (fragment)
N:Alternate names: glycosylasparaginase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 28-Apr-1993
C:Accession: S04228
R:Tollersrud, O.K.; Aronson Jr., N.N.
Biochem. J. 260, 101-108, 1989
A:Title: Purification and characterization of rat liver glycosylasparaginase.
A:Reference number: S04228; MUID:89374025
A:Accession: S04228
A:Molecule type: protein
A:Residues: 1-22 <TOL>
C:Keywords: hydrolase

Query Match 22.2%; Score 24; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTGH 10
| | | |
Db 9 KTGH 12

RESULT 23
PH1907
T-cell receptor alpha chain (clone A21) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 17-Mar-1999
C:Accession: PH1907
R:Sensi, M.; Salvi, S.; Castelli, C.; Maccallì, C.; Mazzocchi, A.; Mortarini, R.; Nic
J. Exp. Med. 178, 1231-1246, 1993
A:Title: T cell receptor (TCR) structure of autologous melanoma-reactive cytotoxic T
HLA-A2-restricted and melanocyte-lineage-specific CTL clone.
A:Reference number: PH1907; MUID:93389388
A:Accession: PH1907
A:Molecule type: mRNA
A:Residues: 1-25 <SEN>
A:Cross-references: EMBL:X74392
A:Experimental source: lymphocyte
C:Keywords: receptor

Query Match 22.2%; Score 24; DB 2; Length 25;
Best Local Similarity 55.6%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TLKYAIKGTG 9
| | | |
Db 7 TYKYIFGTG 15

RESULT 24
S42587
cell protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995

Search completed: February 5, 2001, 10:49:30
Job time: 743 sec

C:Accession: S42587
R:Guzzo, A.; DuBow, M.S.
Mol. Gen. Genet. 242, 455-460, 1994
A:Title: A luxAB transcriptional fusion to the cryptic celf gene of Escherichia coli
A:Reference number: S42587; MUID:94166755

A:Accession: S42587
A:Molecule type: DNA
A:Residues: 1-11 <GUZ>
C:Genetics:
A:Gene: celf

Query Match 21.3%; Score 23; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TCHPR 12
DB 6 TPHPR 10

RESULT 25

S47355
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47365; S47375; S47396; S47397; S47398; S47355
R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47365
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35690; NID:527471; PIDN:CAA84759.1; PID:9527472; EMBL:Z35679;

A:Accession: S47375
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE2>
A:Cross-references: EMBL:Z35700; NID:527493; PIDN:CAA84769.1; PID:9527494
A:Accession: S47379
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE3>
A:Cross-references: EMBL:Z35708; NID:527509; PIDN:CAA84777.1; PID:9527510

A:Accession: S47396
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE4>
A:Cross-references: EMBL:Z35674; NID:527527; PIDN:CAA84743.1; PID:9527528

A:Accession: S47397
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE5>
A:Cross-references: EMBL:Z35675; NID:527529; PIDN:CAA84744.1; PID:9527530

A:Accession: S47398
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE6>
A:Cross-references: EMBL:Z35676; NID:527531; PIDN:CAA84745.1; PID:9527532
C:Keywords: T-cell receptor

Query Match 21.3%; Score 23; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 AKTGHPRYF 14
DB 4 SIRSSYEYF 13


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CC CHAIN.
KM Oxioreductase; Molybdenum.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2096 MW; 89BD67DAD05A212E CRC64;

Query Match
Best Local Similarity 23.1%; Score 25; DB 1; Length 19;
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 4 YAIKTGHPRENQLS 18
DB 2 YAFSTPPTLDEVS 16

RESULT 3
ALLS MANSE
ID ALLS MANSE STANDARD; PRT; 15 AA.
AC P42559;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALLATOSTATIN (MAS-AS).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
RN [1]
RP SEQUENCE.
RC TISSUE-HEAD:
RX MEDLINE-92052112; PubMed-1946359;
RA Kramer S.J., Toschl A., Miller C.A., Katooka H., Qulstad G.B.,
RA Li J.P., Carney R.L., Schooley D.A.;
RT "Identification of an allatostatin from the tobacco hornworm Manduca
RT sexta."
RL Proc. Natl. Acad. Sci. U.S.A. 88:9458-9462(1991).
CC -1- FUNCTION: STRONGX INHIBITS JUVENILE HORMONE BIOSYNTHESIS IN VITRO
CC BY THE CORPORA ALLATA FROM FIFTH-STADIUM LARVAE AND ADULT FEMALES.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide.
FT MOD.RES 1 1 PYROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 15 AA; 1908 MW; 1605B77CDEBC838E CRC64;

Query Match
Best Local Similarity 22.2%; Score 24; DB 1; Length 15;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 13 YFNQLS 18
DB 8 YFNPIIS 13

RESULT 4
OXYF-SCYCA
ID OXYF-SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE-PITUITARY;
RX MEDLINE-95062247; PubMed-7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RA "Special evolution of neurohypophyseal hormones in cartilaginous
RA fishes: asatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyllorhinus caniculus)."
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RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -1- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERS.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981;
DR PFM; PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KM Hormone; Amidation.
FT DISULFID 1 6 AMIDATION.
FT MOD.RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match
Best Local Similarity 21.3%; Score 23; DB 1; Length 9;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 13 YFNQSTG 20
DB 2 YFNCPVG 9

RESULT 5
FORL MYRGU
ID FORL MYRGU STANDARD; PRT; 16 AA.
AC P81438;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE FORMACIN 1.
OS Myrmecia gulosa (Red bulldog ant).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Formicidae; Formicidae; Myrmecia.
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.
RC TISSUE-HEMOLYMPH;
RX MEDLINE-98165787; PubMed-9497332;
RA MacIntosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;
RT "Isolation from an ant Myrmecia gulosa of two inducible
RT O-glycosylated proline-rich antibacterial peptides."
RL J. Biol. Chem. 273:6139-6143(1998).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E. COLI
CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE
CC BACTERIA.
CC -1- INDUCTION: UPON BACTERIAL CHALLENGE.
CC -1- PTH: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
CC -1- SIMILARITY: TO DROSOPHILA DROSOCIN.
KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
FT CARBOHYD 11 11 O-LINKED (GALNAC...).
SQ SEQUENCE 16 AA; 1794 MW; 80CEA3AABBC2E0AE CRC64;

Query Match
Best Local Similarity 21.3%; Score 23; DB 1; Length 16;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 TGHPR 12
DB 11 TPHPR 15

RESULT 6
PPBH_PSEAE
ID PPBH_PSEAE STANDARD; PRT; 19 AA.
AC P35483;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALKALINE PHOSPHATASE H (EC 3.1.3.1) (H-AP) (FRAGMENT).
OS Pseudomons aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomons.
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RN [1]
 RP SEQUENCE.
 RC STRAIN-H103;
 RX MEDLINE-93202452; PubMed-8454193;
 RA Tan A.S.P., Morobec E.A.;
 RT "Isolation and characterization of two immunologically distinct
 alkaline phosphatases from *Pseudomonas aeruginosa*."
 RL FEMS Microbiol. Lett. 106:281-286(1993).
 CC -1- FUNCTION: HAS ONLY A PHOSPHOMONESTERASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O - AN
 CC ALCOHOL + ORTHOPHOSPHATE (AT A HIGH PH OPTIMUM)
 CC -1- COFACTOR: METALLOENZYME CONTAINING TWO ZINC ATOMS AND A MAGNESIUM
 CC ION.
 CC -1- SUBCELLULAR LOCATION: SECRETED AND PERIPLASMIC.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY.
 CC -1- SIMILARITY: BELONGS TO THE ALKALINE PHOSPHATASE FAMILY.
 DR INTERPRO: IPR001952; .
 DR PROSITE: PS00123; ALKALINE_PHOSPHATASE. PARTIAL.
 KM Hydrolase; Zinc; Magnesium; Periplasmic.
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2131 MW; C51B09D7DB22E799 CRC64;

Query Match 21.3%; Score 23; DB 1; Length 19;
 Best Local Similarity 40.0%; Pred. No. 8.8e+02;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 11 PYYENLSTG 20
 Db 5 PSLFNRQAG 14

RESULT 7
 ID CSFS_STRTR STANDARD; PRT; 21 AA.
 AC P1632;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE COLD SHOCK PROTEIN CSFPT (FRAGMENT).
 OS *Streptococcus thermophilus*.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-PB18;
 RX MEDLINE-99456673; PubMed-10525839;
 RA Perrin C., Guilmont C., Bracquart P., Galliard J.L.;
 RT "Expression of a new cold shock protein of 21.5 kDa and of the major
 cold shock protein by *Streptococcus thermophilus* after cold shock."
 RL Curr. Microbiol. 39:342-347(1999).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- INDUCTION: BY COLD SHOCK.
 CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
 DR INTERPRO: IPR002059; .
 DR PFAM: PF00313; CSD. 1.
 DR PROSITE: PS00352; COLD_SHOCK. PARTIAL.
 KM Transcription regulation; DNA-binding; Activator.
 FT DOMAIN 1 >21
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 2376 MW; 56AA4A2800F345EA CRC64;

Query Match 21.3%; Score 23; DB 1; Length 21;
 Best Local Similarity 44.4%; Pred. No. 9.7e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 KTGHPRYFN 15
 Db 1 KNGTVKWN 9

RESULT 8

PGQ_XENLA
 ID PGQ_XENLA STANDARD; PRT; 24 AA.
 AC P39080;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE ANTIMICROBIAL PEPTIDE PGQ.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
 OC Xenopodinae; *Xenopus*.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-STOMACH;
 RX MEDLINE-92011794; PubMed-1717472;
 RA Moore K.S., Bevins C.L., Brasseur M.M., Tomassini N., Turner K.,
 RA Eck H., Zasloff M.;
 RT "Antimicrobial peptides in the stomach of *Xenopus laevis*."
 RL J. Biol. Chem. 266:19851-19857(1991).
 CC -1- FUNCTION: ANTIMICROBIAL PEPTIDE.
 CC -1- TISSUE SPECIFICITY: IS SYNTHESIZED IN THE STOMACH AND STORED
 CC IN A NOVEL GRANULAR MULTINUCLEATED CELL IN THE GASTRIC MUCOSA.
 CC IT IS STORED AS ACTIVE, PROCESSED PEPTIDES IN LARGE GRANULES
 CC WITHIN THE GRANULAR GLAND SECRETIONS OF THE SKIN.
 CC -1- SIMILARITY: BELONGS TO THE MAGAINTIN FAMILY OF ANTIMICROBIAL
 CC PEPTIDES.
 DR PIR: A41037; A41037.
 KM Antibiotic; Amphibian skin.
 FT NON_TER 24
 SQ SEQUENCE 24 AA; 2457 MW; 76GA87CB7CF22B9C CRC64;

Query Match 21.3%; Score 23; DB 1; Length 24;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 13 YFNOLSTG 20
 Db 9 YLKNLGTG 16

RESULT 9
 ID CBPB_PROAT STANDARD; PRT; 15 AA.
 AC P19628;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE CARBOXYPEPTIDASE B (EC 3.4.17.2) (FRAGMENT).
 OS *Protopleus aethiopicus* (Marbled lungfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Dipnoi; Lepidosireniformes; Protopteridae; Protopterus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-PANCREAS;
 RX MEDLINE-73025047; PubMed-5079891;
 RA Reeck G.R., Neurath H.;
 RT "Isolation and characterization of pancreatic procarboxypeptidase B
 and carboxypeptidase B of the African lungfish."
 RL Biochemistry 11:3947-3955(1972).
 CC -1- CATALYTIC ACTIVITY: PEPTIDYL-L-LYSINE/ARGININE + H(2)O - PEPTIDE +
 CC L-LYSINE/ARGININE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14; ALSO KNOWN AS THE
 CC ZINC CARBOXYPEPTIDASE FAMILY.
 CC PIR: A26212; A26212.
 DR MEROPS: M14.003; .
 DR INTERPRO: IPR00834; .
 DR PROSITE: PS00132; CARBOXYPEPT_ZN_1; PARTIAL.
 DR PROSITE: PS00133; CARBOXYPEPT_ZN_2; PARTIAL.
 KM Hydrolase; Carboxypeptidase; Zinc; Zymogen.
 FT PROPEP 1 >15
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1749 MW; 124C910D937BED65 CRC64;

Query Match 20.4%; Score 22; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 9.8e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 PRYFN 15
 11111
 DB 4 PRSFN 8

RESULT 10
 FRHG_METBA STANDARD; PRT: 19 AA.
 AC P80491;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE COENZYME F420 HYDROGENASE GAMMA SUBUNIT (EC 1.12.99.1) (8-HYDROXY-5-DEAZAFLAVIN-REDUCING HYDROGENASE GAMMA SUBUNIT) (FRAGMENT).
 GN FRHG.
 OS Methanosarcina barkeri.
 OC Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 CC [1]
 RP SEQUENCE.
 RC STRAIN-FUSARO / DSM 804;
 RX MEDLINE-96085134; PubMed-8521835;
 RA Michel R., Massanz C., Kostka S., Richter M., Fiebig K.;
 RT "Biochemical characterization of the 8-hydroxy-5-deazaflavin-reactive hydroxylase from Methanosarcina barkeri Fusaro.";
 RL Eur. J. Biochem. 233:727-735(1995).
 CC -1- FUNCTION: REDUCES THE PHYSIOLOGICAL LOW-POTENTIAL TWO-ELECTRON ACCEPTOR COENZYME F420, AND THE ARTIFICIAL ONE-ELECTRON ACCEPTOR METHYLYLIOGEN.
 CC -1- CATALYTIC ACTIVITY: H(2) + COENZYME F420 - REDUCED COENZYME F420.
 CC -1- COFACTOR: FRH CONTAINS NICKEL, IRON-SULFUR, AND FAD COFACTORS.
 CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS AND A GAMMA CHAIN.
 CC -1- SIMILARITY: TO THE SMALL SUBUNITS OF OTHER NI-CONTAINING HYDROREDUCTASES.
 CC Oxidoreductase; Iron-sulfur; Electron transport.
 KM NON_TER 19
 FT SEQUENCE 19 AA; 2012 MW; C443B09B9E7B9D58 CRC64;
 SQ

Query Match 20.4%; Score 22; DB 1; Length 19;
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 IKTGH 10
 11111
 DB 4 IKIGH 8

RESULT 11
 OXLA_OPNHA STANDARD; PRT: 19 AA.
 AC P81383;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE L-AMINO ACID OXIDASE (EC 1.4.3.2) (LAO) (LAAO) (FRAGMENT).
 OS Ophiophagus hannah (King cobra) (Naja hannah).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae; Elapidae; Elapinae; Ophiophagus.
 CC [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RX MEDLINE-94361525; PubMed-8080286;
 RA Ponnudurai G., Chung M.C.M., Tan N.-H.;
 RT "Purification and properties of the L-amino acid oxidase from Malaysian pit viper (Calloselasma rhodostoma) venom.";

RL Arch. Biochem. Biophys. 313:373-378(1994).
 RN [2]
 RP SEQUENCE OF 1-15.
 RC TISSUE=VENOM;
 RX MEDLINE-97449790; PubMed-9304806;
 RA Ahn M.Y., Lee B.M., Kim Y.S.;
 RT "Characterization and cytotoxicity of L-amino acid oxidase from the venom of king cobra (Ophiophagus hannah).";
 RL Int. J. Biochem. Cell Biol. 29:911-919(1997).
 CC -1- FUNCTION: HAS CYTOTOXIC ACTIVITY (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: A L-AMINO ACID + H(2)O + O(2) - A 2-OXO ACID + NH(3) + H(2)O(2).
 CC -1- COFACTOR: FAD.
 CC -1- SUBUNIT: HOMODIMER (PROBABLE).
 CC -1- PTM: GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOXAMINE OXIDASE FAMILY.
 CC STRONG, TO MOUSE FIG-1.
 KM Oxidoreductase; Flavoprotein; FAD; Glycoprotein; Venom.
 FT CONFLICT 1
 FT NON_TER 19
 FT SEQUENCE 19 AA; 2298 MW; DD91A5B414F1427 CRC64;
 SQ

Query Match 20.4%; Score 22; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 11 PRYFNLS 18
 111111
 DB 12 PRYFNHLS 19

RESULT 12
 PK12_SOLTV STANDARD; PRT: 25 AA.
 ID PK12_SOLTV
 AC P24744;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE KUNITZ-TYPE INHIBITOR-2 (PKI-2) (FRAGMENT).
 OS Solanum tuberosum (Potato).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 CC [1]
 RP SEQUENCE.
 RC STRAIN=CV. RUSSET BURBANK; TISSUE=TUBER;
 RA Walsh T.A., Twichell W.P.;
 RT "Two Kunitz-type proteinase inhibitors from potato tubers.";
 RL Plant Physiol. 97:15-18(1991).
 CC -1- FUNCTION: POTENT INHIBITOR OF SUBTILISIN. MODERATE INHIBITOR OF TRYPSIN AND CHYMOTRYPSIN.
 CC -1- TISSUE SPECIFICITY: CORTEX OF POTATO TUBER.
 CC -1- SIMILARITY: TO SOYBEAN TRYPSIN INHIBITOR (KUNITZ) FAMILY OF PROTEASE INHIBITOR.
 CC INTERPRO: IPR002160; -;
 DR PPRM; PF00197; Kunitz_legume; 1.
 DR PROSITE; PS00283; SOYBEAN_KUNITZ; 1.
 KM Serine protease inhibitor.
 FT NON_TER 25
 FT SEQUENCE 25 AA; 2920 MW; 1F5607405921DFDC CRC64;
 SQ

Query Match 20.4%; Score 22; DB 1; Length 25;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 9 GHPRYFNQ 16
 11111
 DB 11 GHPRLRIGQ 18

RESULT 13


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DCML_PSECH
ID DCML_PSECH STANDARD: PRT: 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT)
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria.
RN [1]
RP MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
  carboxydotrophic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR -> CO(2) + REDUCED
  ACCEPTOR
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
  SMALL.
DR PIR: P10140; P10140.
KM Oxidoreductase; Molybdenum.
FT NON_TER 4
SQ SEQUENCE 4 AA: 441 MW: 7761876F0000000 CRC64:

Query Match 19.4%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GHP 11
Db 2 GHP 4

RESULT 14
AH2_PRUSE
ID AH2_PRUSE STANDARD: PRT: 15 AA.
AC P29260;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE AMGDALIN BETA-GLUCOSIDASE I (EC 3.2.1.17) (AMGDALIN HYDROLASE
  ISOZYME I') (AH I') (FRAGMENT).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
  Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
  Rosales; Rosaceae; Prunus.
RN [1]
RP SEQUENCE.
RC TISSUE=SEED;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase."
RL Plant Physiol. 100:282-290(1992)
CC -1- CATALYTIC ACTIVITY: (R)-AMGDALIN + H(2)O -> (R)-PRUNASIN +
  D-GLUCOSE.
CC -1- SUBUNIT: MONOMER.
CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
  UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
  DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
  EMBRYONAL TISSUES.
CC -1- PFM: GLYCOSYLATED.
KM Glycosidase; Hydrolyase; Glycoprotein; Multigene family.
FT NON_TER 15
SQ SEQUENCE 15 AA: 1650 MW: F7CC4FA321E12EC4 CRC64:

Query Match 19.4%; Score 21; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 7 KTGHRFYNOL 17

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Db 2 KTDPPHFASL 12

RESULT 15
CYCH_MOUSE
ID CYCH_MOUSE STANDARD: PRT: 18 AA.
AC O61458;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYCLIN H (FRAGMENT).
OS Mus musculus (Mouse).
GN CCNH.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=TESTIS;
RA Hall F.L., Wu L.;
RT Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MEMBER OF CAK WHICH ACTIVATES CYCLIN-ASSOCIATED
  CDC2/CDK2/CDK4 BY THREONINE PHOSPHORYLATION. ITS EXPRESSION AND
  ACTIVITY ARE CONSTANT THROUGHOUT THE CELL CYCLE. CAK IS TIGHTLY
  ASSOCIATED WITH A MULTIPROTEIN COMPLEX TRIP1, WHICH PLAYS A DUAL
  ROLE IN TRANSCRIPTION AND DNA REPAIR (BY SIMILARITY).
CC -1- SUBUNIT: MAMMALIAN CAK CONTAINS THREE COMPONENTS: CDK7, CYCLIN H,
  AND AN ASSEMBLY FACTOR CALLED MAT1.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN C SUBFAMILY.
CC -----
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CC -----
DR EMBL: X82441; CA57822.1; -.
DR HSP: P51946; IKXU.
DR INTERPRO: IPR000553; -.
DR PROSITE: PS00292; CYCLINS, PARTIAL.
KM Cyclin; Cell cycle; Cell division; Nuclear protein;
  transcription regulation.
FT NON_TER 1
SQ SEQUENCE 18 AA: 2105 MW: 92964DCF68EB98C7 CRC64:

Query Match 19.4%; Score 21; DB 1; Length 18;
Best Local Similarity 36.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 LKVAIKTGHR 12
Db 1 LNSVMYHPR 11

RESULT 16
MB_SCYCA
ID MB_SCYCA STANDARD: PRT: 18 AA.
AC P01206;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MELANOTROPIN BETA (BETA-MSH).
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
  Elasmobranchii; Galeomorphi; Galeidae; Carcharhiniformes;
  Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.

```

RX MEDLINE-75113445; PubMed-4452470;
 RA Love R.M., Pickering B.T.;
 RT "A beta-MSH in the pituitary gland of the spotted dogfish
 RT (Scyliorhinus canicula): isolation and structure.";
 RL Gen. Comp. Endocrinol. 24:398-404(1974).
 DR PIR. A01470; MTFBEC.
 KW Hormone.
 SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DF4 CRC64;

Query Match 19.4%; Score 21; DB 1; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 KTGHPRY 13
 DB 6 KMGHFRM 12

RESULT 17
 HBB2_UROHA STANDARD; PRT; 19 AA.
 AC P18992;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE HEMOGLOBIN BETA-2 CHAIN (FRAGMENT).
 OS Uromastix hardwickii (Indian spiny-tailed lizard).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Leioloplineae;
 OC Uromastix.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-84029159; PubMed-6628672;
 RA Nagy S., Zaidi Z.H., von Bahr-Lindstrom H., Carlquist M.,
 RA Joernvall H.;
 RT "Characterization of hemoglobin from the lizard Uromastix
 RT hardwickii.";
 RL FEBS Lett. 162:290-295(1983).
 DR INTERPRO: IPR000971; -
 DR PROSITE: PS01033; GLOBIN; PARTIAL.
 KW Heme; Oxygen transport; Respiratory protein; Erythrocyte.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 1914 MW; C40AD8EA30019057 CRC64;

Query Match 19.4%; Score 21; DB 1; Length 19;
 Best Local Similarity 60.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGHPR 12
 DB 15 TGNPK 19

RESULT 18
 DCMS_PSECA STANDARD; PRT; 21 AA.
 ID DCMS_PSECA
 AC P19921;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE CARBON MONOXIDE OXYGENASE [CYTOCHROME B-561] SMALL CHAIN (EC 1.2.2.4)
 DE (FRAGMENT).
 OS Pseudomonas carboxydovorans.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group; Oligotropa.
 RN [1]
 RP SEQUENCE.
 RX STRAIN-OM5;
 RX MEDLINE-90055678; PubMed-2818128;

RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydophilic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + FERROCYTOCHROME B-561 - CO(2) +
 CC 2 H(+) + FERROCYTOCHROME B-561.
 CC -1- CORFACTOR: MOLYBDENUM.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: P10144; P10144.
 DR Oxidoreductase; Molybdenum.
 FT NON_TER 21
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 2270 MW; 68D4380629401B9C CRC64;

Query Match 19.4%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GHP 11
 DB 12 GHP 14

RESULT 19
 NSK1_SARBU STANDARD; PRT; 9 AA.
 ID NSK1_SARBU
 AC P41492;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE NEOSULFAKININ-I (NEB-SK-I).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Sarcophagidae; Sarcophaga.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEAD;
 RX MEDLINE-93083101; PubMed-1360367;
 RA Foaagly A., Schoofs L., Proost P., van Damme J., de Loof A.;
 RT "Isolation and primary structure of two sulfakinin-like peptides from
 RT the fleshfly, Neobellieria bullata.";
 RL Comp. Biochem. Physiol. 103C:135-142(1992).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR INTERPRO: IPR001651; -
 DR PROSITE: PS00259; GASTRIN; 1.
 KW Neuropeptide; Amidation; Sulfation.
 FT MOD_RES 4
 FT MOD_RES 4
 FT MOD_RES 4
 SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691B865A0A CRC64;

Query Match 18.5%; Score 20; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 8.9e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 GHPY 13
 DB 5 GHPY 9

RESULT 20
 LSK2_LEUMA STANDARD; PRT; 10 AA.
 ID LSK2_LEUMA
 AC P09039;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE LEUCOSULFAKININ-II (LSK-II).
 OS Leucophaea maderae (Madeira cockroach), and
 OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 RN [1]
 RP SEQUENCE.
 RC SPECIES=L.MADERAE;
 RX MEDLINE=87048769; PubMed=3778455;
 RA Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
 RT "Leucosulfakinin-II, a blocked sulfated insect neuropeptide with
 RT homology to cholecystokinin and gastrin."
 RL Biochem. Biophys. Res. Commun. 140:357-364(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.AMERICANA; TISSUE=CORPORA CARDIACA;
 RX MEDLINE=90137190; PubMed=2615921;
 RA Veenstra J.A.;
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
 RT the American cockroach homologous to the leucosulfakinins."
 RL Neuropeptides 14:145-149(1989).
 CC -1- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF
 CC THE COCKROACH HINDGUT. STIMULATES MUSCLE CONTRACTION OF HINDGUT.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PIR: A26335; GMR02.
 DR INTERPRO: IPR001651;
 DR PROSITE: PS00259; GASTRIN: 1.
 KW Hormone; Amidation; Sulfatation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 5 5 SULFATATION (IN L.MADERAE, BUT NOT IN
 FT AMIDATION).
 FT MOD_RES 10 10 AMIDATION.
 FT SEQUENCE 10 AA; 1255 MW; 9BAF5391E8B5AAA CRC64;
 QY 9 GHPRY 13
 DB 6 GHMRF 10
 Query Match 18.5%; Score 20; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 21
 LSK1_LEUMA STANDARD; PRT; 11 AA.
 AC P04428;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE LEUCOSULFAKININ-1 (LSK-1).
 OS Leucophaea maderae (Madelira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86315858; PubMed=3749893;
 RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
 RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
 RT gastrin and cholecystokinin."
 RL Science 234:71-73(1986).
 CC -1- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF
 CC THE COCKROACH HINDGUT. INHIBITS MUSCLE CONTRACTION OF HINDGUT.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PIR: A01622; GMR01.
 DR INTERPRO: IPR001651;
 DR PROSITE: PS00259; GASTRIN: 1.
 KW Hormone; Amidation; Sulfatation.
 FT MOD_RES 6 6 SULFATATION.
 FT MOD_RES 11 11 AMIDATION.
 FT SEQUENCE 11 AA; 1459 MW; 7EA06080E8B5AAB CRC64;

Query Match 18.5%; Score 20; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 9 GHPRY 13
 DB 7 GHMRF 11
 Query Match 18.5%; Score 20; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 22
 LSKP_PERAM STANDARD; PRT; 11 AA.
 AC P36885;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE PERISULFAKININ (PSA-SK-1).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=CORPORA CARDIACA;
 RX MEDLINE=90137190; PubMed=2615921;
 RA Veenstra J.A.;
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
 RT the American cockroach homologous to the leucosulfakinins."
 RL Neuropeptides 14:145-149(1989).
 CC -1- FUNCTION: STIMULATES HINDGUT CONTRACTIONS.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PIR: A60656; A60656.
 DR INTERPRO: IPR001651;
 DR PROSITE: PS00259; GASTRIN: 1.
 KW Hormone; Amidation; Sulfatation.
 FT MOD_RES 6 6 SULFATATION.
 FT MOD_RES 11 11 AMIDATION.
 FT SEQUENCE 11 AA; 1445 MW; 8BAE06080E8B5AAA CRC64;
 QY 9 GHPRY 13
 DB 7 GHMRF 11
 Query Match 18.5%; Score 20; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 23
 LSK1_LOCOMI STANDARD; PRT; 12 AA.
 AC P47733;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE SULFAKININ (LOW-SK).
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Caelifera;
 OC Acridoidea; Acrididae; Locusta.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=BRAIN;
 RX Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;
 RT (In) Mc Caffery A. J. Wilson I. (eds.);
 RL Chromatography and isolation of insect hormones and pheromones,
 RL pp. 231-241, Plenum Press, New York (1990).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR INTERPRO: IPR001651;
 DR PROSITE: PS00259; GASTRIN: 1.

KW Hormone: Amidation; Sulfatation.
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 7 7 SULFATATION (POTENTIAL).
 FT MOD.RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA: 1440 MW; 9B5B5DA9BD6B5A5A CRC64;

Query Match 18.5%; Score 20; DB 1; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 GHPRY 13
 11 1:
 Db 8 GHMRF 12

RESULT 24
 NSK2_SARBU STANDARD; PRT; 14 AA.
 ID NSK2_SARBU
 AC P41493;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE NEOSULFAKININ-TI (NEB-SK-II).
 OS Sarcophaga bullata (grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Sarcophagidae; Sarcophaga.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-HEAD;
 RX MEDLINE-93083101; PubMed-1360367;
 RA Fonagy A., Schoofs L., Proost P., Van Damme J., de Loof A.;
 RT "Isolation and primary structure of two sulfakinin-like peptides from
 the fleshfly, Neobellieria bullata."
 RL Comp. Biochem. Physiol. 103C:135-142(1992).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR INTERPRO; IPRO01651; -;
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Neuropeptide; Amidation; Sulfatation.
 FT MOD.RES 9 9 SULFATATION (POTENTIAL).
 FT MOD.RES 14 14 AMIDATION (POTENTIAL).
 SQ SEQUENCE 14 AA: 1794 MW; 8B4E06D5B61C62AA CRC64;

Query Match 18.5%; Score 20; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 GHPRY 13
 11 1:
 Db 10 GHMRF 14

RESULT 25
 UC08_MAIZE STANDARD; PRT; 15 AA.
 ID UC08_MAIZE
 AC P80614;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 159)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-COLEOPTILE;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Perollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated

RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.4, ITS MW IS: 38.8 KDA.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR MAIZE-2DPAGE; P80614; COLEOPTILE.
 DR MAIZEDB; 123934; -;
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA: 1785 MW; 1978B1D6A84D8D CRC64;

Query Match 18.5%; Score 20; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 2.1e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 YAIKRGH 10
 11 1:
 Db 8 YFVYPGH 14

Search completed: February 5, 2001, 10:56:01
 Job time: 501 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:55:24 ; Search time 93.77 Seconds
(without alignments)
24.999 Million cell updates/sec

Title: US-08-981-824-4
Sequence: 1 TLKYAIKTHPRYFNQLSTG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_minc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_ricent:*
13: sp_virus:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	29.6	21	4 09UCAT	09UCAT7 homo sapien
2	30.5	28.2	23	10 09S821	09S821 hordeum vul
3	30	27.8	25	2 026056	026056 helicobacte
4	29.5	27.3	20	5 09TWM2	09TWM2 octopus vul
5	29	26.9	24	2 09R5S1	09R5S1 enterococcu
6	29	26.9	24	4 015133	015133 homo sapien
7	28	25.9	19	2 053502	053502 lactobacilli
8	28	25.9	20	2 09R500	09R500 streptomyc
9	28	25.9	25	2 09R550	09R550 enterococcu
10	27	25.0	12	4 016452	016452 homo sapien
11	26.5	24.5	19	6 094149	094149 saccharomyc
12	26	24.1	19	6 09TRR4	09TRR4 ovicollaguc
13	26	24.1	20	3 013594	013594 saccharomyc
14	26	24.1	21	6 09TR06	09TR06 bos taurus
15	25	23.1	10	12 085462	085462 avian sarco
16	25	23.1	15	7 09TNO1	09TNO1 mus sp. bet
17	25	23.1	18	10 P82242	P82242 plantago la
18	25	23.1	21	12 093191	093191 porcine cit
19	25	23.1	23	2 09ZEJ4	09ZEJ4 anabaena sp

20	25	23.1	25	11 09TK04	09TK04 mus musculu
21	24	22.2	8	11 09JLD7	09JLD7 mesocricetu
22	24	22.2	15	2 052135	052135 enterococcu
23	24	22.2	22	1 09UWK5	09UWK5 methanobact
24	24	22.2	22	4 09UCK8	09UCK8 homo sapien
25	23	21.3	13	11 09QW04	09QW04 mus sp. pl.
26	23	21.3	15	8 099586	099586 sus scrofa
27	23	21.3	15	12 09PXC5	09PXC5 tobacco etc
28	23	21.3	16	10 09S8A0	09S8A0 pinus monti
29	23	21.3	16	12 090049	090049 human cytom
30	23	21.3	18	10 09S7E5	09S7E5 arabidopsis
31	23	21.3	18	12 041588	041588 human immun
32	23	21.3	22	11 062538	062538 mus spreus
33	23	21.3	22	13 09PRN2	09PRN2 petromyzon
34	23	21.3	23	4 09UCB0	09UCB0 homo sapien
35	23	21.3	23	13 013029	013029 boreogadus
36	23	21.3	25	5 026087	026087 polycelis n
37	23	21.3	25	12 084040	084040 influenza a
38	22	20.4	13	10 043174	043174 solanum tub
39	22	20.4	15	8 095751	095751 brachylophu
40	22	20.4	16	4 014495	014495 homo sapien
41	22	20.4	16	6 09TRL1	09TRL1 canis famill
42	22	20.4	17	2 052210	052210 staphylococ
43	22	20.4	19	8 09TMN2	09TMN2 begonia for
44	22	20.4	19	8 09TMN1	09TMN1 begonia tai
45	22	20.4	19	8 09T304	09T304 begonia tai

ALIGNMENTS

RESULT 1
ID 09UCAT7 PRELIMINARY; PRT; 21 AA.
AC 09UCAT7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
DE AMELOGENIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=4163560; PubMed=8118759;
RA Catalano-Sherman J., Laskov R., Palmon A., David S., Deutsch D.;
RT "Production of a monoclonal antibody against human amelo-genin.";
RL Calcif. Tissue Int. 54:76-80(1994).
SQ SEQUENCE 21 AA; 2367 MW; 21440C1415CB578F CRC64;

Query Match 29.6%; Score 32; DB 4; Length 21;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 GHPRFN 15
Db 8 GHPGYN 14
RESULT 2
ID 09S821 PRELIMINARY; PRT; 23 AA.
AC 09S821;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE LIGHT-HARVESTING ANTENNA OF PHOTOSYSTEM I 680A, LHCI 680A.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
OX NCBI_TaxID=4513;

RN [1]
RP SEQUENCE.
RX MEDLINE=92267013; PubMed=1587270;
RA Knoetzel J., Svendsen I., Simpson D.J.;
RT "Identification of the photosystem I antenna polypeptides in barley
RT isolation of three pigment-binding antenna complexes.";
RL Eur. J. Biochem. 206:209-215(1992).
SQ SEQUENCE 23 AA; 2282 MW; 194B21969A17581E CRC64;

Query Match	28.28;	Score 30.5;	DB 10;	Length 23;
Best Local Similarity	39.18;	Pred. No. 2.9e+02;		
Matches	9;	Conservative	1;	Mismatches 8;
			Indels	5;
			Gaps	1

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QY      3 KYAIKTGHPRY-----FNQLSTG 20
          || : || | || | |
Db      1 KYLGSGDPAYPGPIFNPLGFG 23
```

RESULT 3
026056

ID	PRELIMINARY:	PRT:	25 AA.
AC	O26056;		
DT	01-JAN-1998 (TREMBLrel. 05, Created)		
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)		
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
DE	HYPOTHEITICAL 3.1 KDA PROTEIN.		
GN	HR1528		
OS	Helicobacter pylori (Campylobacter pylori).		
OC	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group.		
OC	Helicobacter.		
NCBI_taxid=210;			

RA SEQUENCE FROM N.A.
 RP STRAIN-26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kellavage A.R., Clayton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glöck A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weldman J.M., Fujii C., Bowman C., Watthey J., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.,
 RA The complete genome sequence of the gastric pathogen *Helicobacter*
 RT pylori".
 RT Nature 388:539-547(1997).
 RL EMBL: AF000651. AAD08577.1. -.
 DR TIGR: HP1528. -.
 DR Hypothetical protein.
 QO SEQUENCE 25 AA; 3075 MW; E080E93A41CE396E CRC64;

Query Match	27.8%	Score 30;	DB 2;	Length 25;
Best Local Similarity	37.5%	Pred. No. 3.8e+02;		
Matches	6;	Conservative	4;	Mismatches 6;
			Indels	0;
			Gaps	0

```

QY      2 LKVAIKTGHPRYENQL 17
          | | : : | | : | : |
Db      10 LDYSLKKGGLVKVINRL 25

```

RESULT	4
Q9TWM2	
ID	Q9TWM2
AC	Q9TWM2;
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE	GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18).
OS	Octopus vulgaris (Octopus).
OC	Eumetazoa; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;

OC Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=6645;

RN 121
 RP
 RX MEDLINE=95217318; PubMed=7702742;
 RA Tang S.S., Lin C.C., Chang G.G.;
 RT "Isolation and characterization of octopus hepatopancreatic
 glucuronide S-transferase. Comparison of digestive gland enzyme with
 RT lens S-crystallin.";
 RL J. Protein Chem. 13:609-618(1994).
 SO SEQUENCE 20 AA; 2524 MW; 57C23D23DA8B3D9D CRC64;

Query Match	27.38;	Score 29.5;	DB 5;	Length 20;
Best Local Similarity	42.18;	Pred. No. 3.5e+02;		
Matches	8;	Conservative	1;	Mismatches 5;
			Indels	5;
			Gaps	1.

```
QY      2 LKYAIKTGHPRYFNQLSTG 20
          ||| :| ||| |
Db      1 LKYEK-----YENVRGRC 14
```

RESULT	5	
Q9R5S1		
ID	Q9R5S1	PRELIMINARY;
NO	CONFEST.	PRT; 24 AA

DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PENICILLIN-BINDING PROTEIN 4, Bbp4.
OS Enterococcus hirae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1354;
RN [1]
RP
RP SEQUENCE:
RA MEDLINE=92038914; PubMed=1936941;
RA Jacques P., el Kharroubi A., Van Beunen J., Piras G., Coyette J.,
RA Ghysen J.M.;
RT "Mode of membrane insertion and sequence of a 32-amino acid peptide
RT stretch of the penicillin-binding protein 4 of Enterococcus hirae.",
RT FEBS Microbiol. Lett. 66:119-123(1991).
RL
RL SEQUENCE 24 AA: 2561 MW: CD2FC3BD76C2F220B CRC64:

Query Match	26.9%	Score 29;	DB 2;	Length 24;
Best Local Similarity	40.0%	Pred. No. 5.2e+02;		
Matches	8;	Conservative	2;	Mismatches 10;
				Indels 0;
				Gaps 0;

```
QY 1 TLKYAIKTGHPRYFNQLSTG 20
    || : || || : ||
Db 2 TLTLTQTSPRCMIYDNTG 21
```

RESULT	6
Q15133	
ID	Q15133
PRELIMINARY;	
PRT;	24 AA.

DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE GHE-1 TRANSSCRIPTION FACTOR (FRAGMENT).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RX MEDLINE=95237623; PubMed=7721104;
 RA Delhaese M., Viala V., Hooghe-Peters E.L., Castillo J.L.;
 "A novel placental transcription factor is produced by alternatively

Db 5 QTCGP 9

RESULT 11

ID 094149 PRELIMINARY; PRT; 25 AA.

AC 094149; 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PROBABLY NOT EXPRESSED DUE TO SNRNA OVERLAPPING (FRAGMENT).
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomycetes.
 RN NCBI_TaxID=4932;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Boyer J., Fairhead C., Gallon L., Galisson F., Michaux G.,
 RA Thery A., Dujon B.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.

RA MIPS:
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 275144; CAA9457.1;
 FT NON_TER 1 1
 SQ SEQUENCE 25 AA; 3023 MW; D6C9225838A38D04 CRC64;

Query Match 24.1%; Score 26.5; DB 3; Length 25;
 Best Local Similarity 31.6%; Pred. No. 1.4e+03;
 Matches 6; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

OY 2 LKYAIKTGHPRYFNOLSTG 20
 DB 4 LQYVI---YPKHFTKKPG 19

RESULT 12

ID 09TRR4 PRELIMINARY; PRT; 19 AA.

AC 09TRR4; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 13, Last annotation update)
 DE CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN
 DE L-21 FRAGMENT.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN NCBI_TaxID=9986;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=92250478; PubMed=1533622;
 RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
 RT "A calyculin-associated protein is a newly identified member of the
 CA2+/phospholipid-binding proteins, annexin family."
 RL J. Biol. Chem. 267:8919-8924(1992).
 DR HSSP; P79134; IAVC.
 SQ SEQUENCE 19 AA; 2186 MW; 576DC1604E19BCB8 CRC64;

Query Match 24.1%; Score 26; DB 6; Length 19;
 Best Local Similarity 35.3%; Pred. No. 1.2e+03;
 Matches 6; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 TLKYAIKTGHPRYFNOL 17
 DB 1 TLEBAIRSDTSGHFORL 17

RESULT 13

OY 013594

ID 013594 PRELIMINARY; PRT; 20 AA.

AC 013594; 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE ORF YOR222W (FRAGMENT).
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomycetes.
 RN NCBI_TaxID=4932;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Boyer J., Fairhead C., Gallon L., Galisson F., Michaux G.,
 RA Thery A., Dujon B.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.

RA MIPS:
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 275131; CAA9442.2;
 FT NON_TER 1 1
 SQ SEQUENCE 20 AA; 2420 MW; 6685F6B03B1E695 CRC64;

Query Match 24.1%; Score 26; DB 3; Length 20;
 Best Local Similarity 31.6%; Pred. No. 1.3e+03;
 Matches 6; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

OY 2 LKYAIKTGHPRYFNOLSTG 20
 DB 1 LMLVFTGMNFFRDLKXG 19

RESULT 14

ID 09TRO6 PRELIMINARY; PRT; 21 AA.

AC 09TRO6; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CALCYCLIN-ASSOCIATED PROTEIN PEPTIDE L-13, CAP-50-ANNEXIN.
 DE Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 RN NCBI_TaxID=9913;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=92317074; PubMed=1618851;
 RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
 RA Kobayashi R., Hidaka H.;
 RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
 fibroblast 3Y1 cells."
 RL J. Biol. Chem. 267:13498-13504(1992).
 SQ SEQUENCE 21 AA; 2352 MW; 998D0E8AC173DA19 CRC64;

Query Match 24.1%; Score 26; DB 6; Length 21;
 Best Local Similarity 41.2%; Pred. No. 1.4e+03;
 Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 TLKYAIKTGHPRYFNOL 17
 DB 1 TLEBAIRSDTSGHFOOL 17

RESULT 15

ID 085462 PRELIMINARY; PRT; 10 AA.

AC 085462; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)

DE ENV PROTEIN (FRAGMENT).
 GN ENV.
 OS Avian sarcoma virus.
 OC Viruses; Retroviruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=11876;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88275035; PubMed=2839694;
 RX Katz R.A., Kotler M., Skalka A.M.;
 RT "cis-acting intron mutations that affect the efficiency of avian
 retroviral RNA splicing: implication for mechanisms of control.";
 RL J. Virol. 62:2686-2695(1988).
 DR EMBL; M21395; AAA42413.1; -;
 FT NON_TER 1 1
 FT 10 10
 SO SEQUENCE 10 AA; 1007 MW; 5F751D67B5861A7 CRC64;

Query Match 23.1%; Score 25; DB 12; Length 10;
 Best Local Similarity 57.1%; Pred. NO. 8.8e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 AIRGHP 11
 Db 1 AVLTGTP 7

RESULT 16
 O9TNO1 PRELIMINARY; PRT; 15 AA.
 AC O9TNO1
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE BETA 2M-CLASS I-BINDING PEPTIDE-MAJOR HISTOCOMPATIBILITY COMPLEX
 DE H-2Kb-SPECIFIC MOLECULE POORLY ASSOCIATED WITH BETA 2-MICROGLOBULIN.
 OS Mus sp.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=94240094; PubMed=8183884;
 RA Joyce S., Kuzushima K., Repecs G., Angeletti R.H., Nathanson S.G.;
 RT "Characterization of an incompletely assembled major
 RT histocompatibility class I molecule (H-2Kb) associated with unusually
 RT long peptides: implications for antigen processing and presentation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).
 KM MHC.
 SO SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match 23.1%; Score 25; DB 7; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 11 PRYFNOI 17
 Db 1 PRYLLOI 7

RESULT 17
 P82242 PRELIMINARY; PRT; 18 AA.
 AC P82242
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE MAJOR POLLEN ALLERGEN PLA 1 (FRAGMENT).
 OS Plantago lanceolata (narrow-leaved plantain).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OX Lamiales; Plantaginaceae; Plantago.

OX NCBI_TaxID=39414;
 RN [1]
 RP SEQUENCE.
 RC TRISSUE-POLLEN;
 RA Calabozo B., Barber D., Polo F.;
 RT "Purification and characterization of the main allergen of Plantago
 RT lanceolata pollen, Pla 1.";
 RL J. Allergy Clin. Immunol. 0:0-0(1999).
 KM Allergen.
 FT NON_TER 18 18
 SO SEQUENCE 18 AA; 2054 MW; BD780B5758B53559D CRC64;

Query Match 23.1%; Score 25; DB 10; Length 18;
 Best Local Similarity 44.4%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 KITGPRYFN 15
 Db 2 QTSHPAFH 10

RESULT 18
 O93191 PRELIMINARY; PRT; 21 AA.
 ID O93191
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE ORF8.
 OS porcine circovirus.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=46221;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
 RX MEDLINE=98418498; PubMed=9747726;
 RA Meenan B.M., McNeill F.M., Todd D., Kennedy S., Jewhurst V.,
 RA Ellis J.A., Haasard L.E., Clark E.G., Haines D.M., Allen G.M.;
 RT "Characterization of novel circovirus DNAs associated with wasting
 RT syndromes in pigs.";
 RL J. Gen. Virol. 79:2171-2199(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PORCINE CIRCOVIRUS TYPE II;
 RA Meenan B.M.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF055394; AAC3534.1; -;
 DR EMBL; AF055393; AAC3532.1; -;
 SO SEQUENCE 21 AA; 2369 MW; BAB8F6E2184C1013 CRC64;

Query Match 23.1%; Score 25; DB 12; Length 21;
 Best Local Similarity 27.3%; Pred. No. 2e+03;
 Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 LKVAIKTGHP 12
 Db 3 IDHTVSVDHPR 13

RESULT 19
 O9ZEJ4 PRELIMINARY; PRT; 23 AA.
 ID O9ZEJ4
 AC O9ZEJ4
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DNAJ2 PROTEIN (FRAGMENT).
 GN DNAJ2.
 OS Arabidopsis sp.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=1167;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC 7120;
 RA Pohl B.;
 RL Thesis (1999), University of Bonn, Botanical Institute.
 DR EMBL; AJ132709; CA10746.1; -.
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2493 MW; AC5084286BC591ED CRC64;

Query Match 23.1%; Score 25; DB 2; Length 23;
 Best Local Similarity 36.4%; Pred. No. 2.2e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 7 KTGHPRYFNOL 17
 DB 3 KSEPTYYSL 13

RESULT 20
 ID 09JRK04 PRELIMINARY; PRT; 25 AA.
 AC 09JRK04;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (FRAGMENT).
 GN FBPA5E 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tilmann H., Stein S., Liehr T., Eschrich K.;
 RT "Structure and chromosomal localization of the human and mouse muscle
 fructose-1,6-bisphosphatase genes.";
 RL Gene 247:241-253(2000).
 DR EMBL; AJ243025; CAB9672.1; -.
 KW Hydrolyase.
 FT NON_TER 1 1
 FT NON_TER 25 25
 SQ SEQUENCE 25 AA; 2898 MW; EA7A6F50F3A3ID3 CRC64;

Query Match 23.1%; Score 25; DB 11; Length 25;
 Best Local Similarity 27.3%; Pred. No. 2.4e+03;
 Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 5 AIKTGHPRYFN 15
 DB 1 SLNEGAKYFD 11

RESULT 21
 ID 09JLD7 PRELIMINARY; PRT; 8 AA.
 AC 09JLD7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE P53 TUMOR SUPPRESSOR (FRAGMENT).
 OS Mesocricetus auratus (Golden Hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-KIDNEY.
 RA Laverdiere M., Beaudoin J., Lavigne A.;
 RT "Species-specific regulation of alternative splicing in the C-terminal
 region of the p53 tumor suppressor gene.";

RL Nucleic Acids Res. 28:1489-1497(2000).
 DR EMBL; AF190271; AAF43279.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 969 MW; 1DB6D9CDA1761E7 CRC64;

Query Match 22.2%; Score 24; DB 11; Length 8;
 Best Local Similarity 80.0%; Pred. No. 3.7e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 10 HPRYF 14
 DB 2 HPRAF 6

RESULT 22
 ID 052135 PRELIMINARY; PRT; 15 AA.
 AC 052135;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE PLASMD PADI SEX PHEROMONE INHIBITOR (PADI) DETERMINANT.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-91261999; PubMed-2128961;
 RA Clewell D.B., Pontius L.T., An F.Y., Ike Y., Suzuki A., Nakayama J.;
 RT "Nucleotide sequence of the sex pheromone inhibitor (PADI) determinant
 of Enterococcus faecalis conjugative plasmid PADI.";
 RL Plasmid 24:156-161(1990).
 DR EMBL; M62888; AAA98040.1; -.
 KW Plasmid.
 SQ SEQUENCE 15 AA; 1874 MW; 0D9D07E3079E3559 CRC64;

Query Match 22.2%; Score 24; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 YAIKTGHPRYF 14
 DB 2 YTVHYIPREF 12

RESULT 23
 ID 09UWK5 PRELIMINARY; PRT; 22 AA.
 AC 09UWK5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE 65 KDA TUNGSTEN CONTAINING FORMYLMEETHANOFURAN DEHYDROGENASE
 (FRAGMENT).
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacterium.
 OX NCBI_TaxID=2166;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE-94213570; PubMed-8161283;
 RA Bertam P.A., Schmitz R.A., Linder D., Thauer R.K.;
 RT "Tungstate can substitute for molybdate in sustaining growth of
 Methanobacterium thermoautotrophicum. Identification and
 characterization of a tungsten isoenzyme of formylmethanofuran
 dehydrogenase.";
 RL Arch. Microbiol. 161:220-228(1994).
 SQ SEQUENCE 22 AA; 2575 MW; EC412A8DC463A33 CRC64;

Search completed: February 5, 2001, 10:55:26
 Job time: 915 sec

Query Match 22.2%; Score 24; DB 1; Length 22;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 LKVAIKTG 9
 |||||
 DB 1 MEYIKNG 8

RESULT 24

O9UCK8 PRELIMINARY; PRT; 22 AA.
 AC O9UCK8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ASPARTYLGLUCOSAMINIDASE ALPHA SUBUNIT (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93111925; PubMed=1281977;
 RA Rip J.W., Coulter-Mackie M.B., Rupa C.A., Gordon B.A.;
 RT "Purification and structure of human liver aspartylglucosaminidase.";
 RL Biochem. J. 288:1005-1010(1992).
 DR HSP; P20933; IAPY.
 SQ SEQUENCE 22 AA; 2179 MW; 9628EC8CFBDA28F CRC64;

Query Match 22.2%; Score 24; DB 4; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 KTGH 10
 |||||
 DB 9 KTGH 12

RESULT 25

O9QW04 PRELIMINARY; PRT; 13 AA.
 AC O9QW04;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE Pl.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94043690; PubMed=7693750;
 RA Barnett L.A., Whitton J.L., Wada Y., Fujinami R.S.;
 RT "Enhancement of autoimmune disease using recombinant vaccinia virus
 encoding myelin proteolipid protein.";
 RL J. Neuroimmunol. 48:120-120(1993).
 SQ SEQUENCE 13 AA; 1538 MW; 2A33FF99B5807733 CRC64;

Query Match 21.3%; Score 23; DB 11; Length 13;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 9 GHPRYF 14
 |||||
 DB 8 GHPDKF 13

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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:47:31 ; Search time 68.99 Seconds
(without alignments)
9.913 Million cell updates/sec

Title: US-08-981-824-4

Sequence: 108
1 TLKXAKTGHPREYFQNLSTG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 141170

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq.36.*
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.*
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11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT.*
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20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	108	100.0	20	W18845	65 KD Glutamic ac1
2	108	100.0	20	W01796	Human 65 KD glutam
3	108	100.0	20	W12404	GAD65 residues 173
4	72	66.7	20	R72272	Glutamic acid deca
5	72	66.7	20	Y59572	GAD65 fragment, pe
6	60	55.6	20	R72271	Glutamic acid deca
7	60	55.6	20	Y59571	GAD65 fragment, pe
8	55	50.9	20	W18846	65 KD Glutamic, pe
9	55	50.9	20	W01797	Human 65 KD glutam
10	48	44.4	14	R76657	Peptide derived fr
11	48	44.4	14	W18865	65 KD Glutamic ac1
12	48	44.4	15	W12405	GAD65 residues 177

13	34	31.5	24	20	Y36566
14	32	29.6	14	15	R49436
15	32	29.6	24	15	R49435
16	31	28.7	20	21	Y91936
17	30	27.8	11	21	Y57311
18	30	27.8	16	14	R43130
19	30	27.8	16	14	W35218
20	30	27.8	16	18	W35210
21	30	27.8	16	19	W82934
22	30	27.8	17	19	W82926
23	30	27.8	17	19	W80790
24	29	26.9	9	20	Y01008
25	29	26.9	15	20	W92558
26	29	26.9	15	20	W92559
27	29	26.9	12	21	Y58198
28	28	25.9	13	19	W70635
29	28	25.9	13	21	Y99311
30	28	25.9	15	16	R68754
31	28	25.9	15	16	R68755
32	28	25.9	15	20	Y13251
33	28	25.9	15	20	Y13300
34	28	25.9	15	20	Y13277
35	28	25.9	16	15	R57905
36	28	25.9	16	17	R90371
37	28	25.9	20	20	W74168
38	28	25.9	23	13	R20236
39	28	25.9	25	16	R74073
40	28	25.9	25	20	Y39991
41	28	25.9	25	20	Y26613
42	27.5	25.5	24	7	P60962
43	27	25.0	9	15	R62231
44	27	25.0	9	16	R79703
45	27	25.0	9	21	Y67904

ALIGNMENTS

RESULT 1
W18845
W18845 standard; peptide; 20 AA.
XX
AC W18845;
XX
DT 05-JAN-1998 (first entry)
XX
DE 65 KD Glutamic acid decarboxylase peptide fragment IV.
XX
KW GAD, 65 KD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
KW Insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
KW predisposition; autoimmune; tumour; rheumatoid arthritis;
KW multiple sclerosis.
XX
OS Synthetic.
XX
PN DE19526561-A1.
XX
PD 23-JAN-1997.
XX
PE 20-JUL-1995; 95DE-1026561.
XX
PR 20-JUL-1995; 95DE-1026561.
XX
(BOEF) BOEHRINGER MANNHEIM GMBH.
PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;
PI Pozzilli P, Stahl P;
DR WPI; 1997-088254/09.
XX
XX Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
XX involving intradermal admin. of auto-reactive substances

Fragment of human
Calgranulin B posi
Calgranulin B posi
Hsrec2 peptide res
P. aeruginosa cera
Rhinoviral HRV2 2A
Diastereomer pepit
Diastereomer pepit
Antipathogenic pep
Antipathogenic pep
Peptide 6 from D.
Bacterial immune
Mouse beta-actin a
Mouse beta-actin a
Human STRAP-1 pep
Second generation
HLA class II bindi
Cytotoxic T lympho
Diabetes type I au
Naturally occurin
Naturally occurin
Randomly generated
Residues 10-25 of
HJ loop peptide CA
NAF(3-25) peptide
Superantigen pepit
HIV Negative facto
HIV-derived lipope
Polypeptide which
Toxoplasma gondii
EGF receptor Tyr K
EGF receptor autop

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PS Claim 11; Page 9; 12pp; German.
CC CC W18642-70 are peptide fragments of the 65 kD human glutamic acid
CC deкарбоxyлаse (GAD). The fragments are autoreactive substances used for
CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
CC determined by using a claimed method for diagnosis of cell-mediated
CC diseases or a predisposition to cell-mediated diseases, which is effected
CC by administering an autoreactive substance intradermally and establishing
CC the diagnosis on the basis of the occurrence or lack of a positive
CC reaction at the site of administration. The method is used for diagnosis
CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
XX XX Sequence 20 AA:

Query Match 100.0%; Score 108; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 TLKVAIKTGHPRYPFYNQLSTG 20
   |||||
Db 1 tlkvaiktghpryfnqlstg 20

RESULT 2
W01796
W01796 standard; peptide; 20 AA.
W01796;
15-OCT-1997 (first entry)

Human 65 kD glutamine decarboxylase peptide.

Human: glutamine decarboxylase; GAD; diagnosis; predisposition;
tumour; immunological disease; autoimmune; diabetes; reagent;
determination; T cell; subpopulation; medicament; treatment;
prevention; production; antigen; immunogen; tolerogen; isolation;
rejection; inactivation.

OS Homo sapiens.
XX XX DEL95525784-A1.
PN 16-JAN-1997.
XX XX
XX PF 14-JUL-1995; 95DE-1025784.
XX PR 14-JUL-1995; 95DE-1025784.
PA (BOEHRINGER MANNHEIM GMBH:
PI Albert W., Boltard C., Endl J., Jung G., Schendel D;
PI Stahl P., Van Endernt P;
DR MPI: 1997-078452/08.
XX XX
PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of
XX diabetes, etc.
XX
XX Claim 1; Page 12; 15pp; German.

The present peptide is a fragment of the human 65 kD glutamine
decarbоxyлаse (GAD), which can be used to diagnose, or diagnose a
predisposition to, a tumour or immunological disease, preferably an
autoimmune disease, especially diabetes. It can also be used as a
reagent to determine specific T cell subpopulations, in medicaments
to treat or prevent immunological diseases, preferably autoimmune
diseases, especially diabetes, to produce antigens, especially
immunogens or tolerogens and to isolate specific T cell
subpopulations, which can be used to produce antigens or for
rejection, optionally after inactivation.

```

SQ	Sequence	20 AA:
XX	Query Match	100.0%; Score 108; DB 18; Length 20;
XX	Best Local Similarity	100.0%; Prd. NO.1.8e-12;
XX	Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 TLKYAIKTHPRPYENQLSTG 20	
DB	1 tlkyaitkthprpyrnfqstg 20	
RESULT 3		
ID W12404	w12404 standard; peptide; 15 AA.	
AC W12404:		
DT 08-OCT-1997	(first entry)	
DE GAD65 residues 173-187.		
XX 65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;		
KW neuron; central nervous system; type I diabetes; autoimmune response;		
KW T cell; therapy.		
OS Homo sapiens.		
XX Key	Location/Qualifiers	
FH Misc-difference 1..15		
FT /note= "optionally substituted, providing at least 7		
FT residues remain wild type"		
XX WO9700891-A1.		
PN 09-JAN-1997.		
XX 24-JUN-1996;	96WO-US10790.	
XX PF 23-JUN-1995;	95US-0494624.	
XX PR (KENN-) KENNEDY INST RHEUMATOLOGY.		
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.		
PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.		
PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Londel M;		
XX WPI: 1997-087322/08.		
PT New human glutamic acid decarboxylase peptide(s) - used for		
PT treatment, diagnosis and determining predisposition to diabetes and		
PT for ameliorating auto-immune responses.		
PS Claim 22; Page -: 28pp; English.		
CC w12403-w12413 represent fragments and analogues of the 65 kD isoform		
CC of human glutamic acid decarboxylase (GAD65) (see w12402 for full length		
CC wild type protein). GAD is an enzyme expressed in the beta cells of the		
CC pancreas, and in neurons of the central nervous system. There are two		
CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of		
CC GAD65 have been identified in Type I diabetic patients. These GAD65		
CC fragments, and analogues, are used in the methods of the invention. The		
CC methods are for detecting or treating diabetes or a predisposition to		
CC diabetes. The peptides can also be used for ameliorating an autoimmune		
CC response in a patient. Alteration of the native peptides with selective		
CC changes of crucial residues can induce unresponsiveness or change the		
CC responsiveness of antigen-specific autoreactive T cells. The peptide		
CC analogues compete for binding to MHC and do not cause proliferation of		
CC the corresponding native peptide-specific T cells.		
XX Sequence 15 AA:		

Query Match 68.5%; Score 74; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGHPRYFNOLSTG 20
| | | | | | | | | | | | | | |
Db 1 tghpryfnqstg 13

RESULT 4

R72272
ID R72272 standard; Peptide; 20 AA.

XX AC R72272;

XX DT 13-NOV-1995 (first entry)

DE Glutamic acid decarboxylase (GAD65) fragment.

XX glutamic acid decarboxylase; GAD65; autoimmune disorders;

KW Insulin-dependent diabetes mellitus; stiff man disease.

XX Homo sapiens.

XX WO9507992-A.

XX 23-MAR-1995.

XX 24-AUG-1994; 94WO-US09478.

XX 17-SEP-1993; 93US-0123859.

XX (REGC) UNIV CALIFORNIA.

XX PI Clare-Saltzer MJ, Erlander MG, Kaufman DL, Tobin AJ;

XX WPI; 1995-131360/17.

XX New polypeptide fragments of glutamic acid decarboxylase - for

PT diagnosis and treatment of autoimmune disease, esp. insulin

PT antibodies, hybridoma(s) etc.

XX Example 11; Page 76; 100pp; English.

XX Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic

CC acid decarboxylase (GAD65) respectively, from which the GAD65

CC fragments described in R72261-R72298 were derived. These fragments

CC can be used to detect autoantibodies against GAD, e.g. to diagnose

CC and treat GAD-related autoimmune disorders, such as insulin

CC dependant diabetes mellitus or stiff man disease.

XX SO Sequence 20 AA;

Query Match 66.7%; Score 72; DB 16; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.5e-06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTGHPRYFNOLSTG 20
| | | | | | | | | | | | | | |
Db 1 kyghpryfnqstg 14

RESULT 5

Y59572
ID Y59572 standard; Peptide; 20 AA.

XX AC Y59572;

XX DT 03-APR-2000 (first entry)

DE GAD65 fragment, peptide #12.

XX GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;

KW Insulin dependent diabetes mellitus; stiff man disease; diagnosis;

XX Homo sapiens.

XX US598366-A.

XX 07-DEC-1999.

XX 09-APR-1997; 97US-0827618.

XX 07-JUN-1995; 95US-0485725.

XX 21-SEP-1990; 90US-0586536.

XX 18-JUN-1991; 91US-0716909.

XX (REGC) UNIV CALIFORNIA.

XX PI Tobin AJ, Kaufman DL, Erlander MG;

XX WPI; 2000-095930/08.

XX Ameliorating glutamic acid decarboxylase associated autoimmune

XX disorders such as insulin dependent diabetes mellitus and stiff man

XX disease -

XX Example 11; Column 42; 61pp; English.

XX This sequence represents a fragment of the glutamic acid decarboxylase 65

CC (GAD65) protein. The invention relates to a method of ameliorating GAD

CC associated autoimmune disorders by administering a GAD65 peptide to the

CC patient. The method can be used for ameliorating GAD associated

CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)

CC and stiff man disease. GAD65 can also be useful for screening drugs that

CC alter GAD function, for generating monoclonal antibodies and in

CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM

CC and the diagnosis is quite easy. It is also possible to obtain much

CC larger quantities of polypeptide via recombinant techniques than are

XX available from natural sources.

XX SQ Sequence 20 AA;

Query Match 66.7%; Score 72; DB 21; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.5e-06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTGHPRYFNOLSTG 20
| | | | | | | | | | | | | | |
Db 1 kyghpryfnqstg 14

DE Glutamic acid decarboxylase (GAD65) fragment.

XX Glutamic acid decarboxylase; GAD65; autoimmune disorders;

KW Insulin-dependent diabetes mellitus; stiff man disease.

XX Homo sapiens.

XX WO9507992-A.

XX 23-MAR-1995.

PF 24-AUG-1994; 94WO-US09478.
 XX
 XX 17-SEP-1993; 93US-0123859.
 XX
 XX (REGC) UNITV CALIFORNIA.
 XX
 XX Clare-Salzler MJ, Erlander MG, Kaufman DL, Toblin AJ;
 PI WPI; 1995-131360/17.
 DR
 XX New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hydridoma(s) etc.
 XX
 XX Claim 1; Page 76; 100pp; English.
 PS
 XX Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependant diabetes mellitus or stiff man disease.
 XX
 SQ Sequence 20 AA;

Query Match 55.6%; Score 60; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLKYAIKTGHP 11
 |||||
 DB 10 TLKYAIKTGHP 20

RESULT 7
 Y59551
 ID T59551 standard; peptide: 20 AA.

XX Y59551;
 AC
 XX
 XX 03-APR-2000 (first entry)
 DT
 XX
 XX

DE GAD65 fragment, peptide #11.

XX GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
 KW therapy.
 XX
 XX

OS Homo sapiens.

XX

XX US5998366-A.

XX 07-DEC-1999.

XX 09-APR-1997; 97US-0827618.

XX 07-JUN-1995; 95US-0485725.

PR 21-SEP-1990; 90US-0586536.

PR 18-JUN-1991; 91US-0716909.

XX (REGC) UNITV CALIFORNIA.

XX Toblin AJ, Kaufman DL, Erlander MG;

DR WPI; 2000-095930/08.

XX Ameliorating glutamic acid decarboxylase associated autoimmune
 PT disorders such as insulin dependent diabetes mellitus and Stiff man
 CC disease ;
 XX
 PS Claim 1; Column 42; 61pp; English.

XX This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorders by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 CC and Stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.
 XX
 SQ Sequence 20 AA;

Query Match 55.6%; Score 60; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLKYAIKTGHP 11
 |||||
 DB 10 TLKYAIKTGHP 20

RESULT 8
 W18846
 ID W18846 standard; peptide: 20 AA.

XX W18846;

DT 05-JAN-1998 (first entry)

DE 65 kD glutamic acid decarboxylase peptide fragment V.

XX GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
 KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
 KW predisposition; autoimmune; tumour; rheumatoid arthritis;
 KW multiple sclerosis.
 XX
 XX

OS Synthetic.

XX DE19526561-A1.

XX 23-JAN-1997.

XX 20-JUL-1995; 95DE-1026561.

XX 20-JUL-1995; 95DE-1026561.

XX (BOE) BOEHRINGER MANNHEIM GMBH.

XX Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;

XX Pozzilli P, Stahl P;

XX WPI; 1997-088254/09.

XX Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
 PT involving intradermal admn. of auto:reactive substances
 XX
 XX

PS Claim 11; Page 9; 12pp; German.

XX W18842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 XX

SQ Sequence 20 AA:

Query Match 50.9%; Score 55; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PRYFNQLSTG 20
 |||||
 Db 1 pryfnglstg 10

RESULT 9

W01797
 ID W01797 standard; peptide; 20 AA.

AC W01797;

DT 15-OCT-1997 (first entry)

DE Human 65 kD glutamine decarboxylase peptide.

XX Human: glutamine decarboxylase; GAD; diagnosis; predisposition;
 KW tumour; immunological; disease; autoimmune; diabetes; reagent;
 KW determination; T cell; subpopulation; medication; treatment;
 KW prevention; production; antigen; immunogen; tolerogen; isolation;
 KW reinjection; inactivation.

XX Homo sapiens.

PN DE19525784-A1.

PD 16-JAN-1997.

PE 14-JUL-1995; 95DE-1025784.

PR 14-JUL-1995; 95DE-1025784.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Albert W, Bollard C, Endl J, Jung G, Schendel D;

PI Stahl P, Van Enderst P;

DR WPI: 1997-078452/08.

XX Glutamine decarboxylase peptide(s) - for diagnosis and therapy of
 PT diabetes, etc.

PS Claim 1; Page 12; 15pp; German.

XX The present peptide is a fragment of the human 65 kD glutamine
 CC decarboxylase (GAD), which can be used to diagnose, or diagnose a
 CC predisposition to, a tumour or immunological disease, preferably an
 CC autoimmune disease, especially diabetes. It can also be used as a
 CC reagent to determine specific T cell subpopulations, in medicaments
 CC to treat or prevent immunological diseases, preferably autoimmune
 CC diseases, especially diabetes, to produce antigens, especially
 CC immunogens or tolerogens and to isolate specific T cell
 CC subpopulations, which can be used to produce antigens or for
 CC reinjection, optionally after inactivation.

XX Sequence 20 AA:

Query Match 50.9%; Score 55; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PRYFNQLSTG 20
 |||||
 Db 1 pryfnglstg 10

RESULT 10

R76657
 ID R76657 standard; peptide; 14 AA.

AC R76657;

DT 05-MAR-1996 (first entry)

DE Peptide derived from human glutamic acid decarboxylase 16.

XX diabetes; T-cell subpopulation; detection; antigen production;
 KW diagnosis; autoimmune disease.

XX Homo sapiens.

PN DE4418091-A1.

PD 27-JUL-1995.

PE 24-MAY-1994; 94DE-4418091.

PR 04-FEB-1994; 94DE-4403522.

PR 20-JAN-1994; 94DE-4401629.

PA (ENDL) ENDL J.

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Albert W, Dormair K, Endl J, Jung G, Mehl E;

PI Stahl P, Schendel D;

DR WPI: 1995-264505/35.

XX Antigen-specific activated T-lymphocytes and their detection - by
 PT interaction with inventive peptide(s) of peptide-MHC complexes;
 PT useful in diagnosis of e.g. diabetes and autoimmune diseases

PS Claim 1; Fig 2; 21pp; German.

XX R76642-62 are derived from human glutamic acid decarboxylase and
 CC specifically react with T-cell sub-populations isolated from recently
 CC diagnosed Type-I diabetes. Pharmaceutical compns. contg. these
 CC peptides and those shown in R7571-72, are useful for the diagnosis of
 CC a disease or predispositions of immune system diseases, tumours, and
 CC autoimmune diseases, including diabetes. The peptides are able to detect
 CC specific T-cell subpopulations that are then used for antigen prodn.,
 CC e.g. by reinjection.

SQ Sequence 14 AA:

Query Match 44.4%; Score 48; DB 16; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 RYFNQLSTG 20
 |||||
 Db 1 ryinglstg 9

RESULT 11

W18865
 ID W18865 standard; peptide; 14 AA.

AC W18865;

DT 05-JAN-1998 (first entry)

DE 65 kD Glutamic acid decarboxylase peptide fragment 16.

XX GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
 KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
 KW predisposition; autoimmune; tumour; rheumatoid arthritis;
 KW multiple sclerosis.

```

XX OS Synthetic.
XX PN DE19526561-A1.
XX PD 23-JUN-1997.
XX PF 20-JUL-1995; 95DE-1026561.
XX PR 20-JUL-1995; 95DE-1026561.
XX PA (BOEF) BOEHRINGER MANNHEIM GMBH.
XX PI Donie F, Endl J, Ganz M, Jung G, Kientsch-engel R;
XX PI Pozzilli P, Stahl P;
XX DR WPI; 1997-088254/09.
XX PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
XX PT Involving intradermal admn. of auto-reactive substances
XX PS Claim 11; Fig 2; 12pp; German.
XX CC W18842-10 are peptide fragments of the 65 kd human glutamic acid
XX CC decarboxylase (GAD). The fragments are autoreactive substances used for
XX CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
XX CC determined by using a claimed method for diagnosis of cell-mediated
XX CC diseases or a predisposition to cell-mediated diseases, which is effected
XX CC by administering an autoreactive substance intradermally and establishing
XX CC the diagnosis on the basis of the occurrence or lack of a positive
XX CC reaction at the site of administration. The method is used for diagnosis
XX CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
XX CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
XX SQ Sequence 14 AA;

Query Match 44.4%; Score 48; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RYFNOLSTG 20
DB 1 rYfnlsgt 9

RESULT 12
W12405
ID W12405 standard; peptide; 15 AA.
AC W12405;
XX 08-OCT-1997 (first entry)
XX DE GAD65 residues 177-191.
XX KW 65 kd glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;
XX KW neuron; central nervous system; type I diabetes; autoimmune response;
XX KW T cell; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..15
XX FT /note- "optionally substituted, providing at least 7
XX PN residues remain wild type"
XX PD 09-JAN-1997.
XX PF 24-JUN-1996; 96WO-US10790.
XX

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PR 23-JUN-1995; 95US-0494624.
XX (KENN-) KENNEDY INST RHEUMATOLOGY.
XX PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.
XX PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;
XX DR WPI; 1997-087322/08.
XX PT New human glutamic acid decarboxylase peptide(s) - used for
XX PT treatment, diagnosis and determining predisposition to diabetes and
XX PT for ameliorating auto-immune responses.
XX PS Claim 23; Page -; 28pp; English.
XX CC W12403-W12413 represent fragments and analogues of the 65 kd isoform
XX CC of human glutamic acid decarboxylase (GAD65) (see W12402 for full length
XX CC wild type protein). GAD is an enzyme expressed in the beta cells of the
XX CC pancreas, and in neurons of the central nervous system. There are two
XX CC isoforms of GAD, a 67 kd isoform, and GAD65. Immunodominant regions of
XX CC GAD65 have been identified in Type I diabetic patients. These GAD65
XX CC fragments, and analogues, are used in the methods of the invention. The
XX CC methods are for detecting or treating diabetes or a predisposition to
XX CC diabetes. The peptides can also be used for ameliorating an autoimmune
XX CC response in a patient. Alteration of the native peptides with selective
XX CC changes of crucial residues can induce unresponsiveness or change the
XX CC responsiveness of antigen-specific autoreactive T cells. The peptide
XX CC analogues compete for binding to MHC and do not cause proliferation of
XX CC the corresponding native peptide-specific T cells.
XX SQ Sequence 15 AA;

Query Match 44.4%; Score 48; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RYFNOLSTG 20
DB 1 rYfnlsgt 9

RESULT 13
Y36566
ID Y36566 standard; Protein; 24 AA.
AC Y36566;
XX 17-SEP-1999 (first entry)
XX DE Fragment of human secreted protein encoded by gene 39.
XX KW Human; secreted protein; cancer; tumour; developmental abnormality;
XX KW foetal deficiency; blood disorder; immune system disorder; inflammation;
XX KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
XX KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
XX KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
XX KW digestive disorder; endocrine disorder; infection; AIDS.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..15
XX FT /note- "optionally substituted, providing at least 7
XX PN residues remain wild type"
XX PD 24-JUN-1999.
XX PF 17-DEC-1998; 98WO-US27059.
XX PR 19-DEC-1997; 97US-0068369.
XX PR 18-DEC-1997; 97US-0068006.
XX PR 18-DEC-1997; 97US-0068007.
XX PR 18-DEC-1997; 97US-0068008.
XX PR 18-DEC-1997; 97US-0068053.
XX

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DR WPI: 1994-082825/10.
 XX Novel immunomodulatory peptide(s) and nucleic acids - useful for
 PT treatment of auto-immune diseases, transplant rejection and for
 PT vaccination
 PS Disclosure: Page 92, 139pp; English.
 XX
 CC The sequences given in R49291-505 and R46981-7038 represent peptide
 CC fragments of naturally-occurring immunomodulatory proteins. These
 CC fragments are between 10-30 residues in length and bind to a human
 CC major histocompatibility complex (MHC) class II allotype. These
 CC peptides may be used for therapy of autoimmune diseases, such as
 CC type I diabetes, rheumatoid arthritis and multiple sclerosis, and to
 CC reduce transplant rejection. They may also be used for vaccination
 CC providing an exclusively T-cell-mediated response, which can be
 CC class I or class-II based, or both, depending on the length and
 CC character of the immunogenic peptides.
 CC
 CC Sequence 24 AA:
 SQ
 Query Match 29.6%; Score 32; DB 15; Length 24;
 Best Local Similarity 60.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 7 RTGHPRYFNQ 16
 Db 1 k1ghpdt1ng 10
 RESULT 16
 Y91936
 ID Y91936 standard; Peptide; 20 AA.
 AC Y91936;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE HsRec2 peptide residues 153-172.
 XX
 KW HsRec2; serine kinase; homologous pairing; strand transfer; RAD51;
 KW phosphorylation; cyclin E; p53; cell cycle; substrate.
 XX
 OS Synthetic.
 XX
 PN WO200017329-A1.
 PD 30-MAR-2000.
 XX
 PF 17-SEP-1999; 99WO-US21642.
 XX
 PR 21-SEP-1998; 98US-0157603.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 PA (CORR.) CORNELL RES FOUND INC.
 PA (KIME-) KIMERAGEN INC.
 PI
 PI Havre PA, Rice MC, Holloman WK, Kmiec EB;
 DR WPI: 2000-283562/24.
 XX
 PT Phosphorylating a serine-containing substrate by incubating it with
 PT adenosine triphosphate and Rec2 kinase and measuring the level of
 PT phosphorylation, useful for discovering specific antagonists or
 PT agonists of Rec2
 XX
 PS Example 3; Page 14; 41pp; English.
 XX
 CC The present sequence is hRec2 peptide, residues 153-172, a substrate
 CC which was not phosphorylated by hRec2, a human serine kinase. HsRec2
 CC is in the same supergene family as the mammalian protein having
 CC homologous pairing and strand transfer activities, RAD51 and was

CC isolated because of its homology to the homologous pairing and strand
 CC transfer protein of *Ustilago maydis*. In particular, hRec2
 CC phosphorylates several proteins that control the cell cycle, especially
 CC cyclin E and p53. The invention permits the phosphorylation of cell
 CC cycle control proteins at sites that are physiologically relevant. The
 CC invention can be practiced with either murine or human Rec2 or a mutin
 CC or chimera of these proteins. In particular the mutin has the sequence
 CC of a Rec2 kinase containing other than a Tyr at position 163. The
 CC invention comprises a method of phosphorylating a serine-containing
 CC substrate comprising incubating the substrate with ATP (adenosine
 CC triphosphate) and Rec2 kinase or a mammalian Rec2 and measuring the level
 CC of phosphorylation. The method is useful for discovering compounds which
 CC are specific antagonists or agonists of Rec2.
 CC
 CC Sequence 20 AA:
 SQ
 Query Match 28.7%; Score 31; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 11 PRYFN 15
 Db 9 pryfn 13
 RESULT 17
 Y57311
 ID Y57311 standard; peptide; 11 AA.
 AC Y57311;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE P. aeruginosa ceramidase partial fragment C-86.
 XX
 KW Ceramidase; ceramide; sphingosine; fatty acid; atopic dermatitis;
 KW lipid engineering; anti-dermatitis.
 XX
 OS Pseudomonas aeruginosa.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3 /note="unspecified"
 XX
 PN EP980912-A1.
 PD 23-FEB-2000.
 XX
 PF 20-AUG-1999; 99EP-0116154.
 XX
 PR 20-AUG-1998; 98JP-0234769.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Okino N, Ito M;
 PI
 DR WPI: 2000-258590/23.
 XX
 PT New Pseudomonas aeruginosa alkaline ceramidase gene, useful for
 PT diagnosis, treatment and prevention of atopic dermatitis -
 XX
 PS Example 1; Page 21; 32pp; English.
 XX
 CC The invention provides an alkaline ceramidase from *P. aeruginosa*.
 CC Ceramidase can be produced by standard recombinant methodology.
 CC Ceramidase converts ceramide to sphingosine and a fatty acid, causes, or
 CC exacerbates, atopic dermatitis. The ceramidase gene, polypeptide, derived
 CC oligonucleotides and ceramidase-specific antibodies are used to prevent
 CC and/or treat atopic dermatitis. The gene and the polypeptide can be used
 CC as reagents for lipid engineering and for analyzing the structure and
 CC activity of ceramides. Sequences Y57308-313 represent partial fragments
 CC of the ceramidase protein, used for designing primers for amplifying the

CC ceramidase gene.
XX
SQ Sequence 11 AA;

Query Match 27.8%; Score 30; DB 21; Length 11;
Best Local Similarity 62.5%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 AIKTGHPR 12
| | | | |
Db 4 afvghpk 11

RESULT 18
R43130
ID R43130 standard; peptide; 16 AA.

AC R43130;

DT 27-APR-1994 (first entry)

DE Rhinoviral HRV2 2A proteinase inhibitor WMP-1.

KW Human rhinovirus; HRV; infection; cleavage site;
host cell shut-off; picornavirus; proteinase.

OS Synthetic.

FT Key Location/Qualifiers

FT Cleavage-site 8..9

PD EP564801-A.

PD 13-OCT-1993.

PF 27-FEB-1993; 93EP-0103159.

PR 04-MAR-1992; 92DE-4206769.

PR 30-MAY-1992; 92DE-4217929.

PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

DR WPI; 1993-322123/41.

PT Analysis of host cell shut-offs caused by picornaviruses - and

PT Inhibitor of rhinoviral HRV2 2A proteinase

PS Claim 21; Fig 23; 88pp; English.

CC Inhibitors of rhinoviral HRV2 2A proteinase, are derived from the

CC natural cleavage sequence given in R43119, comprising 10-16 amino

CC acid residues and have the amino acid pattern RXH/LTXGP (where X

CC is any amino acid residue). Such inhibitors are given in R43120-

CC R43131.

PS Sequence 16 AA;

OY Query Match 27.8%; Score 30; DB 14; Length 16;

Db Best Local Similarity 45.5%; Pred. No. 59;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

RESULT 19

W35218
ID W35218 standard; peptide; 16 AA.

AC W35218;

DT 14-APR-1998 (first entry)

DE Diastereomer peptide 79.

KW Diastereomer peptide; infection; therapy; excitatory neurotoxin;

KW Honey bee venom; pardaxin; cytolytic activity; cancer;

KW non-haemolytic; preservative; agricultural produce; bacterial cell lysis;

OS agricultural pesticide; cell wall lysis.

FT Synthetic.

FT Key Location/Qualifiers

FT MISC-difference 2 /note- "D-form residue"

FT MISC-difference 3 /note- "D-form residue"

FT MISC-difference 4 /note- "D-form residue"

FT MISC-difference 5 /note- "D-form residue"

FT MISC-difference 6 /note- "D-form residue"

FT MISC-difference 7 /note- "D-form residue"

FT MISC-difference 8 /note- "D-form residue"

FT MISC-difference 9 /note- "D-form residue"

FT MISC-difference 10 /note- "D-form residue"

FT MISC-difference 11 /note- "D-form residue"

FT MISC-difference 12 /note- "D-form residue"

FT MISC-difference 13 /note- "D-form residue"

FT MISC-difference 14 /note- "D-form residue"

FT MISC-difference 15 /note- "D-form residue"

FT MISC-difference 16 /note- "D-form residue"

PN W09731019-A2.

PD 28-AUG-1997.

PF 20-FEB-1997; 97WO-IL00066.

PR 22-FEB-1996; 96IL-0117223.

PA (YEDA) YEDA RES & DEV CO LTD.

DR WPI; 1997-435088/40.

PT Peptide(s) having selective cytolytic activity - against pathogens

PT and malignant cells, but no haemolytic activity, used for treating

PS Infections and cancer

PS Example 5; Page 47; 80pp; English.

CC This sequence represents a diastereomer peptide of the

CC invention. The peptides of the invention have: (a) cytolytic activity on

CC pathogenic cells (pathogens and malignant cells not naturally present in

CC the body); but (b) no haemolytic activity, or such activity only at a

CC concentration significantly higher than that at which they lyse

CC pathogens. The peptides, their complexes and mixtures are used to treat

CC infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses)

CC or cancer, in human and veterinary medicine. Also, they can be used as

CC preservatives for food, cosmetics and agricultural produce, or as

CC agricultural pesticides. The absence of haemolytic activity (associated

CC with disturbance of alpha-helical structures) means that the peptides

CC have few if any toxic effects, and those that include D-aa will have

CC increased resistance to proteolytic degradation. Non-haemolytic,

CC cytotoxic random copolymers of pardaxin, each has a specific spectrum of
 CC activity, allowing selection of agents for particular applications. Since
 CC these random copolymers induce total lysis of bacterial cell walls,
 CC resistance to them is unlikely to develop.
 XX
 SQ Sequence 16 AA;

Query Match 27.8%; Score 30; DB 18; Length 16;
 Best Local Similarity 50.0%; Pred. No. 59;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 HPRYFNOL 17
 |||| :
 Db 7 hprylkkl 14

RESULT 20
 W35210
 ID W35210 standard; peptide: 16 AA.

AC W35210;

DT 14-APR-1998 (first entry)

DE Diastereomer peptide 71.

XX Diastereomer peptide; infection; therapy; excitatory neurotoxin;

KW Honey bee venom; pardaxin; cytolytic activity; cancer;

KW non-haemolytic; preservative; agricultural produce; bacterial cell lysis;
 KW agricultural pesticide; cell wall lysis.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 3 /note= "D-form residue"

FT Misc-difference 4 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 10 /note= "D-form residue"

FT Misc-difference 11 /note= "D-form residue"

FT Misc-difference 13 /note= "D-form residue"

FT Misc-difference 14 /note= "D-form residue"

FT Misc-difference 16 /note= "D-form residue"

PN WO9731019-A2.

XX 28-AUG-1997.

PD 20-FEB-1997; 97WO-IL00066.

XX 22-FEB-1996; 96IL-0117223.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Oren Z, Shai Y;

DR WPI: 1997-435088/40.

PT Peptide(s) having selective cytolytic activity - against pathogens
 PT and malignant cells, but no haemolytic activity, used for treating
 PT infections and cancer

XX Example 5; Page 47; 80pp; English.

PS This sequence represents a diastereomer peptide of the
 XX invention. The peptides of the invention have: (a) cytolytic activity on
 CC pathogenic cells (pathogens and malignant cells not naturally present in
 CC the body); but (b) no haemolytic activity, or such activity only at a
 CC concentration significantly higher than that at which they lyse
 CC pathogens. The peptides, their complexes and mixtures are used to treat
 CC infections (caused by bacteria, fungi, protozoa, mycoplasma or viruses)
 CC or cancer, in human and veterinary medicine. Also, they can be used as
 CC preservatives for food, cosmetics and agricultural produce, or as
 CC agricultural pesticides. The absence of haemolytic activity (associated
 CC with disturbance of alpha-helical structures) means that the peptides
 CC have few if any toxic effects, and those that include D-aa will have
 CC increased resistance to proteolytic degradation. Non-haemolytic,
 CC cytotoxic random copolymers of pardaxin, each has a specific spectrum of
 CC activity, allowing selection of agents for particular applications. Since
 CC these random copolymers induce total lysis of bacterial cell walls,
 CC resistance to them is unlikely to develop.

XX SQ Sequence 16 AA;

Query Match 27.8%; Score 30; DB 18; Length 16;
 Best Local Similarity 50.0%; Pred. No. 59;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 HPRYFNOL 17
 |||| :
 Db 7 hprylkkl 14

RESULT 21

W82934
 ID W82934 standard; peptide: 16 AA.

AC W82934;

DT 19-MAY-1999 (first entry)

DE Antipathogenic peptide.

KW Non-haemolytic; cytolytic; selective cytolytic activity; pathogen;

KW cancer; infection; disinfectant; contact lens wetting solution;

KW preservative; pesticide; fungicide; bactericide.

OS Synthetic.

PN WO9837090-A1.

XX 27-AUG-1998.

PD 19-FEB-1998; 98WO-IL00081.

XX 20-FEB-1997; 97WO-IL00066.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Oren Z, Shai Y;

DR WPI: 1998-594464/50.

XX New non-haemolytic cytolytic agent useful in treating cancer or
 PT infections - is a peptide comprising a moiety which disrupts the
 PT continuity of an alpha-helical structure

PS Example 5; Page 46; 126pp; English.

CC The present peptide is used to produce the agents of the invention. The
 CC specification describes a non-haemolytic, cytolytic agent, which is a
 CC peptide, a complex of bundled peptides, a mixture of peptides or a random
 CC peptide copolymer. The agent has a selective cytolytic activity on

CC pathogenic cells. The agent is selected from a cyclic derivative of a
 CC peptide which has a net positive charge greater than 1, comprises L-amino
 CC acid residues and/or D-amino acid residues and comprises an alpha-helix
 CC breaker moiety, or a peptide (or cyclic derivative of this) which
 CC (comprises L-amino acid residues and D-amino acid residues, has a net
 CC positive charge greater than 1 and has an amino acid sequence such that
 CC a corresponding amino acid sequence comprising only L-amino acid residues
 CC is not found in nature. The cytolytic agents may be used for treatment of
 CC cancer or for treatment of several diseases caused by pathogens,
 CC including bacterial, fungal, viral, mycoplasma and protozoan infections.
 CC They may be used in both human and veterinary medicine. They may also be
 CC used as disinfectants for destruction of microorganisms, i.e. in
 CC solutions for wetting contact lenses, as preservatives, e.g., in the
 CC cosmetic and food industries, as pesticides (e.g. fungicides or
 CC bactericides) or for preservation of agricultural products.

Sequence 16 AA:

Query Match 27.8%; Score 30; DB 19; Length 16;
 Best Local Similarity 50.0%; Pred. No. 59;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 HPRYFNOL 17
 DB 7 hpryikl 14

RESULT 22

W82926 W82926 standard; peptide: 16 AA.

AC W82926;

DT 19-MAY-1999 (first entry)

DE Antipathogenic peptide.

XX Non-haemolytic; cytolytic; selective cytolytic activity; pathogen;

KW cancer; infection; disinfectant; contact lens wetting solution;

KM preservative; pesticide; fungicide; bactericide.

OS Synthetic.

PN W09837090-A1.

PD 27-AUG-1998.

PF 19-FEB-1998; 98WO-1100081.

PR 20-FEB-1997; 97WO-1100066.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Oren Z, Shai Y;

DR WPI; 1998-594464/50.

PT New non-haemolytic cytolytic agent useful in treating cancer or

PT infections - is a peptide comprising a moiety which disrupts the

PT continuity of an alpha-helical structure

XX Example 5; Page 46; 126pp; English.

CC The present peptide is used to produce the agents of the invention. The
 CC specification describes a non-haemolytic, cytolytic agent, which is a
 CC peptide, a complex of bundled peptides, a mixture of peptides or a random
 CC peptide copolymer. The agent has a selective cytolytic activity on
 CC pathogenic cells. The agent is selected from a cyclic derivative of a
 CC peptide which has a net positive charge greater than 1, comprises L-amino
 CC acid residues and/or D-amino acid residues and comprises an alpha-helix
 CC breaker moiety, or a peptide (or cyclic derivative of this) which
 CC (comprises L-amino acid residues and D-amino acid residues, has a net

CC positive charge greater than 1 and has an amino acid sequence such that
 CC a corresponding amino acid sequence comprising only L-amino acid residues
 CC is not found in nature. The cytolytic agents may be used for treatment of
 CC cancer or for treatment of several diseases caused by pathogens,
 CC including bacterial, fungal, viral, mycoplasma and protozoan infections.
 CC They may be used in both human and veterinary medicine. They may also be
 CC used as disinfectants for destruction of microorganisms, i.e. in
 CC solutions for wetting contact lenses, as preservatives, e.g., in the
 CC cosmetic and food industries, as pesticides (e.g. fungicides or
 CC bactericides) or for preservation of agricultural products.

Sequence 16 AA:

Query Match 27.8%; Score 30; DB 19; Length 16;
 Best Local Similarity 50.0%; Pred. No. 59;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 10 HPRYFNOL 17
 DB 7 hpryikl 14

RESULT 23

W80790 W80790 standard; peptide: 17 AA.

AC W80790;

DT 07-DEC-1998 (first entry)

DE Peptide 6 from D. discoideum Dp1 protein.

XX Dictyostelium; Dp1; discoidin II; human Dp1; hdp1; cyclophilin; Ddcyp2;

KW bisphosphonate binding protein; calcium metabolism; cyclosporine;

KM osteoporosis; hypercalcaemia; bone metabolism; bone metastases.

OS Dictyostelium discoideum.

XX Key Location/Qualifiers

FT Misc-difference 1 /note="unknown"

PN W09836064-A1.

PD 20-AUG-1998.

PF 13-FEB-1998; 98WO-US02709.

PR 14-FEB-1997; 97US-0039738.

PA (PROC) PROCTER & GAMBLE CO.

PI (UYSH-) UNIV SHEFFIELD MED SCHOOL.

PI Cook JS, Ebelino FH, Ibbotson KJ, Ji X, Rogers MJ;

PI Russell RGR, Watts DJ, Xiong XJ;

DR WPI; 1998-506311/43.

PT Bisphosphonate binding protein - used to treat calcium metabolism

PT disorders, including bone metabolism, hypercalcaemia, bone

PT metastases, and osteoporosis

XX Example 1; Page 28; 98pp; English.

CC Sequences shown in W80785 to W80793 represent peptides from Dp1 produced
 CC by endoprotease digestion, used for peptide sequencing. The invention
 CC provides sequences encoding Dictyostelium Dp1, human Dp1 (hdp1) and
 CC Dictyostelium cyclophilin (Ddcyp2) which are bisphosphonate binding
 CC proteins. The invention also provides methods for purifying and producing
 CC such bisphosphonate binding proteins. The bisphosphonate binding protein,
 CC or an antibody which binds to the binding protein can be used in the
 CC diagnosis of calcium metabolism disorders. They can also be used to treat

CC calcium metabolism disorders, where the treatment is for the regulation
 CC of bone metabolism, hypercalcaemia, bone metastases, and osteoporosis,
 CC especially by regulation of bone metabolism via interaction with
 CC cyclosporine.

XX Sequence 17 AA;

Query Match 27.8%; Score 30; DB 19; Length 17;
 Best Local Similarity 55.6%; Pred. No. 64;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 HPRYENQLS 18
 ||| | : |
 Db 7 hptynhis 15

RESULT 24

Y01008 Y01008 standard; peptide; 9 AA.

AC Y01008;

DT 02-JUN-1999 (first entry)

DE Bacterial immunogenic peptide clone 18c.

KW Immunogenic peptide; epitope unit; immune response; in vivo protection;
 KW pathogenic microorganism; microorganism infection; diagnosis; therapy.

OS Synthetic.

PN W09911660-A2.

PD 11-MAR-1999.

PF 03-SEP-1998; 98WO-EP05575.

PR 04-SEP-1997; 97US-0057906.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX (INSP) INST PASTEUR.

PI Cortese R, Felici F, Kraehenbuhl J, Phalipon A;

PI Sansonetti P;

DR WPI; 1999-205131/17.

PT New immunogenic polypeptide which induces an immune response in vivo
 PT - useful for inducing a stronger protective immune response against
 PT pathogenic microorganisms

PT Disclosure; Fig 5; 64pp; English.

CC This sequence represents an immunogenic polypeptide of the invention, and
 CC is capable of inducing an immune response in vivo against a pathogenic
 CC microorganism. The peptides can be used for pharmaceutical compositions
 CC for in vivo protection against pathogenic microorganisms. Antibodies
 CC recognising the peptides are useful for diagnosing microorganism
 CC infections. The peptides induce a stronger protective immune response to
 CC pathogenic microorganisms compared to prior art peptides. Preparation is
 CC cheaper and less time is consumed than in preparation of polysaccharide
 CC or carbohydrate antigens.

XX Sequence 9 AA;

Query Match 26.9%; Score 29; DB 20; Length 9;

Best Local Similarity 57.1%; Pred. No. 21e+05;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 11 PRYFNQL 17
 | : ||| :

Db 2 phffnql 8

RESULT 25

ID W92558 standard; peptide; 15 AA.

AC W92558;

DT 26-APR-1999 (first entry)

DE Mouse beta-actin array peptide substrate #9.

KW Peptide substrate; CCR; eukaryotic type II chaperonin complex; cyclin;
 KW binding agent; substrate-binding site; SBS; substrate folding; actin;
 KW tubulin; treatment; cancer; anticancer drug; viral infection; screening;
 KW reduced toxicity; mouse.

OS Mus sp.

PN W09853322-A1.

PD 26-NOV-1998.

PF 22-MAY-1998; 98WO-GB01485.

PR 23-MAY-1997; 97GB-0010762.

PA (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

PI Hynes G, Llou AK, Wallison K;

DR WPI; 1999-070162/06.

PT Identifying specific binding agents for substrate binding site in
 PT CCR chaperonin complex - also new peptide binding agents and their
 PT mimetics, and peptides containing a specific CCR binding site, used
 PT for treating cancer

PT Disclosure; Page 87; 97pp; English.

CC This invention describes a method which uses the CCR (eukaryotic type II
 CC chaperonin) complex or part of it, for identifying a binding agent that
 CC can occupy a substrate-binding site (SBS) on the CCR complex. By binding
 CC to the CCR complex, the binding agents block an SBS so that biological
 CC activity of the CCR complex is affected, particularly its ability to fold
 CC substrates such as actin, tubulin and cyclin. The binding agents are
 CC useful for treatment of cancer, particularly when used in combination
 CC with an anticancer drug, or viral infections. Nucleic acid fragments are
 CC used to screen for agents, e.g. binding agents that modulate interaction
 CC between the CCR complex and a protein that is to be folded. The binding
 CC agents may target cells that are actively synthesising tubulin etc.
 CC (unlike known microtubule-stabilising agents that affect all cells), so
 CC should have reduced toxicity for normal cells. W92550-W92628 are
 CC peptide substrates used in the method of the invention.

XX Sequence 15 AA;

Query Match 26.9%; Score 29; DB 20; Length 15;

Best Local Similarity 66.7%; Pred. No. 82;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 TLKTAIKTG 9
 |||| | : |
 Db 6 tlkypfeng 14

Search completed: February 5, 2001, 10:47:33
 Job time: 627 sec

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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:49:30 ; Search time 58.67 Seconds
(without alignments)
23.147 Million cell updates/sec

Title: US-08-981-824-5

Perfect score: 109
Sequence: 1 PRYFNQSTGIDMVGGLADW 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 5001

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	28.4	25	2	gene HEXA protein
2	28	25.7	15	2	phosphoribulokinase
3	25	25.7	25	2	alpha-2u-globulin
4	27	24.8	13	2	urinary tract ston
5	27	24.8	16	2	protein kinase C 1
6	26	23.9	21	2	gene CTLA-1 protei
7	26	23.9	21	2	NF1/CAT-binding t
8	25	22.9	13	2	S36874 cytochrome P450 CM
9	25	22.9	16	2	major outer membra
10	25	22.9	19	2	homeobox 3 protein
11	25	22.9	19	2	homeobox 4 protein
12	25	22.9	20	2	comartin 7-monooxy
13	25	22.9	20	2	kinase-related tra
14	25	22.9	23	2	photosystem I 8.0K
15	25	22.9	25	2	ubiquitin thiolest
16	25	22.9	25	2	aryldialkylphospha
17	24	22.0	12	2	gene HEXA protein
18	24	22.0	15	2	allatostatin - tob
19	24	22.0	16	2	multicatalytic end
20	24	22.0	18	2	TCR delta chain V-
21	24	22.0	20	2	multicatalytic end
22	24	22.0	23	2	exo-poly-alpha-gal
23	24	22.0	25	2	amidase (EC 3.5.1.
24	23	21.1	17	2	hypothetical prote
25	23	21.1	17	2	Ig heavy chain CRD
26	23	21.1	19	2	UDPglucose--glycos
27	23	21.1	19	2	photosystem I 8.0K
28	23	21.1	20	2	39k major outer me
29	23	21.1	23	2	heterodisulfide re

adenylate kinase (ribosome-inactivin antimicrobial pept binr protein - Sta benzoyl-CoA ligase carboxypeptidase B protein kinase C 1 phycoobiliprotein 1 annexin 36k chain formylmethanofuran globin - polychaet homeobox 1 protein major outer membra gaegurin 6 - Korea formate dehydrogen triosephosphate 1s

ALIGNMENTS

RESULT 1
164828
gene HEXA protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: 164828
R:Boles, D.J.; Proia, R.L.
Am. J. Hum. Genet. 56: 716-724, 1995
A:Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sa
A:Reference number: 151882; MUID:95193801
A:Accession: 164828
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-25 <RES>
A:Cross-references: GB:S76982; NID:9912780; PIDN:ADD14242.1; PID:94261942
C:Genetics:
A:Gene: GDB:HEXA
A:Cross-references: GDB:120040; OMIM:272800
A:Map position: 15q23-15q24
C:Superfamily: beta-hexosaminidase

Query Match 28.4% Score 31; DB 2; Length 25;
Best Local Similarity 50.0% Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PRYFNQSTGID 12
DB 1 PWYLNRIISYGP 12

RESULT 2
PS0276
phosphoribulokinase (EC 2.7.1.19) - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C:Accession: PS0276
R:Tsugita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0276
A:Molecule type: protein
A:Residues: 1-15 <TSD>
A:Experimental source: leaf, chlorophyll, stem
C:Keywords: phosphotransferase

Query Match 25.7% Score 28; DB 2; Length 15;
Best Local Similarity 71.4% Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 13 MWGLAAD 19

Db 7 VIGLAAD 13

RESULT 3

S70348
alpha-2u-globulin - rat (fragment)
N:Alternate names: alpha-2-uglobulin; major urinary protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S70348
R:Bayard, C.; Holmquist, L.; Vesterberg, O.
Biochim. Biophys. Acta 1290, 129-134, 1996
A:Title: Purification and identification of allergenic alpha(2u)-globulin species of rat
A:Reference number: S70347; MUID:96254071
A:Accession: S70348
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-25 <BAV>
C:Superfamily: lipocalin; lipocalin homology

Query Match 25.7%; Score 28; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 11 LDWVGLADW 20
||| : ||
Db 10 LDVAKLNGDW 19

RESULT 4

H56046
urinary tract stone matrix protein 10, 42k - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995
C:Accession: H56046
R:Binette, J.P.; Binette, M.B.; Gawlowski, M.A.; Kendrick, N.
Submitted to the Protein Sequence Database, February 1995
A:Description: Isolation, characterization and sequence of stone proteins.
A:Reference number: A56046
A:Accession: H56046
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BIN>

Query Match 24.8%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 YFNOLSTGLD 12
||| : |
Db 4 YFNDLAETD 13

RESULT 5

S10807
Protein kinase C inhibitor KcIP-1 isoform d - sheep (fragment)
N:Alternate names: Probable lipocortin
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 13-Sep-1998
C:Accession: S10807
R:Tooker, A.; Ellis, C.A.; Sellers, L.A.; Altken, A.
Eur. J. Biochem. 191, 421-429, 1990
A:Title: Protein kinase C inhibitor proteins. Purification from sheep brain and sequence
A:Reference number: S10804; MUID:90345949
A:Accession: S10807
A:Molecule type: protein
A:Residues: 1-16 <TK>
A:Experimental source: brain
C:Superfamily: 14-3-3 protein

Query Match 24.8%; Score 27; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 RYFNOLSTGLD 12
||| : |||
Db 6 RYLAERATGND 16

RESULT 6

I49414
gene CTIA-1 protein - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C:Accession: I49414
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, Mamm. Genome 5, 345-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082
A:Accession: I49414
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-21 <RES>
A:Cross-references: EMBL:U05708; NID:q497037; PIDN:AA60471.1; PID:q497038
C:Genetics:
A:gene: CTIA-1
C:Superfamily: trypsin; trypsin homology

Query Match 23.9%; Score 26; DB 2; Length 21;
Best Local Similarity 35.7%; Pred. No. 6.4e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 PRYFNOLSTGLDW 14
||| : |||
Db 1 PRAFTKVSFLSWI 14

RESULT 7

S69502
NFI/CAAT-binding transcription factor 5 (CTF5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S69502
R:Wenzelides, S.; Altman, H.; Wendler, W.; Winacker, E.L.
Nucleic Acids Res. 24, 2416-2421, 1996
A:Title: CTF5 - a new transcriptional activator of the NFI/CTF family.
A:Reference number: S69502; MUID:96279745
A:Accession: S69502
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-21 <MEN>
A:Cross-references: EMBL:X92857
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

Query Match 23.9%; Score 26; DB 2; Length 21;
Best Local Similarity 62.5%; Pred. No. 6.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 DMWGLAAD 19
||| : |||
Db 1 DLVSLACD 8

RESULT 8

S36874
cytochrome P450 CMB (EC 1.14.-.-) - crab-eating macaque (fragment)
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 09-Jun-1994 #sequence_revision 07-Nov-1997 #text_change 05-Mar-1999
C:Accession: S36874
R:Ohmori, S.; Horie, T.; Guengerich, F.P.; Kluchl, M.; Kitada, M.

Arch. Biochem. Biophys. 305, 405-413, 1993
 A:Title: Purification and characterization of two forms of hepatic microsomal cytochrome
 A:Reference number: S36874; MUID:93384294
 A:Accession: S36874
 A:Molecule type: protein
 A:Residues: 1-13 <OHM>
 C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C:Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; liver;

Query Match 22.9%; Score 25; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 7 LSTGLDNYGLAA 18
 |||||
 Db 2 LAGGLLVALLA 13

RESULT 9
 A49226

major outer membrane protein - Haemophilus somnus (fragment)
 C:Species: Haemophilus somnus
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
 C:Accession: A49226

R:Tagawa, Y.; Ishikawa, H.; Yuasa, N.

Infect. Immun. 61, 91-96, 1993

A:Title: Purification and partial characterization of the major outer membrane protein C
 A:Reference number: A49226; MUID:93114910
 A:Contents: 8025

A:Accession: A49226

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <TAG>

A:Note: sequence extracted from NCBI backbone (NCBIP:121595)

Query Match 22.9%; Score 25; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 7e+02;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 FNOLSTGLDNYG 15
 |||||
 Db 4 YNONGTKYDVCG 15

RESULT 10
 JC2058

homeobox 3 protein - common tobacco (fragment)

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Aug-1994

C:Accession: JC2058

R:Feng, X.H.; Kung, S.D.

Biochem. Biophys. Res. Commun. 198, 1012-1019, 1994

A:Title: Identification of differentially expressed members of tobacco homeobox families
 A:Reference number: JC2057; MUID:94161708

A:Accession: JC2058

A:Molecule type: DNA

A:Residues: 1-19 <FEN>

Query Match 22.9%; Score 25; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 STGLD 12
 |||||
 Db 10 STGLD 14

RESULT 11
 JC2059
 homeobox 4 protein - common tobacco (fragment)

C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 23-Mar-1995
 C:Accession: JC2059

R:Feng, X.H.; Kung, S.D.

Biochem. Biophys. Res. Commun. 198, 1012-1019, 1994

A:Title: Identification of differentially expressed members of tobacco homeobox famill
 A:Reference number: JC2057; MUID:94161708

A:Accession: JC2059

A:Molecule type: DNA

A:Residues: 1-19 <FEN>

A:Experimental source: leaf

C:Genetics:

A:Gene: Hb14

C:Keywords: homeobox

Query Match 22.9%; Score 25; DB 2; Length 19;
 Best Local Similarity 70.0%; Pred. No. 8.5e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

OY 5 NQLS--TGID 12
 |||||
 Db 5 NQLSETGLD 14

RESULT 12
 S21737

coumarin 7-monooxygenase (EC 1.14.14.-) cytochrome P450 2A7 - western baboon (fragmen
 N:Alternate names: coumarin 7-hydroxylase

C:Species: Papio papio (western baboon)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Mar-1999

C:Accession: S21737

R:Dalet-Beluche, I.; Boulenc, X.; Fabre, G.; Mauriel, P.; Bonfils, C.

Eur. J. Biochem. 204, 641-648, 1992

A:Title: Purification of two cytochrome P450 isozymes related to CYP2A and CYP3A gene

A:Reference number: S21737; MUID:92174920

A:Accession: S21737

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <DAL>

C:Genetics:

A:Gene: CYP2A7

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 22.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 9e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 7 LSTGLDNYGLAA 18
 |||||
 Db 2 LAGGLLVALLA 13

RESULT 13
 S00774

kinase-related transforming protein (abl) (EC 2.7.1.-) type II - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999

C:Accession: S00774

R:Bernards, A.; Pasikind, M.; Baltimore, D.

Oncogene 2, 297-304, 1988

A:Title: Four murine c-abl mRNAs arise by usage of two transcriptional promoters and

A:Reference number: S00771; MUID:88202920

A:Accession: S00774

A:Molecule type: DNA

A:Residues: 1-20 <BER>

A:Cross-references: EMBL:X07540; MID:949835; PIDN:CA30413.1; PID:949836

A:Note: the authors translated the codon GAC for residue 12 as His

C:Genetics:

A:Gene: abl

C:Superfamily: human protein-tyrosine kinase abl; protein kinase homology; SH2 homoio

C;Keywords: alternative splicing; ATP; phosphotransferase

Query Match	22.9%;	Score 25;	DB 2;	Length 20;
Best Local Similarity	43.8%;	Pred. No. 9e+02;		
Matches	7;	Conservative	2;	Mismatches 7;
				Indels 0;
				Gaps 0;

Qy	4	FNQLSTGLDMVGLAD	19
		: :	
Db	4	FDDLSDLDLKLVLVD	19

RESULT	14
DO0600	

Photosystem I 8.0K g chain - common tobacco (fragment)
C.Species: Nicotiana tabacum (common tobacco)
C.Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C.Accession: P00690
R.Obkate, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
Plant Physiol. 102, 1259-1267, 1993
Article: Molecular heterogeneity of photosystem I. psad, psae, psaf, psan and psal are 2
A.Reference number: P00667; MUID:94105345
A.Accession: P00690

C;Superfamily: photosystem I chain V
C;keywords: chloroplast; photosynthesis; photosystem I; thylakoid

QY	7	LSTGLDM	13
		11111	:
Db	10	LSTGLSL	16

RESULT 15

ubiquitin thioesterase (EC 3.1.2.15) PGP9.5, brain - bovine (fragment)
 N:Alternate names: 26K protein; gene product 9.5; ubiquitin carboxyl-terminal esterase
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 13-Sep-1998 #text_change 11-Jan-2000
 C:Accession: S17561
 R:Giambanco, I.; Bianchi, R.; Ceccarelli, P.; Pula, G.; Sorci, G.; Antonelli, S.; Bocch
 FEBS Lett. 290, 131-134, 1991
 A>Title: Neuron-specific protein gene product 9.5 (PGP 9.5) is also expressed in glioma
 A:Reference number: S17561; MUID:92008646
 A:Accession: S17561
 A:Molecule type: Protein
 A:Residues: 1-25 <GIA>
 A:Experimental source: brain; glioma cells
 C:Genetics:
 A:Gene: 9.5
 C:Function:
 A:Description: involved in the hydrolysis of esters and amides at the C-terminal glycine
 e during brain development in glial cells
 C:Superfamily: human ubiquitin thioesterase
 C:Keywords: cytosol; thioester hydrolase

Query Match	22.9%	Score 25;	DB 2;	Length 25;
Best Local Similarity	33.3%	Pred. No. 1.1e+03;		
Matches	5;	Conservative	3;	Mismatches 7;
				Indels 0;
				Gaps 0

```
QY      1 PRYFNQLSTGGLDMVG 15
          | |::| |::|
Db      10 PEMLNKVLTRLGVAG 24
```

RESULT 16
PT0088

T008E

arylalkylphosphatase (EC 3.1.8.1) - rat (fragment)
 N.Alternate names: A-esterase; Aryltriphosphatase; Organophosphate hydrolase; Paraoxa
 C.Species: Rattus norvegicus (Norway rat)
 C.Date: 07-Jul-1997 #sequence revised on 18-Jul-1997 #text changed 18-Jul-1997

C:/date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C:/Accession: PT0088

Submitted to JIPID, January 1996
A:Reference number: PT0088
A:Accession: PT0088
A:Molecule type: protein
A:Residues: 1-25 <row>
C:Keywords: phosphoric triester hydrolase

Query Match	22.98;	Score 25;	DB 2;	Length 25;
Best Local Similarity	71.48;	Pred. No. 1.1e+03;		
Matches	5;	Conservative	1;	Indels 0;
				Gaps 0

QY	10	GIDMVL	16
		:	
Db	5	GLTLVL	11

RESULT 17

gene HEXA protein - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 29-May-1998 #sequence-revision 29-May-1998 #text-change 21-Jul-2000
C.Accession: I64829
R.Boles, D.J.; Prola, R.L.
Am. J. Hum. Genet. 56, 716-724, 1995
A.Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs
A.Reference number: I51882; MUID:95193801

A;Gene: GDB:HEXA
A;Cross-references: GDB:120040; OMIM:272800
A;Map position: 15q23-15q24
C;Superfamily: beta-hexosaminidase

Query Match	22.0%;	Score 24;	DB 2;	Length 12;
Best Local Similarity	50.0%;	Pred. No. 7.5e+02;		
Matches	4;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0

QY	1	PRYENOLS	8
		::	
Db	1	PWYLNKRS	8

RESULT 18

A01612
allatostatin - tobacco hornworm
C:Species: *Manduca sexta* (tobacco hornworm)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 11-Jul-1997
C:Accession: A61612
R:Krimmer, S.J.; Troschl, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carne-
Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991
A:Title: Identification of an allatostatin from the tobacco hornworm *Manduca sexta*.
A:Reference number: A61612; MUID:92052112
A:Accession: A61612
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <KRA>
C:Keywords: neuropeptide; pyroglutamic acid
E:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

```
query match      22.0%; Score 24; DB 2; Length 15
```

3800

Best Local Similarity 66.7%; Pred. No. 9.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 YFNOLS 8
|||:|
Db 8 YFNPI5 13

RESULT 19

PC3320 multicatalytic endopeptidase complex (EC 3.4.99.46), HC10-II chain - human (fragment)

N:Alternate names: proteasome

C:Species: Homo sapiens (man)

C>Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 26-May-2000

C:Accession: PC3320

R:Kristensen, P.; Johnsen, A.H.; Uerkvitz, M.; Tanaka, K.; Hendll, K.B.

Biochem. Biophys. Res. Commun. 205, 1785-1789, 1994

A:Title: Human proteasome subunits from 2-dimensional gels identified by partial sequence

A:Reference number: PC3315; MUID:95110324

A:Accession: PC3320

A:Molecule type: protein

A:Residues: 1-16 <KRI>

A:Experimental source: placenta

C:Comment: The proteasome consists of subunits of 21k-30k arranged in 4 stacked rings.

C:Superfamily: multicatalytic endopeptidase complex chain C9

C:Keywords: hydrolase; proteinase.

Query Match 22.0%; Score 24; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

RESULT 20

G49037 Tcr delta chain V-D-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: G49037

R:Rezqueria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.

Eur. J. Immunol. 22, 491-498, 1992

A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T

A:Reference number: A49037; MUID:92164730

A:Accession: G49037

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-18 <EAO>

A:Cross-references: GB:S90657; NID:9246300; PIDN:AB21553.1; PID:9246301

A:Experimental source: dendritic epidermal T-cell lines

A>Note: sequence extracted from NCBI backbone (NCBIN:90657, NCBIIP:90668)

Query Match 22.0%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 21

F42762 multicatalytic endopeptidase complex (EC 3.4.99.46) subunit 13 - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000

C:Accession: F42762

R:DiCK, L.R.; Moormaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.

Biochemistry 31, 7347-7355, 1992

A:Title: Identification and localization of a cysteinyl residue critical for the tryp

A:Reference number: A42762; MUID:92378961

A:Accession: F42762

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <DIC>

A>Note: sequence extracted from NCBI backbone (NCBIIP:112175)

C:Superfamily: multicatalytic endopeptidase complex chain C9

C:Keywords: hydrolase

Query Match 22.0%; Score 24; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 22

A48968 exo-poly-alpha-galacturonosidase (EC 3.2.1.82) - Clostridium thermosaccharolyticum (f

N:Alternate names: exo-poly-alpha-galacturonate hydrolase

C:Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum

C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 06-Dec-1996

C:Accession: A48968

R:Van Rijssel, M.; Gerwig, G.J.; Hansen, T.A.

Appl. Environ. Microbiol. 59, 828-836, 1993

A:Title: Isolation and characterization of an extracellular glycosylated protein comp

A:Reference number: A48968; MUID:93243759

A:Accession: A48968

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-23 <VAN>

A>Note: sequence extracted from NCBI backbone (NCBIIP:130462)

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 22.0%; Score 24; DB 2; Length 23;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

RESULT 23

PC1105 amylase (EC 3.5.1.4) - Brevibacterium sp. (fragment)

C:Species: Brevibacterium sp.

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PC1105

R:Schubler, F.; Levy-Schil, S.; Mayeux, J.F.; Petre, D.; Arnaud, A.; Crouzet, J.

Gene 116, 99-104, 1992

A:Title: Cloning and primary structure of the wide-spectrum amylase from Brevibacteri

A:Reference number: JC1174; MUID:92331957

A:Accession: PC1105

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-25 <SDU>

C:Keywords: hydrolase

Query Match 22.0%; Score 24; DB 2; Length 25;
Best Local Similarity 45.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 24

S58129
hypothetical protein - moss (Ceratodon purpureus)
C:Species: Ceratodon purpureus
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 31-Oct-1997
C:Accession: S58129
R: Hughes, J.; Mittleman, F.
submitted to the EMBL Data Library, July 1995
A:Description: The moss Ceratodon purpureus contains and expresses a second, conventional
A:Reference number: S58129
A:Accession: S58129
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <HUG>
A:Cross-references: GB:U56698; EMBL:X89725; NID:g1314836; PID:g1322246

Query Match

21.1%; Score 23; DB 2; Length 17;
Best Local Similarity 38.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 4 FMQLSTGLDWGL 16
| : | | : || :
DB 4 FSTSRSLMIVGI 16

RESULT 25

PT0234
Ig heavy chain CDR3 region (clone 1-130) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0234
R: Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:9110837
A:Accession: PT0234
A:Molecule type: DNA
A:Residues: 1-17 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match

21.1%; Score 23; DB 2; Length 17;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 RYFNOLSTG 10
||| : | |
DB 8 RYFDWLGG 16

Search completed: February 5, 2001, 10:49:31
Job time: 744 sec

RL Plant Physiol. 98:82-88(1992).
 CC -1- CARLYTIC ACTIVITY: ATP + D-RIBULOSE 5-PHOSPHATE - ADP +
 CC D-RIBULOSE 1,5-BISPHOSPHATE.
 CC -1- PATHWAY: CALVIN CYCLE.
 CC -1- SUBUNIT: HETERODIMER OF A 40 KDA AND A 41 KDA SUBUNIT.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
 DR INTERPRO: IPR001324; -
 DR PROSITE: PS00567; PHOSPHORIBULOKINASE; PARTIAL.
 KM TRANSFERASE; Kinase; Calvin cycle; ATP-binding.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1455 MW; 07A97BCD2F922C75 CRC64;

Query Match 25.7%; Score 28; DB 1; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 13 MVLGLAD 19
 : : : : :
 Db 7 VIGLAD 13

RESULT 3
 RANR_RANRU STANDARD; PRT; 17 AA.
 AC P08952;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RANATENSIN-R.
 OS Rana rugosa (Frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-84131098; PubMed-6141890;
 RA Nakajima T.;
 RL Unpublished results, cited by:
 RL Erspamer V., Erspamer G.F., Mazzaletti G., Endean R.;
 RL Comp. Biochem. Physiol. 77C:99-108(1984).
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
 CC FAMILY.
 DR INTERPRO: IPR000874; -
 DR PFAM: PF02044; Bombesin; 1.
 DR PROSITE: PS00257; BOMBESIN; 1.
 KM Bombesin family; Amidation.
 FT MOD_RES 17 17
 FT SEQUENCE 17 AA; 2053 MW; 3A876B35A581863E CRC64;

Query Match 24.8%; Score 27; DB 1; Length 17;
 Best Local Similarity 55.6%; Pred. No. 1.9e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 RYFNOLSTG 10
 : : : : :
 Db 6 RRYNOMATG 14

RESULT 4
 LE01_BIOGL STANDARD; PRT; 25 AA.
 ID LE01_BIOGL.
 AC P80742;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE HEMOLYMPH 65 KDA LECTIN BG01 (FRAGMENT).
 GN BG01.
 OS Biomphalaria glabrata (Bloodfluke planorb).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 CC Planorbidae; Biomphalaria.
 RN [1]
 RP SEQUENCE.

RC STRAIN-M-LINE; TISSUE-HEMOLYMPH;
 RX MEDLINE-97385165; PubMed-9238039;
 RA Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;
 RA "A family of fibrogen-related proteins that precipitates parasite-
 RT derived molecules is produced by an invertebrate after infection";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696(1997).
 CC -1- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE
 CC ECHINOSTOMA PARANSEI.
 CC -1- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.
 CC -1- INDUCTION: BY INFECTION.
 KM Lectin.
 FT NON_TER 1 1
 FT NON_TER 25 25
 SQ SEQUENCE 25 AA; 2602 MW; CC3747240B08810B CRC64;

Query Match 23.9%; Score 26; DB 1; Length 25;
 Best Local Similarity 38.5%; Pred. No. 4.2e+02;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 7 LSTGLDMVGLAD 19
 : : : : :
 Db 5 LASGLEMODTTD 17

RESULT 5
 CPA7_PAPSP STANDARD; PRT; 20 AA.
 ID CPA7_PAPSP
 AC P80055;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CYTOCHROME P450 2A7 (EC 1.14.14.1) (CYPIA7) (P450 FI) (COMARIN 7-
 DE HYDROXYLASE) (FRAGMENT).
 GN CYP2A7.
 OS Papio sp. (Baboon).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Papio.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-LIVER;
 RX MEDLINE-92174920; PubMed-1541278;
 RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;
 RA "Purification of two cytochrome P450 isozymes related to CYP2A and
 RT CYP3A gene families from monkey (baboon, Papio) liver
 RT microsomes. Cross reactivity with human forms";
 RL Eur. J. Biochem. 204:641-648(1992).
 CC -1- FUNCTION: EXHIBITS A HIGH COMARIN 7-HYDROXYLASE ACTIVITY.
 CC -1- FUNCTION: EXHIBITS A HIGH COMARIN 7-HYDROXYLASE ACTIVITY.
 CC -1- CARLYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) - ROH +
 CC OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
 CC -1- INDUCTION: BY PHENOBARBITAL.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR PIR: S21737; S21737.
 DR INTERPRO: IPR001128; -
 DR PROSITE: PS00086; CYTOCHROME_P450; PARTIAL.
 KM Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KM Microsome; Endoplasmic reticulum.
 FT UNSURE 14 14
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2045 MW; 693102A1F0B50C96 CRC64;

Query Match 22.9%; Score 25; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 4.8e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 7 LSTGLDMVGLAA 18
 : : : : :
 Db 2 LASGLLVALLA 13


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RESULT 6
UBLI_BOVIN STANDARD: PRT: 25 AA.
AC P23356;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L1 (EC 3.1.2.15) (UCH-
L1) (UBIQUITIN THIOLESTERASE L1) (NEURON CYTOPLASMIC PROTEIN 9.5)
DE (PGP 9.5) (FRAGMENT).
GN UCHL1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC MEDLINE-92008646; PubMed-1833240;
RX Giambanco I., Bianchi R., Ceccarelli P., Pula G., Sorci G.,
RA Antonoli S., Bocchini V., Donato R.;
RT "Neuron-specific" protein gene product 9.5 (PGP 9.5) is also
RT expressed in glioma cell lines and its expression depends on cellular
RT growth state.
RT FEBS Lett. 290:131-134(1991).
RL -1- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUITINATED PROTEINS.
CC THIS ENZYME IS A THIOLESTERASE THAT RECOGNIZES AND HYDROLYZES
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -1- CATALYTIC ACTIVITY: UBIQUITIN C-TERMINAL THIOLESTER + H(2)O =
CC UBIQUITIN + A THIOLE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: NEURONS AND CELLS OF THE DIFFUSE
CC NEUROENDOCRINE SYSTEM AND THEIR TUMORS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12; ALSO KNOWN AS
CC FAMILY 1 OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASES.
DR MEROPS: C12.001.
DR INTERPRO: IPR001578;
DR PROSITE: PS00140; UCH_1; PARTIAL.
FT Ubiquitin conjugation; Hydrolase; Thiol protease; Multigene family.
FT NON_TER 25
SQ SEQUENCE 25 AA: 2812 MW: 2685ADDA0A754D55 CRC64;

Query Match 22.9%; Score 25; DB 1; Length 25;
Best Local Similarity 33.3%; Pred. No. 6.1e+02;
Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 PRYFNOJSTGIDMVG 15
DB 10 PEMLNKVLTRLGAVG 24

RESULT 7
ALLS_MANSE STANDARD: PRT: 15 AA.
AC P42539;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALIATOSTATIN (MAS-AS).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
RN [1]
RP SEQUENCE.
RC TISSUE-HEAD:
RX MEDLINE-92052112; PubMed-1946359;
RA Kramer S.J., Toschl A., Miller C.A., Kataoka H., Qulstad G.B.,
RA Li J.P., Carney R.L., Schooley D.A.;
RT "Identification of an allatostatins from the tobacco hornworm Manduca

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RT sexta.
RL Proc. Natl. Acad. Sci. U.S.A. 88:9458-9462(1991).
CC -1- FUNCTION: STRONGLY INHIBITS JUVENILE HORMONE BIOSYNTHESIS IN VITRO
CC BY THE CORPORA ALATA FROM FIFTH-STADIUM LARVAE AND ADULT FEMALES.
CC -1- SIMILARITY: BELONGS TO THE ALIATOSTATIN FAMILY.
KW Neuropeptide.
FT MOD_RES 1
FT SEQUENCE 15 AA: 1908 MW: 1605B77CDBEC838E CRC64;

Query Match 22.0%; Score 24; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFNOLIS 8
DB 8 YFNPLIS 13

RESULT 8
OXYF_SCYCA STANDARD: PRT: 9 AA.
ID OXYF_SCYCA
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOICIN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE-PITUITARY;
RX MEDLINE-95062247; PubMed-7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: aspartocin and phasvatoicin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -1- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981;
DR PFMW: PF00220; hormone; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
FT Hormone; Amidation.
FT DISULFID 1
FT MOD_RES 9
FT SEQUENCE 9 AA: 1016 MW: 17EDD76EB44449DB CRC64;

Query Match 21.1%; Score 23; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 8.9e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 YFNOLIS 10
DB 2 YFNCPVG 9

RESULT 9
PPBH_PSEAE STANDARD: PRT: 19 AA.
ID PPBH_PSEAE
AC P35483;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALKALINE PHOSPHATASE H (EC 3.1.3.1) (H-AP) (FRAGMENT).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
RN [1]
RP SEQUENCE.

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RC STRAIN-H103;
RX MEDLINE-93202452; PubMed-8454193;
RA Tan A.S.P., Morobec E.A.;
RT "Isolation and characterization of two immunochemically distinct
RT alkaline phosphatases from Pseudomonas aeruginosa.";
RL FEMS Microbiol. Lett. 106:281-286(1993).
CC -1- FUNCTION: HAS ONLY A PHOSPHOMONESTERASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)O -> AN
CC ALCOHOL + ORTHOPHOSPHATE (AT A HIGH PH OPTIMUM).
CC -1- COFACTOR: METALLOENZYME CONTAINING TWO ZINC ATOMS AND A MAGNESIUM
CC ION.
CC -1- SUBCELLULAR LOCATION: SECRETED AND PERIPLASMIC.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY.
CC -1- SIMILARITY: BELONGS TO THE ALKALINE PHOSPHATASE FAMILY.
DR INTERPRO: IPR001952;
DR PROSITE: PS00123; ALKALINE_PHOSPHATASE; PARTIAL.
KW Hydrolase; zinc; Magnesium; Periplasmic.
FT NON_TER 19
FT SEQUENCE 19 AA; 2131 MW; C51B09D7DB22E799 CRC64;

SO
Query Match 21.1%; Score 23; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 PRYFNOLSTG 10
DB 5 PSLFNROAG 14

RESULT 10
ID OMPL_ACTAC STANDARD; PRT; 20 AA.
AC P20242;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE 39 KDA MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Actinobacillus.
RN [1]
RP SEQUENCE.
RC STRAIN-Y4;
RX MEDLINE-91169244; PubMed-2004699;
RA Kokeguchi S., Kato K., Nishimura F., Kurihara H., Murayama Y.;
RT "Isolation and partial characterization of a 39 kda major outer
RT membrane protein of Actinobacillus actinomycetemcomitans Y4.";
RL FEMS Microbiol. Lett. 61:85-89(1991).
KW PIR; A54538; A54538.
KW Outer membrane; Transmembrane; Porin.
FT NON_TER 20
FT SEQUENCE 20 AA; 2316 MW; A837A8C4764F527E CRC64;

SO
Query Match 21.1%; Score 23; DB 1; Length 20;
Best Local Similarity 25.0%; Pred. No. 1e+03;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 RYFNOLSTGLDM 13
DB 2 KVTNOSTKVEL 13

RESULT 11
ID KAD_BACLI STANDARD; PRT; 24 AA.
AC P35140;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (FRAGMENT).

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GN ADK.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93062802; PubMed-1435726;
RA Tschander S., Driessen A.J.M., Freudl R.;
RT "Cloning and molecular characterization of the sec genes from
RT Bacillus licheniformis and Staphylococcus carnosus: comparative
RT analysis of nine members of the Sec family.";
RL Mol. Gen. Genet. 235:147-152(1992).
CC -1- FUNCTION: THIS SMALL UNICITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X70087; -; NOT_ANNOTATED_CDS.
CC PIR; S34405; S34405.
CC HSSP; P27142; 1Z10.
CC INTERPRO: IPR000650;
CC PIRAM; PR00406; adenylatekinase; 1.
CC PROSITE: PS00113; ADENYLATE_KINASE; PARTIAL.
KW Transferase; Kinase; ATP-binding.
FT NP_BIND 7
FT NON_TER 24
FT SEQUENCE 24 AA; 2563 MW; A65B1A5F1B018F21 CRC64;

SO
Query Match 21.1%; Score 23; DB 1; Length 24;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 LDMVGL 16
DB 3 LDMGL 8

RESULT 12
ID PGO_XENLA STANDARD; PRT; 24 AA.
AC P39080;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE ANTIMICROBIAL PEPTIDE PGO.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE.
RC TISSUE-STOMACH;
RX MEDLINE-92011794; PubMed-1717472;
RA Moore K.S., Bevilin C.L., Brasseur M.M., Tomassini N., Turner K.,
RA Eck H., Zaslloff M.;
RT "Antimicrobial peptides in the stomach of Xenopus laevis.";
RL J. Biol. Chem. 266:19851-19857(1991).
CC -1- FUNCTION: ANTIMICROBIAL PEPTIDE.
CC -1- TISSUE SPECIFICITY: IS SYNTHESIZED IN THE STOMACH AND STORED
CC IN A NOVEL GRANULAR MULTILINCEATED CELL IN THE GASTRIC MUCOSA.
CC IT IS STORED AS ACTIVE, PROCESSED PEPTIDES IN LARGE GRANULES
CC WITHIN THE GRANULAR GLAND SECRETIONS OF THE SKIN.

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CC -1- SIMILARITY: BELONGS TO THE MAGAININ FAMILY OF ANTIMICROBIAL
CC PEPTIDES.
DR PIR: A41037; A41037.
KW Antibiotic; Amphibian skin.
SQ SEQUENCE 24 AA; 2457 MW; 7E6A87CB7CE22B9C CRC64;

Query Match 21.1%; Score 23; DB 1; Length 24;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 YFNOLSTG 10
I : I I I
D 9 YLRKLG 16

RESULT 13
CR21_LITSP STANDARD; PRT; 25 AA.
AC P56233;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CAERIN 2.1.
OS Litoria splendida.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-PAROTOID GLAND;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. Structures of the caerins and
J. Chem. Soc. Perkin Trans. 1:3173-3178(1992).
RT caeridin 1 from Litoria splendida."
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE THAT ADOPTS AN ALPHA HELICAL
CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
KW Antibiotic; Amphibian skin.
SQ SEQUENCE 25 AA; 2394 MW; DDCA9BC6B49186B8 CRC64;

Query Match 21.1%; Score 23; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 8 STGDMVGLAD 19
I : I I I
D 5 SIGRAGGLAD 16

RESULT 14
CR22_LITGI STANDARD; PRT; 25 AA.
AC P56234;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CAERIN 2.2 (CONTAINS: CAERIN 2.2.1).
OS Litoria gilleni, and Litoria caerulea.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY OF CAERIN 2.2.
RC SPECIES-L.CAERULEA; TISSUE-PAROTOID GLAND;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. The structures of the caerins from
Litoria caerulea."
RT J. Chem. Res. 138:910-936(1993).

RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY OF CAERIN 2.2.1.
RC SPECIES-L.GILLENI; TISSUE-PAROTOID GLAND;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
caeridins from Litoria gilleni."
RL J. Chem. Res. 139:937-961(1993).
CC -1- FUNCTION: ANTIMICROBIAL PEPTIDE THAT ADOPTS AN ALPHA HELICAL
CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -1- MASS SPECTROMETRY: MM-2464; METHOD-FAB; RANGE-1-25.
CC -1- MASS SPECTROMETRY: MM-1695; METHOD-FAB; RANGE-9-25.
KW Antibiotic; Amphibian skin.
FT PEPTIDE 1 25 CAERIN 2.2.
FT PEPTIDE 9 25 CAERIN 2.2.1.
SQ SEQUENCE 25 AA; 2466 MW; DDCA9BC5D49186B8 CRC64;

Query Match 21.1%; Score 23; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 8 STGDMVGLAD 19
I : I I I
D 5 SIGRAGGLAD 16

RESULT 15
CR23_LITCE STANDARD; PRT; 25 AA.
AC P56235; P82117;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SPENDIPHERIN (CAERIN 2.3).
OS Litoria caerulea, and
Litoria splendida.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC SPECIES-L.CAERULEA; TISSUE-PAROTOID GLAND;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins from
Litoria caerulea."
RL J. Chem. Res. 138:910-936(1993).
RN [2]
RP SEQUENCE.
RC SPECIES-L.SPENDINGA; TISSUE-SKIN SECRETION;
RX MEDLINE-99447035; PubMed-10519546;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT "Aquatic sex pheromone from a male tree frog."
RL Nature 401:444-445(1999).
RN [3]
RP SEQUENCE.
RC SPECIES-L.SPENDINGA; TISSUE-SKIN SECRETION;
RX MEDLINE-20069371; PubMed-10601876;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT "Differences in the skin peptides of the male and female Australian
tree frog Litoria splendida. The discovery of the aquatic male sex
pheromone splendipherin, together with phob caerulein and the
antibiotic peptide caerin 1.20."
RL Eur. J. Biochem. 267:269-275(2000).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE THAT ADOPTS AN ALPHA HELICAL
CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC -1- FUNCTION: ACTS AS A MALE SEX PHEROMONE THAT ATTRACTS FEMALE.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -1- MASS SPECTROMETRY: MM-2364; METHOD-FAB.

KW Antibiotic; Phenomene; Amphibian skin.
SQ SEQUENCE 25 AA; 2366 MW; DDD82C36B4918688 CRC64;

Query Match 21.1%; Score 23; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 8 STGLDMVGLAAD 19
| | : | | |
Db 5 SIGKALGGLAD 16

RESULT 16
ID CR24_LITCE STANDARD; PRT; 25 AA.
AC P56236;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERIN 2.4.
OS Litoria caerulea.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-PAROTOID GLAND;
RA Stone D.J.M., Maugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins from
RT Litoria caerulea.";
J. Chem. Res. 138:910-936(1993).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -1- MASS SPECTROMETRY: MW=2450; METHOD=FPAB.
CC Antibiotic; Amphibian skin.
SQ SEQUENCE 25 AA; 2452 MW; DDD82C35D4959688 CRC64;

Query Match 21.1%; Score 23; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 8 STGLDMVGLAAD 19
| | : | | |
Db 5 SIGKALGGLAD 16

RESULT 17
ID CR25_LITGI STANDARD; PRT; 25 AA.
AC P56237;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERIN 2.5.
OS Litoria gilleni.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-PAROTOID GLAND;
RA Maugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
RT caeridins from Litoria gilleni.";
J. Chem. Res. 139:937-961(1993).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -1- MASS SPECTROMETRY: MW=2448; METHOD=FPAB.
KW Antibiotic; Amphibian skin.
SQ SEQUENCE 25 AA; 2450 MW; DDCA9BC5D48F8758 CRC64;

Query Match 21.1%; Score 23; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 8 STGLDMVGLAAD 19
| | : | | |
Db 5 SIGKALGGLAD 16

RESULT 18
ID CBPR_PROAT STANDARD; PRT; 15 AA.
AC P19628;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE CARBOXYPEPTIDASE B (EC 3.4.17.2) (FRAGMENT).
OS Proteolus aethiopicus (Marbled lungfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Dipnoi; Lepidosireniformes; Protopterygidae; Protopterus.
RN [1]
RP SEQUENCE.
RC TISSUE-PANCREAS;
RX MEDLINE-73025047; PubMed-5079891;
RA Reek G.R., Neurath H.;
RT "Isolation and characterization of pancreatic procarboxypeptidase B
RT and carboxypeptidase B of the African lungfish.";
RT Biochemistry 11:3947-3955(1972).
CC -1- CATALYTIC ACTIVITY: PEPTIDYL-L-LYSINE/ARGININE + H(2)O - PEPTIDE +
CC L-LYSINE/ARGININE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14; ALSO KNOWN AS THE
CC ZINC CARBOXYPEPTIDASE FAMILY.
CC PIR: A26212; A26212.
DR MEROPS; M14.003; -;
DR INTERPRO; IPR000834; -;
DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; PARTIAL.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; PARTIAL.
KW Hydrolase; Carboxypeptidase; Zinc; Zymogen.
FT PROPEP 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1749 MW; 124C910D937BED65 CRC64;

Query Match 20.2%; Score 22; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PRYFN 5
| | |
Db 4 PRSFN 8

RESULT 19
ID OXLA_OPHHA STANDARD; PRT; 19 AA.
AC P81383;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE L-AMINO ACID OXIDASE (EC 1.4.3.2) (LAO) (LAAO) (FRAGMENT).
OS Ophiophagus hannah (King cobra) (Naja hannah).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Ophiophagus.
RN [1]
RP SEQUENCE.

RC TISSUE-VENOM;
 RX MEDLINE=94361525; PubMed=8080286;
 RA Ponnudurai G., Chung M.C.M., Tan N.-H.;
 RT "Purification and properties of the L-amino acid oxidase from Malayan
 RT pit viper (Calloselasma rhodostoma) venom.";
 RL Arch. Biochem. Biophys. 313:373-378(1994).
 RN [2]
 RP SEQUENCE OF 1-15.
 RC TISSUE-VENOM;
 RX MEDLINE=97449790; PubMed=9304806;
 RA Ahn M.Y., Lee B.M., Kim Y.S.;
 RT "Characterization and cytotoxicity of L-amino acid oxidase from the
 RT venom of King cobra (Ophiophagus hannah).";
 RL Int. J. Biochem. Cell Biol. 29:911-919(1997).
 CC -1- FUNCTION: HAS CYTOTOXIC ACTIVITY (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: A L-AMINO ACID + H(2)O + O(2) -> A 2-OXO ACID +
 CC NH(3) + H(2)O(2).
 CC -1- COFACTOR: FAD.
 CC -1- SUBUNIT: HOMODIMER (PROBABLE).
 CC -1- PTM: GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOXAMINE OXIDASE FAMILY.
 CC STRONG, TO MOUSE FIG-1.
 KM Oxidoreductase: Flavoprotein; FAD; Glycoprotein; Venom.
 FT CONFLICT 1 1 H -> S (IN REF. 2).
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2298 MW; DD911A5B414F1427 CRC64;

Query Match 20.28; Score 22; DB 1; Length 19;
 Best Local Similarity 50.08; Pred. No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 PXYENOLS 8
 DB 12 PEYENHLLA 19

RESULT 20
 FIBR_PACLE STANDARD; PRT; 20 AA.
 AC P81070;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE FIBRINOGEN (VHDL) (FRAGMENT).
 OS Pacificastacus leniusculus (Signal crayfish).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Astacoidae; Astacidae; Pacificastacus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96074573; PubMed=7488215;
 RA Hall M., van Heusden M.C., Soederhaell K.;
 RT "Identification of the major lipoproteins in crayfish hemolymph as
 RT proteins involved in immune recognition and clotting.";
 RL Biochem. Biophys. Res. Commun. 216:939-946(1995).
 CC -1- FUNCTION: INVOLVED IN LIPID TRANSPORT. PLAYS A ROLE IN HEMOLYMPH
 CC CLOTTING. MAY BE INVOLVED IN WOUND HEALING IN THE CUTICLE.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: SECRETED INTO THE HEMOLYMPH.
 CC -1- SIMILARITY: TO VITELLOGENINS.
 KM Coagulation; Glycoprotein; Lipid-binding; Hemolymph.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2311 MW; 1C04BC596B9FC47 CRC64;

Query Match 20.28; Score 22; DB 1; Length 20;
 Best Local Similarity 30.08; Pred. No. 1.5e+03;
 Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RYFNQSTGL 11
 DB 10 RYSGRVASGI 19

RESULT 21
 SOD2_PICAB STANDARD; PRT; 21 AA.
 AC P29428;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUPEROXIDE DISMUTASE [CU-ZN] II (EC 1.15.1.1) (SOD II) (FRAGMENT).
 OS Picea abies (Norway spruce) (Picea excelsa).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Coniferopsida; Coniferales; Pinaceae; Picea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-NEEDLE;
 RA Koenigler W., Rensenberg H., Polle A.;
 RT "Purification of two superoxide dismutase isozymes and their
 RT subcellular localization in needles and roots of Norway spruce (Picea
 RT abies L.) trees.";
 RL Plant Physiol. 100:334-340(1992).
 CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -1- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) -> O(2) + H(2)O(2).
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: DOMINANT ISOZYME IN ROOTS.
 CC -1- MISCELLANEOUS: EUKARYOTIC CELLS CONTAIN A MITOCHONDRIAL
 CC MN-CONTAINING ENZYME & A CYTOPLASMIC CU-ZN-CONTAINING ENZYME.
 CC PLANTS ALSO HAVE A CHLOROPLAST CU-ZN ENZYME.
 CC -1- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
 CC DR HSP; P15107; 1XSO.
 DR INTERPRO: IPR001424;
 DR PFAM: PF00080; sodcu; 1.
 DR PROSITE: PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE: PS00332; SOD_CU_ZN_2; PARTIAL.
 KM Oxidoreductase; Copper; Zinc; Multigene family.
 FT NON_TER 21 21
 SQ SEQUENCE 21 AA; 2100 MW; 6CF0E108CAF03D65 CRC64;

Query Match 20.28; Score 22; DB 1; Length 21;
 Best Local Similarity 50.08; Pred. No. 1.6e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGLDMVGL 16
 DB 10 TGDVRCV 17

RESULT 22
 ALL4_OLEU STANDARD; PRT; 24 AA.
 AC P80741;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MAJOR POLLEN ALLERGEN OLE E 4 (OLE E IV) (FRAGMENTS).
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Lamiales; Oleaceae; Olea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-POLLEN;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea.";
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -1- DISEASE: MAJOR ALLERGEN FROM OLIVE POLLEN. IMPORTANT IN
 CC MEDITERRANEAN COUNTRIES (BY SIMILARITY).
 KM Allergen.

FT NON_TER 1 1
 RT NON_CONS 10 11
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA; 2711 MW; ADAC5DA9F577D60 CRC64;

Query Match
 Best Local Similarity 20.2%; Score 22; DB 1; Length 24;
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 8 SNGLDVGL 16
 DB 4 NTGVELVSI 12

RESULT 23
 GAE6.RANRU STANDARD; PRT; 24 AA.

AC P80400;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE GAEGRIN-6.
 OS Rana rugosa (Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 RN [1]
 RP TISSUE=SKIN.
 RC MEDLINE=95091844; PubMed=7999137;
 RA Park J.M., Jung J.-E., Lee B.J.;
 RT "Antimicrobial peptides from the skin of a Korean frog, Rana
 rugosa."
 RL Biochem. Biophys. Res. Commun. 205:948-954(1994).
 CC -1- FUNCTION: HAS A NON-HEMOLYTIC ACTIVITY. HAS A BROAD SPECTRUM OF
 ACTIVITY AGAINST BOTH GRAM POSITIVE AND GRAM NEGATIVE BACTERIA,
 FUNGI AND PROTOZOA.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: SKIN.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 FAMILY.
 KW Amphibian skin; Antiploic. BY SIMILARITY.
 FT DISULFID 18 24
 SQ SEQUENCE 24 AA; 2610 MW; 09918123FF90CCD CRC64;

Query Match
 Best Local Similarity 20.2%; Score 22; DB 1; Length 24;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 13 MVLGADW 20
 DB 5 LAGLANF 12

RESULT 24
 NODD.RHILLO STANDARD; PRT; 18 AA.
 AC 052838;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE NODULATION PROTEIN D (FRAGMENT).
 GN NODD.
 OS Rhizobium loti (Mesorhizobium loti).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Phyllobacteriaceae; Mesorhizobium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NZP 2213;
 RX MEDLINE=97002748; PubMed=8850088;
 RA Scott D.B., Young C.A., Collins-Emerison J.M., Terzaghi E.A.,

RA Rockman E.S., Lewis P.E., Pankhurst C.E.;
 RT "Novel and complex chromosomal arrangement of Rhizobium loti
 nodulation genes."
 RL Mol. Plant Microbe Interact. 9:187-197(1996).
 CC -1- FUNCTION: NODD REGULATES THE EXPRESSION OF THE NOD ABCF GENES
 WHICH ENCODE OTHER NODULATION PROTEINS. NODD IS ALSO A NEGATIVE
 REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONOIDS AS INDUCERS.
 CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
 REGULATORS.
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 CC -----

DR EMBL; L06241; AAB47350.1; -
 DR INTERPRO; IPR000847; -
 DR PROSITE; PS00044; PTR_LYSR_FAMILY; PARTIAL.
 KW Nodulation; Transcription regulation; DNA-binding; Activator;
 KW Repressor.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2170 MW; 89BA8A62B591136 CRC64;

Query Match
 Best Local Similarity 19.7%; Score 21.5; DB 1; Length 18;
 Matches 5; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

OY 10 GLDM-VGLADW 20
 DB 5 GDLNLLVPPDM 16

RESULT 25
 CN2.LITGI STANDARD; PRT; 15 AA.
 AC P56247;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CAERIDIN 2.
 OS Litorea gilleni.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 RN [1]
 RP TISSUE=PAROTOID GLAND;
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins and
 caeridins from Litorea gilleni."
 RL J. Chem. Res. 139:937-961(1993).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 ANTI-BIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR POSTAL
 GLANDS.
 CC -1- MASS SPECTROMETRY: MW=1408; METHOD=FAE.
 KW Amphibian skin; Amidation.
 FT MOD_RES 15 15
 SQ SEQUENCE 15 AA; 1410 MW; 06F1BBF72550CBF CRC64;

Query Match
 Best Local Similarity 19.3%; Score 21; DB 1; Length 15;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 LDMVG 15
 DB 3 LDMVG 7

Tue Feb 6 08:48:22 2001

Search completed: February 5, 2001, 10:56:02
Job time: 502 sec

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OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RP [1]
 RN SEQUENCE.
 RX MEDLINE=94259890; PubMed=8201051;
 RA Shida K., Takamizawa K., Nagaoka M., Kushiro A., Osawa T., Tsuji T.,
 RT "Enterotoxin-binding glycoproteins in a protease-peptone fraction of
 RT heated bovine milk."
 RL J. Dairy Sci. 77:930-939(1994).
 DR HSP: P02754; IBSY.
 SQ SEQUENCE 20 AA; 2266 MW; C8236200247ABA66 CRC64;

Query Match 27.5%; Score 30; DB 6; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 6 Q1STGDMVGLADW 20
 DB 5 Q1MKGLDIOKVGCTW 19

RESULT 3
 ID 089021; PRELIMINARY; PRT; 24 AA.
 AC 089021;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MUSCULAR CHLORIDE CHANNEL 1 (FRAGMENT).
 GN CLC1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-SKELETAL MUSCLE;
 RA Vullhorst D.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ011106; CAA09489.1;
 FT NON_TER 1 1
 SQ SEQUENCE 24 AA; 2502 MW; B1AB8650DC0BF64 CRC64;

Query Match 24.8%; Score 27; DB 11; Length 24;
 Best Local Similarity 38.1%; Pred. No. 1e+03;
 Matches 8; Conservative 1; Mismatches 6; Indels 6; Gaps 1;

OY 6 Q1STG-----IDMVGGLADW 20
 DB 1 Q1KSGPLAGISLGMVCGRAW 21

RESULT 4
 ID 092WY2; PRELIMINARY; PRT; 25 AA.
 AC 092WY2;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE ILEX, STX2A, STX2B, GENES AND 25 ORF'S.
 OS Bacteriophage 933W.
 OC Viruses; dsDNA viruses, no RNA stage; unclassified dsDNA phages.
 OX NCBI_TaxID=10730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97076910; PubMed=8975608;
 RA Datz M., Janetzki-Mittmann C., Franke S., Gunzer F., Schmidt H.,
 RA Karch H.;
 RT "Analysis of the enterohemorrhagic Escherichia coli O157 DNA region
 RT containing lambdoid phage gene p and Shiga-like toxin structural
 RT genes."

RL Appl. Environ. Microbiol. 62:791-797(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97257502; PubMed=9103976;
 RA Schmidt H., Scheef J., Janetzki-Mittmann C., Datz M., Karch H.;
 RT "An ilex cRNA gene is located close to the Shiga toxin II operon in
 RT enterohemorrhagic Escherichia coli O157 and non-O157 strains."
 RL FEMS Microbiol. Lett. 149:39-44(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Karch H., Schmidt H., Janetzki-Mittmann C., Scheef J., Kroeger M.;
 RT "Shiga toxins, even when different are encoded in identical positions
 RT in related temperate bacteriophages."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y10775; CAB39286.1;
 SQ SEQUENCE 25 AA; 2779 MW; F2504C217C2A905C CRC64;

Query Match 24.8%; Score 27; DB 9; Length 25;
 Best Local Similarity 33.3%; Pred. No. 1.1e+03;
 Matches 6; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 3 YFNOLSTGDMVGLADW 20
 DB 4 YTFELITGLVIAGLFIW 21

RESULT 5
 ID 048860; PRELIMINARY; PRT; 25 AA.
 AC 048860;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE HOMEOBOX PROTEIN (FRAGMENT).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IRB21;
 RA Liu G., Yang J., Zhai W., He P., Li X., Lu J., Li S., Zhu L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003599; AAB94484.1;
 DR INTERPRO; IPR001356;
 DR PROSITE; PS50071; HOMEOBOX_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 FT NON_TER 1 1
 FT NON_TER 25 25
 SQ SEQUENCE 25 AA; 2861 MW; CC14641CF1E5BFCE CRC64;

Query Match 24.8%; Score 27; DB 10; Length 25;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 STGLDM 13
 DB 10 STGLDL 15

RESULT 6
 ID 09XT42; PRELIMINARY; PRT; 12 AA.
 AC 09XT42;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE ALPHA 5 CHAIN COLLAGEN TYPE IV (FRAGMENT).
 GN COL4A5.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99293036; PubMed-10362815;
 RA Zheng K., Harvey S., Sado Y., Naito I., Ninomiya Y., Jacobs R.,
 RT "Absence of the alpha6(IV) chain of collagen type IV in Alport
 syndrome is related to a failure at the protein assembly level and
 RT does not result in diffuse glomerulonephritis.";
 RL Am. J. Pathol. 154:1883-1891(1999).
 DR EMBL; AF128530; AAD45500.1; -
 KW Collagen.
 FT NON_TER
 SQ SEQUENCE 12 AA; 1289 MW; 2FBC5925EE3A2C8 CRC64;

Query Match 23.9%; Score 26; DB 6; Length 12;
 Best Local Similarity 71.4%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 14 VGLADW 20
 DB 6 VSLAGW 12

RESULT 7
 062538 PRELIMINARY; PRT; 21 AA.
 AC 062538;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE GRANTYME B(G,H) (EC 3.4.21.79) (CYTOTOXIC CELL PROTEASE 1) (CCP1)
 DE (CTLA-1) (FRAGMENTIN 2) (FRAGMENT).
 GN GZMB OR CTLA-1.
 OS Mus spretus (Western wild mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SECRET/ET;
 RX MEDLINE-94319082; PubMed-8043949;
 RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,
 RT Nadeau J.H.;
 RL Mamm. Genome 5:349-355(1994).
 CC "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
 CC -1- FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-
 CC MEDIATED IMMUNE RESPONSES. IT CLEAVES AFTER ASP. SEEMS TO BE
 CC LINKED TO AN ACTIVATION CASCADE OF CASPASES (ASPARTATE-SPECIFIC
 CC CYSTEINE PROTEASES) RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES
 CC CASPASE-3, -7, -9 AND 10 TO GIVE RISE TO ACTIVE ENZYMES MEDIATING
 CC APOPTOSIS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ASP-1-XAA >> ASN-1-XAA
 CC > MET-1-XAA, SER-1-XAA.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES OF CYTOLYTIC T-
 CC LYMPHOCYTES AND NATURAL KILLER CELLS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. STRONGEST TO OTHER GRANZYMES AND TO MAST CELL
 CC PROTEASES.
 DR EMBL; U05708; AAB60471.1; -
 DR HSSP; P04187; 2CPL.
 DR MEROPS; S01.136; -
 KM MGD; MGI:109267; Gmb.
 KW Hydrolyase; Serine protease; Zymogen; T-cell; Cytolysis; Apoptosis.
 FT NON_TER
 SQ SEQUENCE 21 AA; 2430 MW; 9DAC8253DFB1AE6 CRC64;

Query Match 23.9%; Score 26; DB 11; Length 21;
 Best Local Similarity 35.7%; Pred. No. 1.3e+03;
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 PRYFNOLSTGLDNY 14
 DB 1 PRAFTKVSFLSWI 14

RESULT 8
 085543 PRELIMINARY; PRT; 22 AA.
 AC 085543;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
 GN OMP-1.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-REF A12B;
 RA Hsieh Y.-H., Bobo L.D.;
 RT "Diversity of major outer membrane protein (omp-1) of Chlamydia
 RT trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF070327; AAC25298.1; -
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 22 AA; 2237 MW; 3BD2052033F8097D CRC64;

Query Match 23.9%; Score 26; DB 2; Length 22;
 Best Local Similarity 54.5%; Pred. No. 1.4e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 9 TGLDNGVLAD 19
 DB 4 TTSVDVGLERD 14

RESULT 9
 09TN01 PRELIMINARY; PRT; 15 AA.
 ID 09TN01
 AC 09TN01;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE BETA 2M-CLASS I-BINDING PEPTIDE-MAJOR HISTOCOMPATIBILITY COMPLEX
 DE H-2KB-SPECIFIC MOLECULE POORLY ASSOCIATED WITH BETA 2-MICROGLOBULIN.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-94240094; PubMed-8183884;
 RA Joyce S., Kuzushima K., Kepes G., Angelelli R.H., Nathenson S.G.;
 RT "Characterization of an incompletely assembled major
 RT histocompatibility class I molecule (H-2Kb) associated with unusually
 RT long peptides: implications for antigen processing and presentation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:4145-4149(1994).
 KW MHC.
 SQ SEQUENCE 15 AA; 1754 MW; 2CEACDA0F1180DC7 CRC64;

Query Match 22.9%; Score 25; DB 7; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PRYFNOL 7
 DB 1 PRYFNOL 7

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RESULT 10
099386 PRELIMINARY; PRT; 15 AA.
AC 099386: 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE CYTOCHROME OXIDASE SUBUNIT 2 (FRAGMENT).
GN COIT.
OS Sus scrofa (Pig).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE=98403943; PubMed=9734874;
RA Tartaglia M., Saulle E.;
RT "Rapid communication: nucleotide sequence of porcine and ovine
RL TRN(Lys) and ATPase8 mitochondrial genes.";
DR J. Anim. Sci. 76:2207-2208(1998).
KM EMBL; AF039170; AAD05063.1; -.
FT Mitochondrion.
SQ NON_TER 1
SEQUENCE 15 AA; 1788 MW; 2B93E0B6A0588CB3 CRC64;

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Query Match 22.9%; Score 25; DB 8; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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OY 2 RYFNOLSTGL 11
:|:|:|:|:|
DB 3 KYFEKWTSM 12

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RESULT 11
0994F2 PRELIMINARY; PRT; 16 AA.
AC 0994F2: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE RES-701-2-ENDOTHELIN TYPE B RECEPTOR ANTAGONIST.
OS Streptomyces.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae.
OX NCBI_TaxID=1883;
RN [1]
RP SEQUENCE.
RX MEDLINE=96139410; PubMed=8557586;
RA Yano K., Yamasaki M., Yoshida M., Matsuda Y., Yamaguchi K.;
RT "RES-701-2, a novel and selective endothelin type B receptor
RT antagonist produced by Streptomyces sp. II. Determination of the
RT primary structure.";
RL J. Antibiot. 48:1368-1370(1995).
SQ SEQUENCE 16 AA; 2061 MW; 4E7B0E0789E244DB CRC64;

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Query Match 22.9%; Score 25; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 15 GLAADV 20
| | | | |
DB 5 GTAPDW 10

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RESULT 12
09R5E9 PRELIMINARY; PRT; 16 AA.
ID 09R5E9

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AC 09R5E9: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
OS Haemophilus somnus.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=731;
RN [1]
RP SEQUENCE.
RX MEDLINE=93114910; PubMed=8418069;
RA Tagawa Y., Ishikawa H., Yusa N.;
RT "Purification and partial characterization of the major outer membrane
RT protein of Haemophilus somnus.";
RL Infect. Immun. 61:91-96(1993).
SQ SEQUENCE 16 AA; 1709 MW; 910FCA6B728D0D65 CRC64;

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Query Match 22.9%; Score 25; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 1.4e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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OY 4 FNOJSTGLDMVG 15
:|:|:|:|:|
DB 4 YNONGTKVDVG 15

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RESULT 13
09OVJ9 PRELIMINARY; PRT; 19 AA.
AC 09OVJ9: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE MEPRIN-B PEPTIDE B1.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373354; PubMed=1894622;
RA Kounnas M.Z., Wolz R.L., Gorbica C.M., Bond J.S.;
RT "Meprln-A and -B: Cell surface endopeptidases of the mouse kidney.";
RL J. Biol. Chem. 266:17350-17357(1991).
SQ SEQUENCE 19 AA; 2157 MW; 81E66F19417E20C5 CRC64;

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Query Match 22.9%; Score 25; DB 11; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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OY 4 FNOJSTGLDMVG 15
| | | | |
DB 1 FNOVSITNDNIG 12

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RESULT 14
047529 PRELIMINARY; PRT; 22 AA.
AC 047529: 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-NOV-1996 (TREMBlrel. 08, Last annotation update)
DE ORF1 AND ORF2.
GN HEMA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-K-12; MEDLINE-931171869; PubMed-7679718;
 RA Post D.A., Hore-Jensen B., Switzer R.L.;
 RT "Characterization of the hemA-prs region of the Escherichia coli and
 RT Salmonella typhimurium chromosomes: Identification of two open reading
 RT frames and implications for prs expression."
 RL J. Gen. Microbiol. 139:259-266(1993).
 DR EMBL: M77237; AAA24432.1; -
 SQ SEQUENCE 22 AA; 2340 MW; 25802412BB5B4E51 CRC64;

Query Match 22.9%; Score 25; DB 2; Length 22;
 Best Local Similarity 38.5%; Pred. No. 2e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 STGLDMVGLADW 20
 : : : : :
 Db 6 NTNDVRSLLASY 18

RESULT 15
 ID 04861 PRELIMINARY; PRT; 22 AA.
 AC 04861;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE HOMEOBOX PROTEIN (FRAGMENT).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
 OX NCBI_TaxID-4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IRB21;
 RA Liu G., Yang J., Zhai W., He P., Li X., Lu J., Li S., Zhu L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003600; AAB94485.1; -
 KW Homeobox; DNA-binding; Nuclear protein.
 FT NON_TER 1
 FT NON_TER 22
 SQ SEQUENCE 22 AA; 2337 MW; B18E95E52F6CE9C CRC64;

Query Match 22.9%; Score 25; DB 10; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 STGLD 12
 : : : : :
 Db 8 STGLD 12

RESULT 16
 ID 09723 PRELIMINARY; PRT; 23 AA.
 AC 09723;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE 8 KDA PHOTOSYSTEM I PSBG PROTEIN (FRAGMENT).
 OS Nicotiana glauca (Wood tobacco).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID-4096;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE-94105345; PubMed-8278548;
 RA Oookata J., Mikami K., Hayashida N., Nakamura M., Sugiyama M.;
 RT "Molecular heterogeneity of photosystem I. psad, psae, psaf, psah, and
 RT psal are all present in isoforms in Nicotiana spp.";

RL Plant Physiol. 102:1259-1267(1993).
 SQ SEQUENCE 23 AA; 2415 MW; E56CC139D095A968 CRC64;

Query Match 22.9%; Score 25; DB 8; Length 23;
 Best Local Similarity 71.4%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 LSTGLDM 13
 : : : : :
 Db 10 LSTGLSL 16

RESULT 17
 ID 090V05 PRELIMINARY; PRT; 16 AA.
 AC 090V05;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE IRI HEAVY CHAIN-RELATED PROTEIN (FRAGMENT).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10118;
 RN [1]
 RP SEQUENCE.
 RA Choi-Miura N.H., Sano Y., Oda E., Nakano Y., Tobe T., Yanagishita T.,
 RA Tanigawa M., Katagiri T., Tomita M.;
 RA J. Biochem. 117:400-407(1995).
 SQ SEQUENCE 16 AA; 1809 MW; 89436CB4C81609C7 CRC64;

Query Match 22.0%; Score 24; DB 11; Length 16;
 Best Local Similarity 40.0%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 10 GLDMVGLAD 19
 : : : : :
 Db 4 GIDIVSLTVD 13

RESULT 18
 ID 069392 PRELIMINARY; PRT; 23 AA.
 AC 069392;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
 DE THE FIRST 23 CODONS OF PRV GC ALLELE ASGRL PRECURSOR (FRAGMENT).
 OS GC.
 OS Pseudorabies virus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 OX NCBI_TaxID-10345;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BECKER;
 RX MEDLINE-95081163; PubMed-7989378;
 RA Tomlino M., Wilkinson K.S., Ryan P.;
 RT "Can a signal sequence become too hydrophobic?";
 RL J. Biol. Chem. 269:32016-32021(1994).
 DR EMBL: L36971; AAA79968.1; -
 KW Signal.
 FT SIGNAL 1
 FT SIGNAL 22
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2188 MW; B7069865A1406F3F CRC64;

Query Match 22.0%; Score 24; DB 13; Length 23;
 Best Local Similarity 54.5%; Pred. No. 3.1e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 8 STGLDMVGLAA 18
1 1 1 1 1
DB 3 SIGLAMLALLA 13

RESULT 19

O9S941 PRELIMINARY; PRT; 13 AA.
AC O9S941:
ID 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE H(+)-TRANSLUCATING (PYROPHOSPHATE-ENERGIZED) INORGANIC
DE PYROPHOSPHATASE BETA-2 POLYPEPTIDE (EC 3.6.1.1) (FRAGMENT1).
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons, core eudicots; Caryophyllales;
OC Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=3555;
RN [1]
RP MEDLINE=92179265; PubMed=1311852;
RA Sarafian V., Kim Y., Poole R.J., Rea P.A.;
RT "Molecular cloning and sequence of cDNA encoding the pyrophosphate-
energized vacuolar membrane proton pump of Arabidopsis thaliana.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).
SQ SEQUENCE 13 AA; 1243 MW; C9DB193C37C22AD CRC64;

Query Match 21.1%; Score 23; DB 10; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 GLDMVG 15
1 1 1 1 1
DB 5 GADLVG 10

RESULT 20

O9PXC5 PRELIMINARY; PRT; 15 AA.
AC O9PXC5:
ID 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE SMALL NUCLEAR INCLUSION POLYPEPTIDE CLEAVAGE PRODUCT.
OS Tobacco etch virus (TEV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12227;
RN [1]
RP MEDLINE=91306428; PubMed=1853555;
RA Dougherty W.G., Parks T.D.;
RT "Post-translational processing of the tobacco etch virus 49-kDa small
nuclear inclusion polypeptide: identification of an internal cleavage
site and delimitation of VPg and proteinase domains.";
RL Virology 183:449-456(1991).
SQ SEQUENCE 15 AA; 1680 MW; 2273B6E461D0F28C CRC64;

Query Match 21.1%; Score 23; DB 12; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PTFENOLS 8
1 1 1 1 1
DB 8 PRDYNPIS 15

RESULT 21

O9UCP7 PRELIMINARY; PRT; 17 AA.
ID O9UCP7

AC O9UCP7:
ID 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE HML-1 BETA SUBUNIT, SMALLER HML-1 SUBUNIT, BETA 7
DE INTEGRIN-HETERODIMERIC PROTEIN COMPLEX RECOGNIZED BY THE HUMAN
DE MUCOSAL LYMPHOCYTE 1 MONOCLONAL ANTIBODY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=92179294; PubMed=1542691;
RA Parker C.M., Ceppek K.L., Russell G.J., Shaw S.K., Posnett D.N.,
RA Schartling R., Brenner M.B.;
RT "A family of beta 7 integrins on human mucosal lymphocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1924-1928(1992).
SQ SEQUENCE 17 AA; 1903 MW; 053C3931745A8BA2 CRC64;

Query Match 21.1%; Score 23; DB 4; Length 17;
Best Local Similarity 26.7%; Pred. No. 3.2e+03;

Matches 4; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 6 QUSTGLDMVGLADW 20
1 1 1 1 1 1 1
DB 1 ELDAKIPSTGDATFW 15

RESULT 22

O9TRD9 PRELIMINARY; PRT; 17 AA.
AC O9TRD9:
ID 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE V2 VASOPRESSIN RECEPTOR (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=94079886; PubMed=8257689;
RA Kojima E., Eich P., Gimpl G., Fahrenholz F.;
RT "Direct identification of an extracellular agonist binding site in the
renal V2 vasopressin receptor.";
RL Biochemistry 32:13537-13544(1993).
SQ SEQUENCE 17 AA; 1904 MW; E3C89EB346200E57 CRC64;

Query Match 21.1%; Score 23; DB 6; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.2e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 11 LDMVGLAA 18
1 1 1 1 1 1
DB 9 LQWGVKTA 16

RESULT 23

O24445 PRELIMINARY; PRT; 17 AA.
ID O24445:
AC O24445:
ID 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE THIS ORF RESIDES IN THE 5' UTR OF CPHYX2.
OS Ceratodon purpureus (Moss).
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Bryopsida;
OC Dicranidae; Dicranales; Ditrichaceae; Ceratodon.

Search completed: February 5, 2001, 10:55:27
Job time: 916 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:47:33 ; Search time 68.99 Seconds
(without alignments)
9.913 Million cell updates/sec

Title: US-08-981-824-5

Perfect score: 109
Sequence: 1 PRYFNLSTGLDMVGLADW 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 segs, 34193795 residues

Total number of hits satisfying chosen parameters: 141170

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_36:*

1:	/SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
2:	/SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
3:	/SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
4:	/SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
5:	/SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
6:	/SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
7:	/SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
8:	/SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*
9:	/SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*
10:	/SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
11:	/SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
12:	/SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
13:	/SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
14:	/SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
15:	/SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
16:	/SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
17:	/SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*
18:	/SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
19:	/SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
20:	/SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
21:	/SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	109	100.0	20	18	W18846	65 KD Glutamic ac1
2	109	100.0	20	18	W01197	Human 65 KD glutam
3	84	77.1	20	16	R72272	Glutamic acid deca
4	84	77.1	20	21	Y59572	GAD65 fragment, pe
5	77	70.6	15	18	W12405	GAD65 residues 177
6	73	67.0	14	16	R76657	Peptide derived fr
7	73	67.0	14	18	W18865	65 KD Glutamic ac1
8	65	59.6	15	18	W12404	GAD65 residues 173
9	55	50.5	20	18	W18845	65 KD Glutamic ac1
10	55	50.5	20	18	W01196	Human 65 KD glutam
11	50	45.9	20	16	R72273	Glutamic acid deca
12	50	45.9	20	21	Y59573	GAD65 fragment, pe

13	36	33.0	14	19	W70362	Epitope tag WTGLD,
14	36	33.0	14	19	W70363	Epitope tag WTGLD,
15	36	33.0	15	19	W70361	Epitope tag WTGLD,
16	36	33.0	22	16	R65046	Random biotinylati
17	36	33.0	22	19	W46649	Biotinylation pept
18	36	33.0	22	20	Y29339	Biotinylation pept
19	32	29.4	15	21	Y79295	Human protein pro
20	32	29.4	15	21	Y67045	B. lentus protease
21	32	29.4	15	21	Y54682	Fragment of p53 bl
22	31	28.4	18	16	W13198	Human WBPI immunog
23	31	28.4	18	19	W57351	Human WBPI immunog
24	31	28.4	19	21	Y79452	Rat kynurenine am1
25	31	28.4	20	21	Y91936	Hsrec2 peptide res
26	31	28.4	24	16	W13206	Fragment of p53 bl
27	31	28.4	24	19	W57367	Human WBPI immunog
28	30	27.5	17	20	Y27549	Rat P-450c peptide
29	30	27.5	18	16	R66373	Chlamydial MOMP VD
30	30	27.5	18	16	R65374	Chlamydial MOMP VD
31	30	27.5	19	15	R65378	Helper T cell epit
32	30	27.5	19	16	R82589	Escherichia coli T
33	30	27.5	19	17	W05615	E. coli tra T help
34	30	27.5	19	21	Y80074	Pathogen derived T
35	30	27.5	19	21	Y54556	T helper cell (Th)
36	30	27.5	19	21	Y58780	Unidentified pepti
37	30	27.5	20	18	W33044	Human heat shock p
38	30	27.5	20	18	W12352	Human hsp60 peptid
39	30	27.5	21	13	R22911	Bacterial immunoge
40	29	26.6	9	20	Y01008	Rat sp. AMPK-alpha
41	29	26.6	12	18	W29922	Lys-C peptide 293
42	29	26.6	13	16	R64138	Calcium sensor pro
43	29	26.6	13	17	R97212	Human calcium sens
44	29	26.6	13	19	W43316	Peptide derived fr
45	29	26.6	14	16	R76647	

ALIGNMENTS

RESULT	1
W18846	W18846 standard; peptide; 20 AA.
ID	W18846;
AC	W18846;
XX	
DT	05-JAN-1998 (first entry)
XX	
DE	65 KD Glutamic acid decarboxylase peptide fragment V.
XX	
KW	GAD; 65 KD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
KW	Insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
KW	predisposition; autoimmune; tumour; rheumatoid arthritis;
KW	multiple sclerosis.
XX	
OS	Synthetic.
XX	
FN	DE19526561-A1.
XX	
PD	23-JAN-1997.
XX	
PF	20-JUL-1995; 95DE-1026561.
XX	
PR	20-JUL-1995; 95DE-1026561.
XX	
PA	(BOEF) BOEHRINGER MANNHEIM GMBH.
XX	
PI	Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;
PI	Pozzilli P, Stahl P;
XX	
DR	WPI; 1997-088254/09.
XX	
PT	skin test for diagnosis of cell-mediated diseases, esp. diabetes -
XX	Involving intradermal admn. of auto-reactive substances

PS Claim 11; Page 9; 12pp; German.
 XX
 CC W18842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 109; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.2e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRYFNOLSTGLDMVGLADW 20
 |||||
 Db 1 pryfnglstglmvglaadw 20

RESULT 2

W01797
 ID W01797 standard; peptide: 20 AA.

XX
 AC W01797;

XX
 DT 15-OCT-1997 (first entry)

XX
 DE Human 65 kD glutamine decarboxylase peptide.

XX
 KM Human; glutamine decarboxylase; GAD; diagnosis; predisposition;
 KM tumour; immunological; disease; autoimmune; diabetes; reagent;
 KM determination; T cell; subpopulation; medication; treatment;
 KM prevention; production; antigen; immunogen; tolerogen; isolation;
 KM reinfection; inactivation.
 XX

OS Homo sapiens.

XX
 PN DE19525784-A1.

XX
 PD 16-JAN-1997.

XX
 PF 14-JUL-1995; 95DE-1025784.

XX
 PR 14-JUL-1995; 95DE-1025784.

XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX
 PI Albert W, Boltard C, Endl J, Jung G, Schendel D;

XX
 PI Stahl P, Van Endert P;

XX
 DR WPI; 1997-078452/08.

XX
 PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of

XX
 PT diabetes, etc.

XX
 PS Claim 1; Page 12; 15pp; German.

XX
 CC The present peptide is a fragment of the human 65 kD glutamine
 CC decarboxylase (GAD), which can be used to diagnose, or diagnose a
 CC predisposition to, a tumour or immunological disease, preferably an
 CC autoimmune disease, especially diabetes. It can also be used as a
 CC reagent to determine specific T cell subpopulations, in medicaments
 CC to treat or prevent immunological diseases, preferably autoimmune
 CC diseases, especially diabetes, to produce antigens, especially
 CC immunogens or tolerogens and to isolate specific T cell
 CC subpopulations, which can be used to produce antigens or for
 CC reinfection, optionally after inactivation.

XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 109; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.2e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRYFNOLSTGLDMVGLADW 20
 |||||
 Db 1 pryfnglstglmvglaadw 20

RESULT 3

R72272
 ID R72272 standard; Peptide: 20 AA.

XX
 AC R72272;

XX
 DT 13-NOV-1995 (first entry)

XX
 DE Glutamic acid decarboxylase (GAD65) fragment.

XX
 KM Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KM insulin-dependent diabetes mellitus; stiff man disease.
 XX

OS Homo sapiens.

XX
 PN W09507992-A.

XX
 PD 23-MAR-1995.

XX
 PF 24-AUG-1994; 94WO-US09478.

XX
 PR 17-SEP-1993; 93US-0123859.

XX
 PA (REBC) UNIV CALIFORNIA.

XX
 PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;

XX
 DR WPI; 1995-131360/17.

XX
 PT New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hybridoma(s) etc.
 XX

PS Example 11; Page 76; 100pp; English.

XX
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependent diabetes mellitus or stiff man disease.
 XX

XX
 SQ Sequence 20 AA;

Query Match 77.1%; Score 84; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRYFNOLSTGLDMVGL 16
 |||||
 Db 5 pryfnglstglmvgyl 20

RESULT 4

Y59572
 ID Y59572 standard; peptide: 20 AA.

XX
 AC Y59572;

```

XX 03-APR-2000 (first entry)
DT GAD65 fragment, peptide #12.
XX
XX GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
KW insulin dependent diabetes mellitus; stiff man disease; diagnosis;
KM therapy.
XX
XX Homo sapiens.
OS
XX US5998366-A.
PN
XX 07-DEC-1999.
PD
XX
XX 09-APR-1997; 97US-0827618.
PF
XX
XX 07-JUN-1995; 95US-0485725.
PR 21-SEP-1990; 90US-0586536.
PR 18-JUN-1991; 91US-0716909.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX Tobin AJ, Kaufman DL, Erlander MG;
PI
XX WPI; 2000-095930/08.
DR
XX
XX Ameliorating glutamic acid decarboxylase associated autoimmune
PT disorders such as insulin dependent diabetes mellitus and stiff man
PT disease -
XX
XX Example 11; Column 42; 61pp; English.
PS
XX This sequence represents a fragment of the glutamic acid decarboxylase 65
CC (GAD65) protein. The invention relates to a method of ameliorating GAD
CC associated autoimmune disorders by administering a GAD65 peptide to the
CC patient. The method can be used for ameliorating GAD associated
CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC and stiff man disease. GAD65 can also be useful for screening drugs that
CC alter GAD function, for generating monoclonal antibodies and in
CC immunosays. GAD65 is an effective diagnostic tool for predicting IDDM
CC and the diagnosis is quite easy. It is also possible to obtain much
CC larger quantities of polypeptide via recombinant techniques than are
CC available from natural sources.
CC
XX
XX Sequence 20 AA:
SQ
Query Match 77.18; Score 84; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PRYFNQLSTGLDMVGL 16
DB 5 prfngqlstgldmvgl 20
RESULT 5
W12405
ID W12405 standard; peptide; 15 AA.
XX
XX W12405;
AC
XX
XX 08-OCT-1997 (first entry)
DE
XX
XX GAD65 residues 177-191.
DE
XX
XX 65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;
KW neuron; central nervous system; type I diabetes; autoimmune response;
KM T cell; therapy.
XX
XX Homo sapiens.
OS
XX

```

```

FH Key Location/Qualifiers
FT MISC-difference 1..15
FT /note- "optionally substituted, providing at least 7
FT residues remain wild type"
XX
XX W09700891-A1.
PN
XX
XX 09-JAN-1997.
PD
XX
XX 24-JUN-1996; 96MO-US10790.
PF
XX
XX 23-JUN-1995; 95US-0494624.
PR
XX
XX (KENN-) KENNEDY INST RHEUMATOLOGY.
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.
XX
XX Conlon PJ, Gaur A, Leslie RDG, Ling N, Londel M;
PI
XX WPI; 1997-087322/08.
DR
XX
XX New human glutamic acid decarboxylase peptide(s) - used for
PT treatment, diagnosis and determining predisposition to diabetes and
PT for ameliorating auto-immune responses.
XX
XX Claim 23; Page -: 28pp; English.
PS
XX
XX W12403-W12413 represent fragments and analogues of the the 65 kD isoform
CC of human glutamic acid decarboxylase (GAD65) (see W12402 for full length
CC wild type protein). GAD is an enzyme expressed in the beta cells of the
CC pancreas, and in neurons of the central nervous system. There are two
CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of
CC GAD65 have been identified in type I diabetic patients. These GAD65
CC fragments, and analogues, are used in the methods of the invention. The
CC methods are for detecting or treating diabetes or a predisposition to
CC diabetes. The peptides can also be used for ameliorating an autoimmune
CC response in a patient. Alteration of the native peptides with selective
CC changes of crucial residues can induce unresponsiveness or change the
CC responsiveness of antigen-specific autoreactive T cells. The peptide
CC analogues compete for binding to MHC and do not cause proliferation of
CC the corresponding native peptide-specific T cells.
CC
XX
XX Sequence 15 AA:
SQ
Query Match 70.6%; Score 77; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RYFNQLSTGLDMVGL 16
DB 1 rfyngqlstgldmvgl 15
RESULT 6
R76657
ID R76657 standard; peptide; 14 AA.
XX
XX R76657;
AC
XX
XX 05-MAR-1996 (first entry)
DE
XX
XX Peptide derived from human glutamic acid decarboxylase 16.
DE
XX
XX diabetes; T-cell subpopulation; detection; antigen production;
KW diagnosis; autoimmune disease.
XX
XX Homo sapiens.
OS
XX
XX DE4418091-A1.
PN
XX
XX 27-JUL-1995.
PD
XX

```

PF 24-MAY-1994; 94DE-4418091.
 XX
 XX 04-FEB-1994; 94DE-4403522.
 PR 20-JAN-1994; 94DE-4401629.
 XX
 PA (ENDL/) ENDL J.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Albert W, Dormair K, Endl J, Jung G, Meinel E;
 PI Stahl P, Schendel D;
 XX WPI; 1995-264505/35.
 DR
 XX Antigen-specific activated T-lymphocytes and their detection - by
 PT interaction with inventive peptide(s) of peptide-MHC complexes;
 PT useful in diagnosis of e.g. diabetes and auto-immune diseases
 XX
 PS Claim 1; Fig 2; 21pp; German.
 XX
 CC R76642-62 are derived from human glutamic acid decarboxylase and
 CC specifically react with T-cell sub-populations isolated from recently
 CC diagnosed Type-I diabetics. Pharmaceutical compns. contg. these
 CC peptides and those shown in R77571-72, are useful for the diagnosis of
 CC a disease or predispositions of immune system diseases, tumours, and
 CC autoimmune diseases, including diabetes. The peptides are able to detect
 CC specific T-cell subpopulations that are then used for antigen prodn.,
 CC e.g. by reinjection.
 CC
 SQ Sequence 14 AA;

Query Match 67.0%; Score 73; DB 16; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RYFNOLSTGLDMVG 15
 |||||
 Db 1 RYFNGLSTGLDMVG 14

RESULT 7
 W18865
 ID W18865 standard; peptide: 14 AA.
 XX
 AC W18865;
 XX
 DT 05-JAN-1998 (first entry)
 XX
 DE 65 KD Glutamic acid decarboxylase peptide fragment 16.
 XX
 KW GAD; 65 KD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
 KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
 KW prediagnosis; autoimmune; tumour; rheumatoid arthritis;
 KW multiple sclerosis.
 XX
 OS Synthetic.
 XX
 PN DE19526561-A1.
 XX
 PD 23-JAN-1997.
 XX
 PF 20-JUL-1995; 95DE-1026561.
 XX
 PR 20-JUL-1995; 95DE-1026561.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;
 PI Pozzilli P, Stahl P;
 XX WPI; 1997-088254/09.
 DR
 XX Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
 PT

PT involving intradermal admin. of auto-reactive substances
 XX
 PS Claim 11; Fig 2; 12pp; German.
 XX
 CC W18842-70 are peptide fragments of the 65 KD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 CC
 SQ Sequence 14 AA;

Query Match 67.0%; Score 73; DB 18; Length 14;
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RYFNOLSTGLDMVG 15
 |||||
 Db 1 RYFNGLSTGLDMVG 14

RESULT 8
 W12404
 ID W12404 standard; peptide: 15 AA.
 XX
 AC W12404;
 XX
 DT 08-OCT-1997 (first entry)
 XX
 DE GAD65 residues 173-187.
 XX
 DE 65 KD glutamic acid decarboxylase: human; GAD65; enzyme; pancreas;
 KW neuron; central nervous system; type I diabetes; autoimmune response;
 KW T cell; therapy.
 XX
 KW Homo sapiens.
 OS
 XX
 FH Key location/Qualifiers
 FT Misc-difference 1.15 /note= "optionally substituted, providing at least 7
 FT residues remain wild type"
 FT

PN W09700891-A1.
 XX
 PD 09-JAN-1997.
 XX
 PF 24-JUN-1996; 96WO-US10790.
 XX
 PR 23-JUN-1995; 95US-0494624.
 XX
 PA (KENN-) KENNEDY INST RHEUMATOLOGY.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.
 PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;
 DR WPI; 1997-087322/08.
 XX
 DR New human glutamic acid decarboxylase peptide(s) - used for
 PT treatment, diagnosis and determining predisposition to diabetes and
 PT for ameliorating auto-immune responses.
 XX
 PS Claim 22; Page -; 28pp; English.
 XX
 CC W12403-W12413 represent fragments and analogues of the 65 KD isoform
 CC of human glutamic acid decarboxylase (GAD65) (see W12402 for full length
 CC wild type protein). GAD is an enzyme expressed in the beta cells of the

pancreas, and in neurons of the central nervous system. There are two isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of GAD65 have been identified in Type I diabetic patients. These GAD65 fragments, and analogues, are used in the methods of the invention. The methods are for detecting or treating diabetes or a predisposition to diabetes. The peptides can also be used for ameliorating an autoimmune response in a patient. Alteration of the native peptides with selective changes of crucial residues can induce unresponsiveness or change the responsiveness of antigen-specific autoreactive T cells. The peptide analogues compete for binding to MHC and do not cause proliferation of the corresponding native peptide-specific T cells.

XX Sequence 15 AA:

Query Match 59.6%; Score 65; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRYFNQSTGID 12
| | | | | | | | | |
Db 4 pryfngstgld 15

RESULT 9
W18845
W18845 standard; peptide: 20 AA.
AC W18845;
DT 05-JAN-1998 (first entry)
XX
DE 65 kD glutamic acid decarboxylase peptide fragment IV.
XX
GAD: 65 kD: human: glutamic acid decarboxylase; autoreactive; diagnosis;
KM insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
KM prediagnosis; autoimmune; tumour; rheumatoid arthritis;
KM multiple sclerosis.
XX
OS Synthetic.
XX
PN DE19526561-A1.
XX
PD 23-JAN-1997.
XX
PF 20-JUL-1995; 95DE-1026561.
XX
PR 20-JUL-1995; 95DE-1026561.
XX
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;
PI Pozzilli P, Stahl P;
XX
DR WPI; 1997-088254/09.
XX
PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
PT Involving intradermal admin. of auto-reactive substances
XX
PS Claim 11; Page 9; 12pp; German.
XX
W18842-70 are peptide fragments of the 65 kD human glutamic acid
CC decarboxylase (GAD). The fragments are autoreactive substances used for
CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
CC determined by using a claimed method for diagnosis of cell-mediated
CC diseases or a predisposition to cell-mediated diseases, which is effected
CC by administering an autoreactive substance intradermally and establishing
CC the diagnosis on the basis of the occurrence or lack of a positive
CC reaction at the site of administration. The method is used for diagnosis
CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
XX
SQ Sequence 20 AA:

Query Match 50.5%; Score 55; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRYFNQSTG 10
| | | | | | | | | |
Db 11 pryfngstg 20

RESULT 10
W01796
W01796 standard; peptide: 20 AA.
XX
AC W01796;
XX
DT 15-OCT-1997 (first entry)
XX
DE Human 65 kD glutamine decarboxylase peptide.
XX
KM Human: glutamine decarboxylase; GAD; diagnosis; predisposition;
KM tumour; immunological; disease; autoimmune; diabetes; reagent;
KM determination; T cell; subpopulation; medicament; treatment;
KM prevention; production; antigen; immunogen; tolerogen; isolation;
KM reinjection; inactivation.
XX
OS Homo sapiens.
XX
PN DE19525784-A1.
XX
PD 16-JAN-1997.
XX
PF 14-JUL-1995; 95DE-1025784.
XX
PR 14-JUL-1995; 95DE-1025784.
XX
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PI Albert W, Bolteard C, Endl J, Jung G, Schendel D;
PI Stahl P, Van Endert P;
XX
DR WPI; 1997-078452/08.
XX
PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of
PT diabetes, etc.
XX
PS Claim 1; Page 12; 15pp; German.
XX
The present peptide is a fragment of the human 65 kD glutamine
CC decarboxylase (GAD), which can be used to diagnose, or diagnose a
CC predisposition to, a tumour or immunological disease, preferably an
CC autoimmune disease, especially diabetes. It can also be used as a
CC reagent to determine specific T cell subpopulations, in medicaments
CC to treat or prevent immunological diseases, preferably autoimmune
CC diseases, especially diabetes, to produce antigens, especially
CC immunogens or tolerogens and to isolate specific T cell
CC subpopulations, which can be used to produce antigens or for
CC reinjection, optionally after inactivation.
XX
SQ Sequence 20 AA:

Query Match 50.5%; Score 55; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRYFNQSTG 10
| | | | | | | | | |
Db 11 pryfngstg 20

RESULT 11

```

R72273
ID R72273 standard; Peptide; 20 AA.
XX
AC R72273;
XX
DT 13-NOV-1995 (first entry)
XX
DE Glutamic acid decarboxylase (GAD65) fragment.
XX
KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
XX insulin-dependant diabetes mellitus; stiff man disease.
XX
OS Homo sapiens.
XX
PN W09507992-A.
XX
PD 23-MAR-1995.
XX
PF 24-AUG-1994; 94MO-US09478.
XX
PR 17-SEP-1993; 93US-0123859.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
XX WPI, 1995-131360/17.
XX
DR New polypeptide fragments of glutamic acid decarboxylase - for
XX diagnosis and treatment of autoimmune disease, esp. insulin
XX dependent diabetes, also related nucleic acid, vectors,
XX antibodies, hybridoma(s) etc.
XX
PS Example 11; Page 76; 100pp; English.
XX
CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
XX acid decarboxylase (GAD65) respectively, from which the GAD65
XX fragments described in R72261-R72298 were derived. These fragments
XX can be used to detect autoantibodies against GAD, e.g. to diagnose
XX CC and treat GAD-related autoimmune disorders, such as insulin
XX dependent diabetes mellitus or stiff man disease.
XX
SQ Sequence 20 AA;

Query Match 45.9%; Score 50; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DMVGLAADM 20
   |||||
   1 dmvglaadm 9

Db

RESULT 12
V59573
ID Y59573 standard; peptide; 20 AA.
XX
AC Y59573;
XX
DT 03-APR-2000 (first entry)
XX
DE GAD65 fragment, peptide #13.
XX
KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
XX insulin, dependent diabetes mellitus; Stiff man disease; diagnosis;
XX therapy.
XX
OS Homo sapiens.
XX
PN US5998366-A;
XX
PD 07-DEC-1999.

```

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XX
PF 09-APR-1997; 97US-0827618.
XX
PR 07-JUN-1995; 95US-0485725.
XX
PR 21-SEP-1990; 90US-0586536.
XX
PR 18-JUN-1991; 91US-0716909.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Tobin AJ, Kaufman DL, Erlander MG;
XX WPI, 2000-095930/08.
XX
DR Ameliorating glutamic acid decarboxylase associated autoimmune
XX disorders such as insulin dependent diabetes mellitus and Stiff man
XX disease -
XX
PS Example 11; Column 42; 61pp; English.
XX
CC This sequence represents a fragment of the glutamic acid decarboxylase 65
XX (GAD65) protein. The invention relates to a method of ameliorating GAD
XX associated autoimmune disorders by administering a GAD65 peptide to the
XX patient. The method can be used for ameliorating GAD associated
XX autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
XX and Stiff man disease. GAD65 can also be useful for screening drugs that
XX alter GAD function, for generating monoclonal antibodies and in
XX immunoassays. GAD65 is an effective diagnostic tool for predicting IDDM
XX and the diagnosis is quite easy. It is also possible to obtain much
XX larger quantities of polypeptide via recombinant techniques than are
XX available from natural sources.
XX
SQ Sequence 20 AA;

```

```

Query Match 45.9%; Score 50; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 DMVGLAADM 20
   |||||
   1 dmvglaadm 9

Db

RESULT 13
W70362
ID W70362 standard; Protein; 14 AA.
XX
AC W70362;
XX
DT 14-DEC-1998 (first entry)
XX
DE Epitope tag WTGLD, open reading frame 2.
XX
KW Target nucleotide; epitope; gene tagging; epitope tagging.
XX
OS Synthetic.
XX
PN W09826094-A1.
XX
PD 18-JUN-1998.
XX
PF 09-DEC-1997; 97WO-US22472.
XX
PR 09-DEC-1996; 96US-0762106.
XX
PA (JARV/) JARVIK J W.
XX
PI Jarvik JW;
XX
DR WPI, 1998-348546/30.
XX
DR N-PSDB; V33280.
XX
PT Epitope tagging of genes, transcripts and polypeptides - using an

```

PT oligonucleotide comprising a nucleotide sequence encoding the
PT epitope independently of the reading frame of the nucleotide
PT sequence
XX
PS Disclosure: Page 15; 46pp; English.

CC The epitope tag is encoded by the nucleotide sequence independently of
CC the reading frame. The epitope and methods disclosed can be used for
CC tagging of genes, transcripts and polypeptides. They can be used for
CC e.g. discovering new genes, determining the size and abundance of
CC proteins produced by newly discovered genes, tracking the movement of
CC proteins within cell membranes, monitoring receptor binding and
CC internalisation of exogenous proteins, identifying the components of
CC functional protein complexes, purifying proteins, discovering the
CC function of proteins. The products, methods and uses are particularly
CC used for proteins that are unstable, are difficult to purify, or share
CC epitopes with a number of other proteins. The methods overcome the
CC inefficiency of epitope tagging caused by reading frame obstacles and
CC orientation obstacles.

SQ Sequence 14 AA;

Query Match	33.0%	Score 36	DB 19	Length 14
Best Local Similarity	66.7%	Pred NO. 3.7		
Matches	8	Conservative	2	Indels 2; Gaps 1

QY	9	TGLDMVGLADW	20
Db	5	tgldwtgl--dw	14

RESULT 14

ID W70363 standard; protein; 14 AA.

AC W70363

DT 14-DEC-1998 (first entry)

DE Epitope tag WTGLD, open reading frame 3.

KW Target nucleotide; epitope; gene tagging; epitope tagging.

Synthetic

PN WO9826094-A1

PD 18-JUN-1998

PF 09-DEC-1997; 97WO-US22472

PR 09-DEC-1996; 96US-0762106.

PA (JARV/) JARVIK J W.

PI JARVlk JTW;

DR WPI; 1998-348546/30

XX
X
+
0
0
+
0
0
+

PT Epitope tagging of genes, transcripts and polypeptides - using an
oligonucleotide comprising a nucleotide sequence encoding the
PT epitope independently of the reading frame of the nucleotide
sequence

PS Disclosure: Page 15; 46pp: English.

CC protein within cell membranes, monitoring receptor binding and
CC internalisation of exogenous proteins, identifying the components of
CC functional protein complexes, purifying proteins, discovering the
CC function of proteins. The products, methods and uses are particularly
CC used for proteins that are unstable, are difficult to purify, or share
CC epitopes with a number of other proteins. The methods overcome the
CC inefficiency of epitope tagging caused by reading frame obstacles and
CC orientation obstacles.

5Q Sequence 14 AA

Query Match	33.0%	Score 36:	DB 19;	Length 14;
Best Local Similarity	66.7%	Pred. No. 3.7;		
Matches	8;	Conservative	0;	Mismatches 2;
			Indels	2;
			Gaps	1

```

0Y      9 TGLDMVGLADW 20
         ||||  ||  ||
Db      3 tglidwtgl--dw 12

```

RESULT 15

ID W70361 standard; Protein; 15 AA

AC W70361;

DT 14-DEC-1998 (first entry)

DE Epitope tag WTGLD, open reading frame 1

KW Target nucleotide; epitope; gene tagging; epitope tagging

OS Synthetic

PN W09826094-A1

PD 18-JUN-1998

PF 09-DEC-1997; 97WO-US22472

PR 09-DEC-1996; 96US-0762106

PA (JARV/) JARVIK J W
xx

PI Jarvik JW

DR WPI; 1998-348546/30.

XXIX

PT Epitope tagging of genes, transcripts and polypeptides - using an
PT oligonucleotide comprising a nucleotide sequence encoding the
PT epitope independently of the reading frame of the nucleotide
PT sequence

CC The epitope tag is encoded by the nucleotide sequence independently of
CC the reading frame. The epitope and methods disclosed can be used for
CC tagging of genes, transcripts and polypeptides. They can be used for
CC e.g. discovering new genes, determining the site and abundance of
CC proteins produced by newly discovered genes, tracking the movement of
CC proteins within cell membranes, monitoring receptor binding and
CC internalisation of exogenous proteins, identifying the components of
CC functional protein complexes, purifying proteins, discovering the
CC function of proteins. The products, methods and uses are particularly
CC used for proteins that are unstable, are difficult to purify, or share
CC epitopes with a number of other proteins. The methods overcome the
CC inefficiency of epitope tagging caused by reading frame obstacles and
CC orientation obstacles.

50 Sequence 15 AA;

Query Match 33.0%; Score 36; DB 19; Length 15;
 Best Local Similarity 66.7%; Pred. No. 4.1;
 Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 9 TGLDMVGLADW 20
 |||||
 Db 2 tgldevtgi--dw 11

RESULT 16

R65046 R65046 standard; Peptide; 22 AA.

AC R65046;

DT 06-OCT-1995 (first entry)

DE Random biotinylation peptide 15.

XX biotinylation; peptide; recombinant; fusion protein; small;

KW specific; defined; purification; BIRA; enzyme; biotin.

XX Synthetic.

OS Key Location/Qualifiers

XX Modified-site 16 /note- "biotin-Lys"

XX W09504069-A.

XX 09-FEB-1995.

XX 28-JUL-1994; 94WO-US08528.

XX 30-JUL-1993; 93US-0099991.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Schatz PJ;

XX WPI: 1995-090609/12.

XX Production of biotinylated proteins by expression of a

XX recombinant DNA vector - which encodes a fusion protein

XX comprising a protein and a biotinylated peptide.

XX Claim 10; Page 136; 146pp; English.

XX A library of small, efficient peptide biotinylation sequences (R65032-46)

XX was generated by using a generic peptide (R65020) and a system known as

XX the "peptides on plasmids" system. At some positions in the sequences,

XX no clear consensus is apparent. At other residues, however, clear trends

XX emerge. A protein can be biotinylated by constructing a recombinant DNA

XX expression vector encoding a fusion protein, comprising a protein and a

XX biotinylation peptide. A host cell, eg. E. coli is transformed with the

XX vector and is cultured in the presence of biotin and a biotinylation

XX enzyme, eg. BIRA.

XX Sequence 22 AA;

XX

ID W46649 standard; peptide; 22 AA.

XX W46649;

AC 28-MAY-1998 (first entry)

XX Biotinylation peptide isolated from random library 1.

XX Biotinylation peptide; biotinylation enzyme; biotin-protein ligase;

KW BIRA; biotin ligase; biotin; purification; immobilisation; labelling;

XX detection; protein.

XX Synthetic.

OS US5723584-A.

XX 03-MAR-1998.

XX 03-FEB-1995; 95US-0383753.

XX 30-JUL-1993; 93US-0099991.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Schatz PJ;

XX WPI: 1998-178542/16.

XX Peptide(s) that can be biotinylated by biotin ligase - and fusion

XX proteins containing them

XX Claim 3; Column 66; 33pp; English.

XX Peptides W46648-49 are non-naturally occurring biotinylation peptides,

XX derived from a library constructed to express peptides of the generic

XX sequence W46623. The library was constructed using oligonucleotides

XX V6118-20. The peptides contain a biotinylatable sequence motif,

XX recognised by a biotinylation enzyme, e.g. biotin-protein ligase (BIRA).

XX The C or N terminus of the peptides can be covalently coupled to a

XX protein that is incapable of being biotinylated by a biotin ligase.

XX The peptides can be biotinylated in vitro or in vivo, especially with

XX BIRA biotin ligase, and used for the purification, immobilisation,

XX labelling or detection of proteins.

XX Sequence 22 AA;

XX

XX Query Match 33.0%; Score 36; DB 19; Length 22;

XX Best Local Similarity 38.9%; Pred. No. 6.5;

XX Matches 7; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

XX QY 7 LSTGID---WVGLADW 20

XX : ||||| : 1: 11

XX Db 2 metgidlrpiltgmkdw 19

XX RESULT 18

XX ID Y29339 standard; peptide; 22 AA.

XX AC Y29339;

XX DT 28-SEP-1999 (first entry)

XX DE Biotinylation peptide SEQ ID NO:28.

XX Biotinylation enzyme; biotin-protein ligase; BIRA; labelling;

KW biotin carboxyl carrier protein; BCCP; Escherichia coli;

KW fusion protein; identification; purification; diagnosis; research;

XX Escherichia coli.

XX OS Synthetic.

XX

PN US5932433-A.
 XX 03-AUG-1999.
 PD 28-OCT-1997; 97US-0959512.
 XX 03-FEB-1995; 95US-0383753.
 PR 30-JUL-1993; 93US-0099991.
 PR 28-OCT-1997; 97US-0959512.
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX Schatz PJ;
 PI WPI: 1999-457113/38.
 DR Identification and biotinylation of proteins synthesized by
 PT recombinant DNA techniques in vivo
 PS Claim 6: Column 66; 35pp; English.
 XX The present invention describes a method for the identification and
 CC biotinylation of proteins synthesized by recombinant DNA techniques
 CC in vivo with a biotinylation peptide of less than 50 amino acids. The
 CC method comprises: (a) on the surface of a substrate, providing a fusion
 CC protein comprising a recombinant protein and a peptide defined by the
 CC sequence given in Y24492, where the peptide is capable of being
 CC biotinylated by a biotin ligase at the lysine residue adjacent to
 CC position 8 and is 13-50 aa in length; (b) in a predefined region of the
 CC surface of the substrate, contacting the fusion protein with an enzyme;
 CC and (c) determining whether the fusion protein has been biotinylated.
 CC The method allows the identification and purification of biotinylated
 CC enzymes e.g. Birt. The method is also useful in research and diagnostic
 CC applications. The method uses small but specific peptides, allowing the
 CC labelling of a protein at a defined site, this provides improved
 CC immobilization and avoids the use of antibodies. Y24493 to Y24548, and
 CC Y29299 to Y29312 represent specifically claimed examples of
 CC biotinylation peptides for use in the method of the invention.
 XX SQ Sequence 22 AA:
 QY 7 LSTGLD---MVGIAADW 20
 Db 2 metgldlrplltgmkmw 19
 RESULT 19
 Y79295
 ID Y79295 standard; Peptide: 15 AA.
 AC Y79295;
 XX 18-JUL-2000 (first entry)
 DT Human prorenin profragment immunogenic antigen.
 DE Human prorenin profragment immunogenic antigen.
 XX Human; prorenin; renin; antibody; immunogen; antigen.
 KW Homo sapiens.
 OS EP994187-A1.
 PN 19-APR-2000.
 PD 13-OCT-1999; 99EP-0308080.
 PF 13-OCT-1998; 98JP-0291124.
 PR 13-OCT-1998; 98JP-0291124.
 XX

PA (TOKU) TOKIMA CHEM IND CO LTD.
 PA (ISHI/) ISHIDA Y.
 XX Murakami K, Nakamura Y, Suzuki F, Ishida Y;
 XX WPI: 2000-273528/24.
 DR Novel renin-active complex comprising human prorenin and at least one
 PT anti-peptide antibody with specific affinity to parts of the human
 PT prorenin profragment -
 XX Example 2; Page 6; 18pp; English.
 PS This peptide is a human prorenin profragment immunogenic antigen
 CC comprising amino acid residues 27-41 of the profragment (see also
 CC Y79293). The peptide was produced by solid-phase synthesis, with
 CC addition of a C-terminal Cys residue, and used to raise
 CC anti-peptide antibodies in New Zealand white rabbit. The invention
 CC provides a novel renin-active complex (I) formed from human
 CC prorenin and an anti-peptide antibody that specifically recognizes
 CC either (a) an amino acid sequence of at least 15 residues in the 33
 CC residues between Ile11 and Arg43 of human prorenin profragment, or
 CC (b) an amino acid sequence comprising residues Ile11-Arg26 of human
 CC prorenin profragment, or (c) an amino acid sequence comprising
 CC residues Gly27-Met41 of human prorenin profragment. In all cases,
 CC (I) may also include a second anti-peptide antibody that specifically
 CC recognizes a sequence of 11 amino acids comprising Leu1-Ile11 of
 CC human prorenin profragment. (I) is useful as a renin substitute.
 CC Greatly enhanced renin activity can be obtained by using a mixed
 CC antibody consisting of equimolar amounts of anti-peptide antibodies.
 XX SQ Sequence 15 AA:
 QY 10 GLDMVGIAADW 20
 Db 1 gydmavrlgpew 11
 RESULT 20
 Y67045
 ID Y67045 standard; Peptide: 15 AA.
 AC Y67045;
 XX 15-MAR-2000 (first entry)
 DT B.lentus protease peptide F10.
 DE B.lentus protease peptide F10.
 XX Subtilisin; allergy; human; bacterium; protease; epitope; detergent;
 KW cosmetic; textile; pet food industry; debridement treatment.
 XX Bacillus lentus.
 OS WO9953078-A2.
 PN 21-OCT-1999.
 PD 15-APR-1999; 99WO-US08177.
 PF 15-APR-1998; 98US-0060854.
 PR (GEWY) GENENCOR INT INC.
 PA Estell D;
 PI WPI: 2000-061971/05.
 DR Modified non-human protease having reduced allergenicity -
 XX

XX
PS Example 2; Fig 7; 38pp; English.
XX
CC Peptides Y66983-Y67070 represent peptides derived from the Bacillus
CC lentus subtilisin protein. The peptides were used for epitope mapping of
CC the bacterial subtilisin. The invention relates to a method of reducing
CC the allergenicity of a non-human protein, especially a bacterial protease
CC such as subtilisin, by identifying an epitope on the non-human protein
CC and replacing it by an analogous region from the human protein. The
CC method is useful for producing proteins, including proteases, that are
CC less likely to cause allergic reactions. Thus the invention can be
CC employed for example in detergents, cosmetics, textile treatment, and
CC pet food industries. The human subtilisin can be used pharmaceutically
CC for debridement treatments.
CC
CC Sequence 15 AA:
SO

Query Match 29.4%; Score 32; DB 21; Length 15;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 FNQJSTGLDMV 14
1:1 111:1
Db 3 fsqygaqidiv 13

RESULT 21
Y54682
ID Y54682 standard; peptide; 15 AA.
XX
AC Y54682;
XX
DT 04-FEB-2000 (first entry)
XX
DE B. lentus protease fragment peptide F10.
XX
KW Subtilisin; protease variant; precursor protease; cleaning composition;
KW detergent; liquid soap application; dish-care formulation; animal feed;
KW contact lens cleaning solution; peptide hydrolysis; waste treatment;
KW cosmetic formulation; fusion-cleavage enzyme; protein production.
XX
OS Bacillus lentus.
XX
PN W09953038-A2.
XX
PD 21-OCT-1999.
XX
PF 14-APR-1999; 99WO-US08253.
XX
PR 15-APR-1998; 98US-0060872.
XX
PA (GEMV) GENENCOR INT INC.
XX
PI Estell DA, Harding FA;
XX
DR WPI; 2000-013100/01.
XX
PT New mutant proteins having lower allergenic response in humans useful
PT in cleaning compositions, animal feed and treating textiles -
XX
PS Example 2; Fig 6a; 43pp; English.
XX
CC This sequence is a fragment of the Bacillus lentus protease. The
CC invention relates to protease variants comprising a substitution at least
CC 1 of the positions in a precursor protease corresponding to K170D, Y171Q
CC and/or S173D of the Bacillus amyloliquefaciens subtilisin. The protease
CC variant can be used in a cleaning composition (e.g. in detergents, in bar
CC or liquid soap application, dish-care formulations, or contact lens
CC cleaning solutions), in animal feed and for treating textiles
CC (e.g. treating wool to prevent felting). The protease variant may also be
CC used for peptide hydrolysis, waste treatment, cosmetic (e.g. skin care)
CC formulations, or as fusion-cleavage enzymes in protein production. The

CC proteins (including enzymes) with reduced antigenicity may be used with
CC significantly less danger of sensitisation for the individuals exposed.
CC Peptides which contain epitopes responsible for initially sensitising an
CC individual may be identified by measuring the proliferation of T-cells
CC due to T-cell epitope recognition.
CC
CC Sequence 15 AA:
SO

Query Match 29.4%; Score 32; DB 21; Length 15;
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 FNQJSTGLDMV 14
1:1 111:1
Db 3 fsqygaqidiv 13

RESULT 22
W13198
ID W13198 standard; Protein; 18 AA.
XX
AC W13198;
XX
DT 19-MAY-1997 (first entry)
XX
DE Fragment of p53 binding protein WBPI.
XX
KW p53; binding protein; WBPI; antibody; diagnosis; treatment;
KW neoplastic; pre-neoplastic; disease; agonist; antagonist;
KW augmentation; inhibition; complex formation; neoplasia; apoptosis;
KW reperfusion; injury; myocardial infarction; stroke; AIDS;
KW traumatic brain; neurodegenerative; aging; ischaemia; toxemia;
KW infection; hepatitis; probe; genetic; forensic identification;
KW fragment.
XX
OS Homo sapiens.
XX
PN W09514777-A1.
XX
PD 01-JUN-1995.
XX
PF 21-NOV-1994; 94WO-US13499.
XX
PR 22-NOV-1993; 93US-0156571.
XX
PA (ONYX-) ONYX PHARM.
XX
PI Bischoff JR, Wu L;
XX
DR WPI; 1995-206934/27.
XX
PT New p53-binding polypeptide(s) WBPI and p53UBC - used to develop
PT prods. for screening assays and for use in diagnosis and therapy of
PT diseases, esp. neoplasia
XX
PS Claim 8; Page 38; 90pp; English.
XX
CC The present sequence is a fragment of the p53 binding protein WBPI,
CC which can be used to generate antibodies for the diagnosis of
CC (pre)neoplastic diseases, and WBPI (ant)agonists. The (ant)agonists
CC augment or inhibit the formation of p53:WBPI complexes and
CC inhibit neoplasia or apoptosis, useful in the treatment of, e.g.
CC reperfusion injury, myocardial infarction, stroke, traumatic brain
CC injury, neurodegenerative diseases, aging, ischaemia, toxemia,
CC infection, AIDS and hepatitis. The WBPI encoding cDNA, which was
CC isolated from a HeLa cell derived cDNA library using the yeast
CC two-hybrid system, can be used to generate probes for the diagnosis
CC of (pre)neoplastic pathological conditions and genetic diseases,
CC and the forensic identification of human individuals.
XX
SO Sequence 18 AA;

Query Match 28.4%; Score 31; DB 16; Length 18;
Best Local Similarity 33.3%; Pred. No. 41;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 PRFNQSTGLDMVG 15
1 : 1 : 1 : 1 :
Db 1 pgqvgqslssmdlsq 15

RESULT 23

W57351
ID W57351 standard; peptide; 18 AA.

AC W57351;

DT 11-AUG-1998 (first entry)

DE Human WBPI immunogenic peptide SEQ ID NO:83.

XX Human; WBPI, p53; cancer; interacting protein; screen; diagnosis;

KW genetic disease; forensic identification; nuclear phosphoprotein;

XX cellular proliferation; neoplastic transformation; p53UBC; immunogen.

OS Homo sapiens.

PN US5756669-A.

PD 26-MAY-1998.

PF 02-MAR-1995; 95US-0399696.

PR 02-MAR-1995; 95US-0399696.

PR 22-NOV-1993; 93US-0156571.

PR 21-NOV-1994; 94WO-US13499.

PA (ONYX-) ONYX PHARM INC.

PI Bischoff JR, Wu L;

DR WPI; 1998-321626/28.

PT WBPI, p53-interacting protein - useful screening agents for

XX treatments of p53 related cancers

XX Disclosure; Column 24; 68pp; English.

XX The present sequence represents an immunogenic peptide from WBPI

XX (cellular proliferation and neoplastic transformation) polypeptide,

XX which can be used to screen bacteriophage antibody display libraries or

XX to immunize a rabbit. WBPI is a p53-interacting protein that can be used

XX to screen for agents for diagnosis or treatment of cancer and genetic

XX diseases and for forensic identification of human individuals. The p53

XX protein is a nuclear phosphoprotein involved in control of cellular

XX proliferation, and mutations in it are associated with human cancers.

XX Sequence 18 AA;

RESULT 24

W79452
ID W79452 standard; peptide; 19 AA.

AC W79452;

XX Y79452;

XX 01-AUG-2000 (first entry)
DT Rat kynurenine aminotransferase variant (aa16-34).
XX

KW Rat; kynurenine aminotransferase; metabolic X syndrome;
KW hypertension; stroke; diabetes; insulin resistance; obesity;
KW dyslipidemia; anorectic; hypotensive; cerebroprotective;
KW vasotropic; antidiabetic; antilipemic; gene therapy; diagnosis;
KW mutant; muten; chromosome 3.

XX Rattus sp.

XX Key Location/Qualifiers

XX Peptide 1..19 /note- "Corresponds to residues 16-34 of

XX FT full-length protein"

XX FT Misc-difference 12 /note- "replaces Glu in wild-type"

XX W020001918-A2.

XX 06-APR-2000.

XX 28-SEP-1999; 99WO-US22494.

XX 28-SEP-1998; 98US-0161939.

XX (CURA-) CURAGEN CORP.

XX Shimkete RA;

XX WPI; 2000-303450/26.

XX Novel genes encoding e.g. CD36, SGLT2, and kynurenine aminotransferase,

XX which are predictive and therapeutic for stroke, hypertension, diabetes

XX and obesity

XX Claim 2; Fig 4B; 79pp; English.

XX This sequence represents amino acids 16-34 of kynurenine

XX aminotransferase (KAT) from a spontaneously hypertensive rat (SHR).

XX This region of KAT carries an amino acid substitution (E27G) when

XX compared to the corresponding region in control Wistar Kyoto (WKY)

XX rats (see Y79453). The mutation changes the charge of a residue

XX that is conserved across all known KAT homologues, from human to

XX Caenorhabditis elegans. The invention discloses genes whose expression

XX is modulated in SHR rat, which is an animal model for human

XX metabolic X syndrome. Heart, brain, fat, liver and kidney tissues

XX from SHR, stroke-prone SHR (SHR-SP) and WKY animals were analysed

XX using GeneCalling methodology to facilitate the identification and

XX characterization of genes which are differentially expressed in the

XX SHR and SHR-SP, as compared with WKY rats. Genes encoding KAT,

XX sodium dependent glucose cotransporter, CD36, aldolase A, atrial

XX natriuretic factor, alpha-cardiac myosin and alpha-tubulin were

XX identified as being potentially associated with hypertension,

XX obesity and insulin resistance. Rat was increased in abundance in

XX SHR and SHR-SP kidney, and was mapped within an SHR-SP

XX hypertension QTL on chromosome 3. Hypotension may be treated by

XX administering kynurenine acid. The polynucleotides and polypeptides

XX of the invention, including isolated proteins comprising the present

XX sequence, are used for treating, preventing and diagnosing ischemic

XX CC and metabolic diseases and disorders, such as stroke, hypertension,

XX CC diabetes and obesity, especially insulin resistivity, dyslipidemia

XX CC and ischemic stroke (all claimed). The polynucleotides may also be

XX CC used in gene therapy and antisense therapy protocols.

XX Sequence 19 AA;

Query Match 28.4%; Score 31; DB 21; Length 19;

Best Local Similarity 46.2%; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy      4  ENQLSTGLDMVGL 16
Db      6  fgkltkydvvn1 18
```

Search completed: February 5, 2001, 10:47:34
Job time: 628 sec

RESULT 25

ID	standard; peptide; 20 AA.
Y91936	

AC Y91936;

DT 19-JUL-2000 (first entry)

DE HSRec2 peptide residues 153-172.

KW HSRec2, serine kinase; homologous pairing; strand transfer; RAD51.
KW phosphorylation; cyclin E; p53; cell cycle; substrate.

OS Synthetic.

PN WO200017329-A1

PD 30-MAR-2000

PF 17-SEP-1999; 99WO-US21642
VY

PR 21-SEP-1998; 98US-0157603
XX XX

PA (UYJE-) UNIV JEFFERSON THOMAS.
PA (CORR) CORNELL RES FOUND INC.
PA (KIME-) KIMERAGEN INC.

PI Havre PA, Rice MC, Holloman WK, Kmiec EB;

DR WPI; 2000-283562/24.

PT Phosphorylating a serine-containing substrate by incubating it with
PT adenosine triphosphate and Rec2 kinase and measuring the level of
PT phosphorylation, useful for discovering specific antagonists or
PT agonists of Rec2

PS Example 3; Page 14; 41pp; English.

CC The present sequence is hsrc2 peptide, residues 153-172, a substrate
CC which was not phosphorylated by hsrc2, a human serine kinase. hsrc2
CC is in the same supergene family as the mammalian protein having
CC homologous pairing and strand transfer activities, RAD51 and vas
CC isolated because of its homology to the homologous pairing and strand
CC transfer protein of *Ustilago maydis*. In particular, hsrc2
CC phosphorylates several proteins that control the cell cycle, especially
CC cyclin E and p53. The invention permits the phosphorylation of cell
CC cycle control proteins at sites that are physiologically relevant. The
CC invention can be practiced with either murine or human Rec2 or a mutant
CC or chimera of these proteins. In particular the muten has the sequence
CC of a Rec2 kinase containing other than a Tyr at position 163. The
CC invention comprises a method of phosphorylating a serine-containing
CC substrate comprising incubating the substrate with ATP (adenosine
CC triphosphate) and Rec2 kinase or a mammalian Rec2 and measuring the level
CC of phosphorylation. The method is useful for discovering compounds which
CC are specific antagonists or agonists of Rec2.

SQ. Sequence 20 AA;

Query Match	28.4%	Score	31	DB	21	Length	20
Best Local	Similarity	100.0%	Pred. No.	46			
Matches	5	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

QY	1	PRYFN	5
Db	9	pryfn	13

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:55:27 ; Search time 93.77 Seconds
(without alignments)
24.999 Million cell updates/sec

Title: US-08-981-824-6

Sequence: 99
1 TYEIAVFEVLEVTLLKMR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_Archaea:*
- 2: sp_Bacteria:*
- 3: sp_Fungi:*
- 4: sp_Human:*
- 5: sp_Invertebrate:*
- 6: sp_Mammal:*
- 7: sp_Mhc:*
- 8: sp_Organelle:*
- 9: sp_Phage:*
- 10: sp_Plant:*
- 11: sp_Rodent:*
- 12: sp_Virus:*
- 13: sp_Vertebrate:*
- 14: sp_Unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29.3	19	2	Q9S625	Q9S625 prochloroto
2	29.3	23	2	Q9S630	Q9S630 prochloroto
3	27.3	18	8	Q9ZYW9	Q9ZYW9 agathidella
4	27.3	23	11	Q63334	Q63334 rattus norv
5	26.3	19	2	Q9X3F0	Q9X3F0 prochloroto
6	26.3	25	11	Q63992	Q63992 rattus norv
7	25.3	18	6	Q9TOR9	Q9TOR9 mamuthus p
8	25.3	18	8	Q9ZYV8	Q9ZYV8 aspiiota sp
9	25.3	19	8	Q9ZYV7	Q9ZYV7 myrmecia fo
10	25.3	22	12	Q34195	Q34195 ehrlichia r
11	25.3	25	1	Q9QP62	Q9QP62 hepatitis c
12	24.2	15	10	Q9UWH4	Q9UWH4 pyrococcus
13	24.2	18	7	Q9SK87	Q9SK87 copitis japo
14	24.2	18	12	Q9TNP1	Q9TNP1 mus sp. mhc
15	24.2	22	8	Q41588	Q41588 human immun
16	24.2	22	8	Q99389	Q99389 ovis aries
17	24.2	24	4	Q9N267	Q9N267 homo sapien
18	24.2	24	4	Q13660	Q13660 homo sapien
19	24.2	25	2	Q9RLN0	Q9RLN0 neisseria m

20	24	24.2	25	8	Q9MQK4	Q9MQK4 rupicepra r
21	23.5	23.7	24	6	Q28200	Q28200 bos taurus
22	23	23.2	18	2	Q50076	Q50076 mycobacteri
23	23	23.2	18	8	Q9ZYX0	Q9ZYX0 blacus sp.
24	23	23.2	25	11	Q9JX04	Q9JX04 mus musculu
25	22.5	22.7	15	2	Q9R022	Q9R022 salmoneilla
26	22	22.2	12	8	Q9XNR6	Q9XNR6 pylaella 1
27	22	22.2	18	12	Q87589	Q87589 chimpanzee
28	22	22.2	18	12	Q87591	Q87591 chimpanzee
29	22	22.2	18	12	Q87593	Q87593 chimpanzee
30	22	22.2	19	5	Q20438	Q20438 caenorhabdi
31	22	22.2	19	8	Q9ZYX2	Q9ZYX2 centistes s
32	22	22.2	19	8	Q9ZYX3	Q9ZYX3 micropylitis
33	22	22.2	19	10	Q9S8E9	Q9S8E9 zea mays (m
34	22	22.2	20	11	Q9R5D0	Q9R5D0 pseudomonas
35	22	22.2	20	13	Q9OV83	Q9OV83 rattus sp.
36	22	22.2	20	13	Q9RFP2	Q9RFP2 gallus gall
37	22	22.2	22	5	P82108	P82108 mythima un
38	22	22.2	22	7	Q9MX47	Q9MX47 oryzias lat
39	22	22.2	22	13	Q9PS00	Q9PS00 micropogon
40	22	22.2	23	4	Q16137	Q16137 homo sapien
41	22	22.2	24	8	Q9MQK1	Q9MQK1 capra ibex
42	22	22.2	25	5	Q94680	Q94680 polyandroca
43	22	22.2	25	8	Q9ZYX1	Q9ZYX1 dlooplus s
44	21.7	21.7	25	4	Q16092	Q16092 homo sapien
45	21	21.2	11	2	Q9R5R4	Q9R5R4 mycoplasma

ALIGNMENTS

RESULT 1	Q9S625	PRELIMINARY;	PRT;	19 AA.
ID	Q9S625			
AC	Q9S625			
DT	01-MAY-2000 (TREMUREL. 13, Created)			
DT	01-MAY-2000 (TREMUREL. 13, Last sequence update)			
DT	01-MAY-2000 (TREMUREL. 13, Last annotation update)			
DE	CYTOCHROME B (FRAGMENT).			
GN	PETB.			
OS	Prochlorococcus sp.			
OC	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;			
OC	Prochlorococcus.			
OX	NCBI_TaxID=1220;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Urbach E., Chisholm S.W.;			
RT	"Genetic diversity in Prochlorococcus populations flow cytometrically			
RT	sorted from the Sargasso Sea and Gulf Stream.";			
RL	Limnol. Oceanogr. 43:1615-1630(1998).			
DR	EMBL; AF070177; AAD20793.1; -			
FT	NON TER			
FT	1			
SO	SEQUENCE	19 AA;	2207 MW;	63744292AB2D51B4 CRC64;
Query Match	29.3%;	Score 29;	DB 2;	Length 19;
Best local Similarity	33.3%;	Pred. No. 3.6e+02;		
Matches	4;	Conservative	6;	Mismatches 2;
				Indels 0;
				Gaps 0;
QY	7 VFVLEVTLLK 18			
DB	1 VFVLEVTLLK 12			
RESULT 2	Q9S630	PRELIMINARY;	PRT;	23 AA.
ID	Q9S630			
AC	Q9S630			
DT	01-MAY-2000 (TREMUREL. 13, Created)			
DT	01-MAY-2000 (TREMUREL. 13, Last sequence update)			
DT	01-MAY-2000 (TREMUREL. 13, Last annotation update)			
DE	CYTOCHROME B (FRAGMENT).			
GN	PETB.			

OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OC NCBI_TaxID=1220;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Urdach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 sorted from the Sargasso Sea and Gulf Stream."
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL: AF070199; AAD23242.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 23 AA; 2720 MW; 1474425C2B9CEE6 CRC64;

Query Match 29.3%; Score 29; DB 2; Length 23;
 Best Local Similarity 33.3%; Pred. No. 4.3e+02;
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 7 VFVLEVTYTLKK 18
 DB 5 VFVLMHFLMIRK 16

RESULT 3
 ID O92YW9 PRELIMINARY; PRT; 18 AA.
 AC O92YW9;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE CYTOCHROME OXIDASE II (FRAGMENT).
 OS Agathella sp.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Ichneumonidae; Braconidae; Agathidinae; Agathella.
 OC NCBI_TaxID=64848;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99152621; PubMed=10028295;
 RA Dowson M., Austin A.D.;
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
 the Hymenoptera."
 RL Mol. Biol. Evol. 16:298-309(1999).
 DR EMBL: AF034592; AAC79740.1; -.
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 18 AA; 2238 MW; FAB24589081FCCD6 CRC64;

Query Match 27.3%; Score 27; DB 8; Length 18;
 Best Local Similarity 50.0%; Pred. No. 7.3e+02;
 Matches 5; Conservative 3; Mismatches -2; Indels 0; Gaps 0;

OY 9 VLEVTYTLKK 18
 DB 1 IVLESTELKK 10

RESULT 4
 ID O63334 PRELIMINARY; PRT; 23 AA.
 AC O63334;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ALPRA-2-MACROGLOBULIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RX [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR;
 RX MEDLINE=85207604; PubMed=2581948;
 RA Northmann W., Heisig M., Kunz D., Heinrich P.C.;
 RT "Molecular cloning of cDNA sequences for rat alpha 2-macroglobulin and
 measurement of its transcription during experimental inflammation."
 RL J. Biol. Chem. 260:6200-6205(1985).
 DR EMBL: M84369; AAA41594.1; -.
 DR INTERPRO: IPR001599; -.
 DR PFM: PF00207; A2M; 1.
 FT NON_TER 1 1
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2526 MW; E2D721FB1B223876 CRC64;

Query Match 27.3%; Score 27; DB 11; Length 23;
 Best Local Similarity 62.5%; Pred. No. 9.4e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 FVLEVTY 15
 DB 8 YVLAAYLT 15

RESULT 5
 ID O9X3F0 PRELIMINARY; PRT; 19 AA.
 AC O9X3F0;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN PETB.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OC NCBI_TaxID=1220;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Urdach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 sorted from the Sargasso Sea and Gulf Stream."
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL: AF070148; AAD20767.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 19 AA; 2247 MW; 4E744292BAD51A3 CRC64;

Query Match 26.3%; Score 26; DB 2; Length 19;
 Best Local Similarity 25.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 7 VFVLEVTYTLKK 18
 DB 1 VFVLMHFLMIRK 12

RESULT 6
 ID O63992 PRELIMINARY; PRT; 25 AA.
 AC O63992;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HOX3.2 HOMEOBOX HOMOLOG (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94271262; PubMed=7911662;
 RA Imura T., Oida S., Takeda K., Maruoka Y., Sasaki S.;

RT "Changes in homeobox-containing gene expression during ectopic bone formation induced by bone morphogenetic protein."
 RL Biochem. Biophys. Res. Commun. 201:980-987(1994).
 DR EMBL: S71317; AAB31008.1; -
 DR HSSP: P02833; 9ANT.
 DR INTERPRO: IPR001356; -
 DR PIRAM: PFO0046; homeobox; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 FT NON_TER 1
 SQ SEQUENCE 25 AA; 3157 MW; 42CAF3D514AD2304 CRC64;

Query Match 26.3%; Score 26; DB 11; Length 25;
 Best Local Similarity 54.5%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 YEAPVFLVLE 12
 DB 12 YEVARVNLNTE 22

RESULT 7
 ID 09TOR9 PRELIMINARY; PRT; 18 AA.
 AC 09TOR9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE VON WILLEBRAND FACTOR (FRAGMENT).
 OS Mammuthus primigenius (Siberian woolly mammoth).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Proboscidea; Elephantidae; Mammuthus.
 OX NCBI_TaxID=37349;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022977; PubMed=10555277;
 RA Greenwood A.D.; Capelli C.; Posenert G.; Paabo S.;
 RT "Nuclear DNA sequences from late Pleistocene megafauna."
 RL Mol. Biol. Evol. 16:1466-1473(1999).
 DR EMBL: AF154874; AAF12750.1; -
 DR EMBL: AF154873; AAF12749.1; -
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1914 MW; DFCB484B41F69236 CRC64;

Query Match 25.3%; Score 25; DB 6; Length 18;
 Best Local Similarity 60.0%; Pred. No. 1.6e+03;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 APVFLLEV 14
 DB 1 APVSVTPV 10

RESULT 8
 ID 09ZYV8 PRELIMINARY; PRT; 18 AA.
 AC 09ZYV8;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE CYTOCHROME OXIDASE II (FRAGMENT).
 OS Aspiota sp.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Ichneumonidae; Braconidae; Alysiinae; Aspilota.
 OX NCBI_TaxID=61200;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99152621; PubMed=10028295;

RA Dowton M., Austin A.D.;
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in the Hymenoptera."
 RL Mol. Biol. Evol. 16:298-309(1999).
 DR EMBL: AF034603; AAC79751.1; -
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 18 AA; 2181 MW; F83846FDAE8BDCD6 CRC64;

Query Match 25.3%; Score 25; DB 8; Length 18;
 Best Local Similarity 55.6%; Pred. No. 1.6e+03;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 9 VLEEVYTLK 17
 DB 1 IVLESVSLK 9

RESULT 9
 ID 09ZYV7 PRELIMINARY; PRT; 19 AA.
 AC 09ZYV7;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE CYTOCHROME OXIDASE II (FRAGMENT).
 OS Myrmica forficata.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata;
 OC Formicoidae; Formicidae; Myrmecia.
 OX NCBI_TaxID=32387;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99152621; PubMed=10028295;
 RA Dowton M., Austin A.D.;
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in the Hymenoptera."
 RL Mol. Biol. Evol. 16:298-309(1999).
 DR EMBL: AF034604; AAC79752.1; -
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2370 MW; 25AE99B2B1F53EB6 CRC64;

Query Match 25.3%; Score 25; DB 8; Length 19;
 Best Local Similarity 33.3%; Pred. No. 1.7e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 9 VLEEVYTLK 17
 DB 1 IVLEVYTNK 9

RESULT 10
 ID 034195 PRELIMINARY; PRT; 22 AA.
 AC 034195;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE GROES. (FRAGMENT).
 GN GROES.
 OS Ehrlichia risticii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Ehrlichieae; Ehrlichia.
 OX NCBI_TaxID=950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97373904; PubMed=9230387;
 RA Sumner J.W., Nicholson W.L., Massung R.F.;
 RT "PCR amplification and comparison of nucleotide sequences from the

RT groESL heat shock operon of *Escherichia* species."
 RL J. Clin. Microbiol. 35:2087-2092(1997).
 DR EMBL: U96732; AAB5632.1;
 DR INTERPRO: IPR001476;
 DR PIRAM; PF00166; cpn10; 1.
 FT NON_TER
 SO SEQUENCE 22 AA; 2504 MW; 21D959D75191F620 CRC64;

Query Match 25.3%; Score 25; DB 2; Length 22;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 11 LEVYTLKK 18
 :||| :||
 Db 5 VEYVWKE 12

RESULT 11
 O90P62 PRELIMINARY; PRT; 25 AA.
 AC O90P62;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE TRUNCATED NS2.
 DE Hepatitis C virus.
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Leng Y., Chen X.Z., Du Y., Wang H.T.;
 RT "Cloning of NS2 cDNA of Hepatitis C virus (HCV) and complexity of NS2
 RT quasispecies in a HCV carrier."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF175472; AAD50790.1;
 SO SEQUENCE 25 AA; 2637 MW; 5684D08FA4DAC202 CRC64;

Query Match 25.3%; Score 25; DB 12; Length 25;
 Best Local Similarity 60.0%; Pred. No. 2.2e+03;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 7 VFVLELVYTL 16
 :||| :||
 Db 13 VEVGLVFLL 22

RESULT 12
 O90WH4 PRELIMINARY; PRT; 15 AA.
 AC O90WH4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE KETO-VALINE-TEREDOXIN OXIDOREDUCTASE ALPHA-SUBUNIT, VOR ALPHA
 DE (FRAGMENT).
 OS Pyrococcus.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae.
 OX NCBI_TaxID=2260;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE-96146528; PubMed-8550513;
 RA Heider J., Mai X., Adams M.W.;
 RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a
 RT new and reversible coenzyme A-dependent enzyme involved in peptide
 RT fermentation by hyperthermophilic archaea."
 RL J. Bacteriol. 178:780-787(1996).
 SO SEQUENCE 15 AA; 1727 MW; 42363C008C9A9CFA CRC64;

Query Match 24.2%; Score 24; DB 1; Length 15;

Best Local Similarity 44.4%; Pred. No. 1.9e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Oy 11 LEVYTLKK 19
 :||| :||
 Db 1 MEYKPIKV 9

RESULT 13
 O9S8K7 PRELIMINARY; PRT; 15 AA.
 AC O9S8K7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE S-ADENOSYL-L-METHIONINE:NORCOCLAURINE 6-O-METHYLTRANSFERASE,
 DE NORCOCLAURINE 6-O-METHYLTRANSFERASE (EC 2.1.1.-) (FRAGMENT).
 OS Coplis japonica (Japanese goldthread).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; Ranunculales; Ranunculaceae; Coplis.
 OX NCBI_TaxID=3442;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE-95010097; PubMed-7925429;
 RA Sato F., Tsujita T., Katagiri Y., Yoshida S., Yamada Y.;
 RT "Purification and characterization of S-adenosyl-L-methionine:
 RT norcochlorine 6-O-methyltransferase from cultured Coplis japonica
 RT cells."
 RL Eur. J. Biochem. 225:125-131(1994).
 SO SEQUENCE 15 AA; 1595 MW; 8762BC05939B6C4C CRC64;

Query Match 24.2%; Score 24; DB 10; Length 15;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 YEIAVVFVLL 11
 :||| :||
 Db 1 YALXPFIATLL 10

RESULT 14
 O9TNP1 PRELIMINARY; PRT; 18 AA.
 AC O9TNP1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE MHC CLASS II H 2EK NATURAL LIGAND (FRAGMENT).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE-96360157; PubMed-8746565;
 RA Schild H., Grunberg U., Pougialis G., Wallny H.J., Kellholz W.,
 RA Stevanovic S., Rammensee H.G.;
 RT "Natural ligand motifs of H-2E molecules are allele specific and
 RT illustrate homology to HLA-DR molecules."
 RL Int. Immunol. 7:1957-1965(1995).
 SO SEQUENCE 18 AA; 1997 MW; A0FD2CD387023F46 CRC64;

Query Match 24.2%; Score 24; DB 7; Length 18;
 Best Local Similarity 71.4%; Pred. No. 2.3e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 12 EYVTLKK 18
 :||| :||
 Db 3 EFGTLKK 9

Query Match 24.2%; Score 24; DB 1; Length 15;

RESULT 15
 ID 041588 PRELIMINARY; PRT; 18 AA.
 AC 041588;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PC13;
 RX MEDLINE-98105804; PubMed-9445059;
 RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
 Walker B.D., Neumann A.U., Vermund S.H., Westceky J., Jackson S.,
 Fendmore E., Cao Y., Gao F., Kalam S., Kunstman K.J., McDonald D.,
 McWilliams N., Tirkola A., Moore J.P., Wolinsky S.M.;
 RT Immunodeficiency and virological analyses of persons infected by human
 immunodeficiency virus type 1 while participating in trials of
 recombinant gp120 subunit vaccines.";
 RL J. VIROL. 72:1552-1576(1998).
 DR EMBL: U84837; AAC5876.1; -.
 DR INTERPRO: IPR000777; -.
 DR PFAM: PF00516; GP120; 1.
 DR Envelope protein.
 FT NON_TER
 SQ SEQUENCE 18 AA; 2050 MW; 656402F80913D46E CRC64;

Query Match 24.2%; Score 24; DB 12; Length 18;
 Best Local Similarity 36.4%; Pred. No. 2.3e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 EIAPEVLEY 13
 : : : : :
 DB 5 KLPPLCVTLKY 15

RESULT 16
 ID 099389 PRELIMINARY; PRT; 22 AA.
 AC 099389;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE ATPASE SUBUNIT 6 (FRAGMENT).
 OS Ovis aries (Sheep).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RX MEDLINE-98403943; PubMed-9734874;
 RA Tartaglia M., Saulle E.;
 RT "Rapid communication: nucleotide sequence of porcine and ovine
 rRNA(Lys) and ATPase mitochondrial genes.";
 RL J. Anim. Sci. 76:2207-2208(1998).
 DR EMBL: AF039171; AAD05068.1; -.
 DR Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 22 AA; 2453 MW; 215F87BDF0E8A1C8 CRC64;

Query Match 24.2%; Score 24; DB 8; Length 22;
 Best Local Similarity 46.2%; Pred. No. 2.8e+03;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 IAPFVLEYVTL 16
 : : : : :
 DB 10 ITPMMLGLPVTL 22
 RESULT 17
 ID 09N267 PRELIMINARY; PRT; 23 AA.
 AC 09N267;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ATP7B (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu Z.Y., Wang N., Murong S.X.;
 RT "Missense mutations of exons 14 and 18 of Wilson's disease gene in
 Chinese patients.";
 RL Chung-Hua I Hsueh I Chuan Hsueh Tsa Chih 16:91-93(1999).
 DR EMBL: AF218354; AAF25685.1; -.
 FT NON_TER
 FT VARIANT 9 9 P -> R.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2483 MW; 23CF54F1868B5DOB CRC64;

Query Match 24.2%; Score 24; DB 4; Length 23;
 Best Local Similarity 38.5%; Pred. No. 3e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 4 IAPFVLEYVTL 16
 : : : : :
 DB 7 VMPVLLGDVATL 19

RESULT 18
 ID 013660 PRELIMINARY; PRT; 24 AA.
 AC 013660;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
 DE MANNOSE 6-PHOSPHATE/INSULIN-LIKE GROWTH FACTOR-II RECEPTOR
 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96083596; PubMed-7493029;
 RA De Souza A.T., Hankins G.R., Washington M.K., Otton T.C., Jittle R.L.;
 RT "M6P/IGF2R gene is mutated in human hepatocellular carcinomas with
 loss of heterozygosity.";
 RL Nat. Genet. 11:447-449(1995).
 DR EMBL: S80763; AAB35664.1; -.
 FT NON_TER
 SQ SEQUENCE 24 AA; 2799 MW; E6F28C7F43E17602 CRC64;

Query Match 24.2%; Score 24; DB 4; Length 24;
 Best Local Similarity 50.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 7 VFVLEYV 14
 : : : : :
 DB 6 VIVLVKY 13

RESULT 19

09RLNO PRELIMINARY: PRT: 25 AA.
 AC 09RLNO:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE PORR. PROTEIN (FRAGMENT).
 GN PORR.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=36/93;
 RA Wedge E., Gaugant D.A., Musacchio A., Saunders N.B., Zollinger W.D.,
 "Redesignation of a purported P1.15 subtype-specific meningococcal
 monoclonal antibody as a P1.19-specific reagent."
 RT Clin. Diagn. Lab. Immunol. 6:639-642(1999).
 RL EMBL; AJ012726; CAA10149.1; -
 DR EMBL; AJ012726; CAA10149.1; -
 FT NON-TER 1 1
 FT SEQUENCE 25 AA: 2480 MW: 3AD7F47D1C4D8378 CRC64;

Query Match 24.2%; Score 24; DB 2; Length 25;
 Best Local Similarity 35.7%; Pred. No. 3.2e+03;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 6 PVFVLELYVTLLK 19
 DB 7 PAYVAENGVAR 20

RESULT 20

09MOK4 PRELIMINARY: PRT: 25 AA.
 AC 09MOK4:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ATPASE SUBUNIT 6 (FRAGMENT).
 OS Ruplicapra rupicapra.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Rupicapra.
 OX NCBI_TaxID=34869;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PERIPHERAL BLOOD;
 RA MEDLINE=20104876; PubMed=10641890;
 RA Saille E., Di Pasquale S., Tartaglia M.,
 "Rapid identification: nucleotide sequence of chamois, alpine ibex, and
 red deer tRNA(Lys) and Arpase8 mitochondrial genes."
 RT J. Anim. Sci. 77:3398-3399(1999).
 RL EMBL; AF104681; AAF43479.1; -
 DR EMBL; AF104681; AAF43479.1; -
 KW Mitochondrion.
 FT NON-TER 25
 FT SEQUENCE 25 AA: 2778 MW: 6FFDC915FF87BDF CRC64;

Query Match 24.2%; Score 24; DB 8; Length 25;
 Best Local Similarity 46.2%; Pred. No. 3.2e+03;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 4 IAPFVLELYVTLL 16
 DB 10 ITPMMLGPLEVTLL 22

RESULT 21

Q28200 PRELIMINARY: PRT: 24 AA.
 AC Q28200:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
 DE TYROSINASE-RELATED PROTEIN-1 (FRAGMENT).
 GN TRP-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96314791; PubMed=8759137;
 RA Noneman D., Shubuya H., Johnson G.S.;
 "A BstUI PCR/RFLP in the bovine tyrosinase-related protein-1 (TYRPI)
 gene."
 RT Anim. Genet. 27:218-219(1996).
 RL EMBL; L43123; AAB38537.1; -
 DR EMBL; L43123; AAB38537.1; -
 FT NON-TER 1 1
 FT SEQUENCE 24 AA: 2719 MW: C72B279D86390579 CRC64;

Query Match 23.7%; Score 23.5; DB 6; Length 24;
 Best Local Similarity 42.1%; Pred. No. 3.8e+03;
 Matches 8; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

OY 1 TYEI---APFVLELYVTLL 16
 DB 5 TYEIQWPSRSFSISGVYI 23

RESULT 22

050076 PRELIMINARY: PRT: 18 AA.
 AC 050076:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE u1400.
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Robison K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U15183; AAA63011.1; -
 SO SEQUENCE 18 AA: 2183 MW: 951B7CD608037D00 CRC64;

Query Match 23.2%; Score 23; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 VFVLELYVTLL 16
 DB 2 VFELYEHTSL 11

RESULT 23

Q92YX0 PRELIMINARY: PRT: 18 AA.
 AC Q92YX0:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)

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DT 01-MAY-1999 (Tremblrel. 10, last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, last annotation update)
DE CYTOCHROME OXIDASE II (FRAGMENT).
OS Blacus sp.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Ichneumonidae; Braconidae; Blacinae; Blacus.
OX NCBI_Taxid=64854;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
the Hymenoptera."
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF034591; AAC79739.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2269 MW; E826148E78157286 CRC64;

Query Match 23.2%; Score 23; DB 8; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 VLEEVTLKK 18
   :|:|:|:
DB 1 IVLEVIELNK 10

RESULT 24
Q9JK04 PRELIMINARY; PRT; 25 AA.
AC Q9JK04;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
DE FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (FRAGMENT).
GN FBPA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
fructose-1,6-bisphosphatase genes."
RL Gene 247:241-253(2000).
DR EMBL; AJ243025; CAB90672.1; -.
KW Hydrolyase.
FT NON_TER 1
FT NON_TER 25
SQ SEQUENCE 25 AA; 2898 MW; E4A7A6F50F3A31D3 CRC64;

Query Match 23.2%; Score 23; DB 11; Length 25;
Best Local Similarity 71.4%; Pred. No. 4.7e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 EYVTLKK 18
   |||
DB 16 EYVOKKK 22

RESULT 25
Q9RQ22 PRELIMINARY; PRT; 15 AA.
AC Q9RQ22;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, last annotation update)

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DE FERRIC HYDROXAMATE UPTAKE PROTEIN (FRAGMENT).
GN FHUB.
OS Salmonella typh.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_Taxid=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ISP1820;
RA Morrow B.J., Graham J.E., Curtiss R. III.;
RT "genomic subtractive hybridization and selective capture of
transcribed sequences identify a novel Salmonella typhimurium fimbrial
operon and putative transcriptional regulator that are absent from the
RT Salmonella typh genome."
RL Infect. Immun. 67:5106-5116(1999).
DR EMBL; AF134977; AAD54116.1; -.
KW Non-terminator.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1825 MW; 036E36EB6455E616 CRC64;

Query Match 22.7%; Score 22.5; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 3.4e+03;
Matches 6; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 5 APVFLLEVYTLKKMR 20
   |||:|:|:|:|:|
DB 3 APYFI---YLLRKQSR 15

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Search completed: February 5, 2001, 10:55:28
 Job time: 917 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:56:02 ; Search time 32.57 Seconds
(without alignments)
19.831 Million cell updates/sec

Title: US-08-981-824-6

Sequence: 1 TTEIAPVFLVEYTLTKMR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1436

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	22.2	6	1 CIP2_MYTED	P13737 mytilus edu
2	21	21.2	6	1 YCX8_ODOSI	P49834 odontella s
3	20.5	20.7	22	1 MORTI_CANFA	P19863 canis fam1
4	20	20.2	13	1 UC20_MAIZE	P80626 zea mays (m
5	20	20.2	19	1 MIFR_TRISP	P81529 trichinella
6	20	20.2	20	1 AMP_FUSNU	P81207 fusobacteri
7	20	20.2	23	1 MDH_THEAL	P33163 thermoleoph
8	19.5	19.7	16	1 PSAI_SPIOL	P17230 spinacia ol
9	19.5	19.7	25	1 PA22_BOTSC	P80963 botrytis chis
10	19	19.2	6	1 CIP1_MYTED	P13736 mytilus edu
11	19	19.2	14	1 ULA4_HUMAN	P30039 homo sapien
12	19	19.2	14	1 UNO4_CLOPA	P81349 clostridium
13	19	19.2	20	1 MIF_PIG	P80928 sus scrofa
14	19	19.2	20	1 SUCE_CANFA	P99507 canis fam1
15	19	19.2	22	1 NUO7_SOLUTU	P80730 solanum tub
16	19	19.2	22	1 VGL6_RABVA	P15199 tables viru
17	19	19.2	25	1 ATPX_SOLUTU	P80497 solanum tub
18	18.5	18.7	13	1 PSAJ_PEA	P17229 pisum sativ
19	18.5	18.7	19	1 CH10_CLOPA	P81338 clostridium
20	18	18.2	11	1 NIFS_BRAJA	P37030 bradyrhizob
21	18	18.2	15	1 MIFR_ONCKE	P81037 oncorhynchu
22	18	18.2	15	1 UC17_MAIZE	P80623 zea mays (m
23	18	18.2	18	1 ALI2_CYDPO	P82153 cydia pomon
24	18	18.2	20	1 AROQ_AMEME	P46380 amycolatops
25	18	18.2	20	1 CPXK_RHORI	P31718 rhodococcus
26	18	18.2	20	1 GTS2_ASCSU	P48429 ascaris sun
27	18	18.2	21	1 DCMS_PSECA	P19931 pseudomonas
28	18	18.2	24	1 CR17_LITXA	P56232 illorria xan
29	18	18.2	25	1 COX6_NEDCR	P001359 neurospora
30	18	18.2	25	1 FRHB_METBA	P80490 methanosarc
31	18	18.2	25	1 SMRB_RAT	P80968 rattus norv
32	17.5	17.7	21	1 CH1C_PEA	P31233 pisum sativ
33	17.5	17.7	22	1 IAD1_ENTFA	P24803 enterococcu

34	17.5	17.7	24	1 THD2_SALTY	P11954 salmonella
35	17	17.2	10	1 TMOF_AEDAE	P19425 aedes aegypt
36	17	17.2	12	1 TM2A_METMA	P80652 methanosarc
37	17	17.2	13	1 ODPK_CANFA	P49823 canis fam1
38	17	17.2	14	1 LPW_ECOLI	P03053 escherichia
39	17	17.2	15	1 ACRA_ACTICA	P28467 acinetobact
40	17	17.2	15	1 KLOM_LUMTE	P1918 lumbricus t
41	17	17.2	15	1 UC14_MAIZE	P80620 zea mays (m
42	17	17.2	15	1 UC19_MAIZE	P80625 zea mays (m
43	17	17.2	16	1 PGTL_PELAC	P80563 pelobacter
44	17	17.2	16	1 UPAB_HUMAN	P31935 homo sapien
45	17	17.2	17	1 APID_BOMPA	P81464 bombus pasc

ALIGNMENTS

RESULT 1
CIP2_MYTED STANDARD; PRT; 6 AA.
ID CIP2_MYTED
AC P13737;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CONTRACTION-INHIBITING PEPTIDE II (MIP II).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytilidae; Mytilinae; Mytilus.
RN [1]
RP SEQUENCE.
RC TISSUE-PEDAL GANGLION;
RX MEDLINE-88240357; PubMed-3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -1- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
CC MUSCLES.
CC -1- SIMILARITY: TO MIP I.
CC PIR: B27696; B27696.
DR PIR: B27696; B27696.
KW Hormone; Amidation.
FT MOD RES
SQ SEQUENCE 6 AA: 621 MW: 72C9C6876D81000 CRC64;
AMIDATION

Query Match 22.2%; Score 22; DB 1; Length 6;
Best local Similarity 80.0%; Pred. No. 8.9e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 APYFV 9
11:11

Db 2 APMFV 6

RESULT 2
YCX8_ODOSI STANDARD; PRT; 25 AA.
ID YCX8_ODOSI
AC P49834;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 3.1 KDA PROTEIN IN PSBJ-TRE INTERGENIC REGION (ORF25).
OS Odontella sinensis.
OC Chloroplast.
OC Eukaryota; streptophytes; Bacillariophyta; Coscinodiscophyceae;
OC Eukaryota; streptophytes; Bacillariophyta; Eupodiscaceae; Odontella.
RN [1]
RP SEQUENCE FROM N.A.
RA Kowalik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freter U.;
RT "The chloroplast genome of a chlorophyll a+c-containing alga,
Odontella sinensis.";
RL Plant Mol. Biol. Rep. 13:336-342(1995).
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 CC -----
 DR EMBL: 267753; CAA91716.1; -
 KM Chloroplast; Hypothetical protein.
 SQ SEQUENCE 25 AA; 3083 MW; 9F50BB79484EAS31 CRC64;

Query Match 21.2%; Score 21; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 1.8e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 7 VFVLEVTYTK 17
 DB 1 MFEISFYIALK 11

RESULT 3
 MOTI_CANFA STANDARD; PRT; 22 AA.
 AC P19863:
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE MOTILIN.
 GN MLN.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=INTESTINE; PubMed=6844663;
 RX MEDLINE=83195948; PubMed=6844663;
 RA Poltras P., Reeve J.R., Jr., Hunziker M.W., Hood L.E., Walsh J.H.,
 RT "Purification and characterization of canine intestinal motilin.";
 RL Regul. Pept. 5:197-208(1983).
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
 CC INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
 CC RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC PIR: S00189; S00189.
 DR PIR: A60313; A60313.
 KM Hormone.
 FT UNSURE
 SQ SEQUENCE 22 AA; 2685 MW; 4BECB840ABE0639F CRC64;

Query Match 20.7%; Score 20.5; DB 1; Length 22;
 Best Local Similarity 40.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

OY 6 PVFVLEVTYTKMR 20
 DB 3 PFTFSE--LOKIR 14

RESULT 4
 UC20_MAIZE STANDARD; PRT; 15 AA.
 AC P80626:
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 445)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

RN [1]
 RP SEQUENCE.
 RC TISSUE=COLEOPTILE;
 RA Touret P., Roccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Perrollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
 CC PROTEIN IS: 6.1, ITS MW IS: 45.3 KDA.
 CC -1- SIMILARITY: TO ADOMET SYNTHETASES.
 DR MAIZE-2DPAGE:P80626; COLEOPTILE.
 DR MAIZE2B: 123952; -
 FT NON_TER
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1597 MW; D2EECE163EB10156 CRC64;

Query Match 20.2%; Score 20; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.6e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 VLEEVY 14
 DB 3 VVVEVY 8

RESULT 5
 MIFH_TRISP STANDARD; PRT; 19 AA.
 AC P81529:
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE L-DOPACHROME-METHYL ESTER TAUOMERASE (MACROPHAGE MIGRATION INHIBITORY
 DE FACTOR HOMOLOG) (FRAGMENT).
 OS Trichinella spiralis.
 OC Eukaryota; Metazoa; Nematoda; Enopleae; Trichocephalida;
 OC Trichocephalina; Trichinelloidea; Trichinelidae; Trichinella.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=99013685; PubMed=9794786;
 RA Pennock J.L., Behnke J.M., Blockle O.D., Devaney E., Grencis R.K.,
 RA Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;
 RT "Rapid purification and characterization of L-dopamine-methyl ester
 RT tauomerase (macrophage migration inhibitory factor) from Trichinella
 RT spiralis, Trichinella muris and Brugia pahangi".
 RL Biochem. J. 335:495-498(1998).
 CC -1- FUNCTION: TAUOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.
 CC -1- INDUCTION: INHIBITED BY FREE FATTY ACIDS AND HAEMATIN.
 CC -1- SIMILARITY: BELONGS TO THE MIF FAMILY.
 CC INTERPRO: IPR001398; -
 DR PROSITE: PS01158; MIF; PARTIAL.
 DR Cyclokin.
 KM NON_TER
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2106 MW; F7CA05F112A628D CRC64;

Query Match 20.2%; Score 20; DB 1; Length 19;
 Best Local Similarity 60.0%; Pred. No. 2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 PVFVL 10
 DB 1 PIFVL 5

RESULT 6
 AMP_FUSNU STANDARD; PRT; 20 AA.
 AC P81207:
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE AMINOPEPTIDASE (EC 3.4.11.-) (AP) (FRAGMENT).
 OS Fusobacterium nucleatum.
 OC Bacteria; Fusobacteria; Fusobacterium.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-ATCC 10953;
 RX MEDLINE-98361026; PubMed-9695913;
 RA Rogers A.H., Gunadi A., Gully N.J., Zilm P.S.;
 RT "An aminopeptidase nutritionally important to Fusobacterium nucleatum." 144:1807-1813(1998).
 RL Microbiology 144:1807-1813(1998).
 CC -1- FUNCTION: CLEAVES A WIDE RANGE OF DIPEPTIDES AND TRIPEPTIDES.
 CC -1- COFACTOR: COBALT.
 CC -1- SUBCELLULAR LOCATION: CELL ENVELOPE-ASSOCIATED.
 KW Hydrolase; Aminopeptidase; Metalloprotease; Cobalt.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2585 MW; 97095B948262C71B CRC64;

Query Match 20.2%; Score 20; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 13 YVTLKK 18
 DB 6 YVDLKE 11

RESULT 7
 MDH_THEAL
 ID MDH_THEAL STANDARD; PRT; 23 AA.
 AC P33163;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37) (FRAGMENT).
 GN MDH.
 OS Thermoleophilum album.
 OC Bacteria; Green non-sulfur bacteria; Thermoleophilum.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-NM;
 RA Novotny J.F., Jr., Perry J.J.;
 RT "Characterization of the malate dehydrogenase from Thermoleophilum album NM.";
 RL Arch. Microbiol. 154:304-307(1990).
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALOACETATE + NADH.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 DR PIR: A60689; A60689.
 DR INTERPRO: IPR001252;
 DR PROSITE: PS00068; MDH; PARTIAL.
 KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2544 MW; 9848F8218EFAF125 CRC64;

Query Match 20.2%; Score 20; DB 1; Length 23;
 Best Local Similarity 60.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 11 LEVYT 15
 DB 17 IEXLT 21

RESULT 8
 PSAL_SPIOL
 ID PSAL_SPIOL STANDARD; PRT; 16 AA.
 AC P17230;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-I) (FRAGMENT).
 GN PSAL.
 OS Spinacia oleracea (Spinach).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales;
 OC Caryophyllales; Chenopodiaceae; Spinacia.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-90242987; PubMed-2185953;
 RA Ikeuchi M., Hirano A., Hiyama T., Inoue Y.;
 RT "Polypeptide composition of higher plant photosystem I complex. Identification of psal, psal and psal gene products." FEBS Lett. 263:274-278(1990).
 CC -1- FUNCTION: MAY HELP IN THE ORGANIZATION OF THE PSAL AND PSAL SUBUNITS.
 CC -1- SIMILARITY: BELONGS TO THE PSAL FAMILY.
 DR PIR: S09732; S09732.
 KW Chloroplast; Photosystem I; Photosynthesis; Transmembrane.
 FT TRANSMEM 6 >16
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1851 MW; A1B8DA6E26E7D110 CRC64;

Query Match 19.7%; Score 19.5; DB 1; Length 16;
 Best Local Similarity 62.5%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 1 TY-ETAPV 7
 DB 6 TYLSAVP 13

RESULT 9
 PA22_BOTSC
 ID PA22_BOTSC STANDARD; PRT; 25 AA.
 AC P80963;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PHOSPHOLIPASE A2 HOMOLOG. MYOTOXIN II (FRAGMENT).
 OS Bothriechis schlegelii (Eyelash viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Bothriechis.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-VENOM;
 RX MEDLINE-97209510; PubMed-9056257;
 RA Angulo Y., Chaves E., Alape A., Rucavado A., Gutierrez J.M., Lomonte B.;
 RT "Isolation and characterization of a myotoxic phospholipase A2 from the venom of the arboreal snake Bothriechis (Bothrops) schlegelii from Costa Rica.";
 RL Arch. Biochem. Biophys. 339:260-266(1997).
 CC -1- FUNCTION: THIS MYOTOXIC PROTEIN LACKS ENZYMATIC ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 DR HSSP: P24605; 1CLP.
 DR INTERPRO: IPR001211;
 DR PFAM: PF000068; phospholipase 1.
 DR PROSITE: PS00118; PA2_HIS; PARTIAL.
 DR PROSITE: PS00119; PA2_ASP; PARTIAL.
 KW Toxin; Venom; Multigene family.
 FT NON_TER 25 25
 SQ SEQUENCE 25 AA; 2725 MW; C578AB09235EA02A CRC64;

Query Match 19.7%; Score 19.5; DB 1; Length 25;
 Best Local Similarity 45.5%; Pred. No. 3.3e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

OY 2 YETAPVFLVE 12

Db 3 YEIGRM-ILLE 12

RESULT 10
CIP1_MYTED STANDARD: PRT: 6 AA.
ID CIP1_MYTED
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CONTRACTION-INHIBITING PEPTIDE I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytilioida;
OC Mytilioidae; Mytilidae; Mytilus.
RN [1]
RP SEQUENCE.
RC TISSUE-PEDAL GANGLION; MEDLINE-88240377; PubMed-3377776;
RX Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.,
RT "Structure and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -I- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
MUSCLES.
CC -I- SIMILARITY: TO MIP II.
DR PIR: A27696; A27696.
KW Hormone; Amidation.
FT MOD_RES
SQ SEQUENCE 6 AA: 637 MW: 72C9C68775B81000 CRC64;

Query Match 19.2%; Score 19; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 APVFEV 9
Db 2 SPWFV 6

RESULT 11
UUA4_HUMAN STANDARD: PRT: 14 AA.
ID UUA4_HUMAN
AC P30039;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 32) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE.
RC TISSUE-LIVER; MEDLINE-93162045; PubMed-1286669;
RX Hochstrasser D.F., Frutiger S., Paquet N., Batroch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargha R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.2, ITS MW IS: 28 KDA.
DR SWISS-2DPAGE; P30039; HUMAN.
FT NON_TER
SQ SEQUENCE 14 AA: 1614 MW: 0F96AC07E93295D0 CRC64;

Query Match 19.2%; Score 19; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 PVFV 9

Db 4 PIFI 7

RESULT 12
UN04_CLOPA STANDARD: PRT: 14 AA.
ID UN04_CLOPA
AC P81349;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE UNKNOWN PROTEIN CP 4 FROM 2D-PAGE (FRAGMENT).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN [1]
RP SEQUENCE.
RC STRAIN-W5; MEDLINE-96291870; PubMed-9629918;
RX Flengrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.7, ITS MW IS: 45.7 KDA.
DR NON_TER
FT NON_TER
SQ SEQUENCE 14 AA: 1608 MW: D424A7069460EBD2 CRC64;

Query Match 19.2%; Score 19; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 YEIAVFEV 9
Db 2 YEIXIVV 9

RESULT 13
MIF_PIG STANDARD: PRT: 20 AA.
ID MIF_PIG
AC P80928;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (GLYCOSYLATION-INHIBITING
DE FACTOR) (GIF) (FRAGMENT).
GN MIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
RN [1]
RP SEQUENCE.
RC RAVIERE S., Bouet F., Menez A., Galat A.;
RL Submitted (MAR-1997) to the SWISS-PROT data bank.
CC -I- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST
CC A ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE
CC IN HOST DEFENSE (BY SIMILARITY).
CC -I- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR HSSP: P14174; MIF.
DR INTERPRO: IPR001398;
DR PROSITE: PS01156; MIF; PARTIAL.
KW Macrophage; Inflammatory response; Cytokine.
FT NON_TER
SQ SEQUENCE 20 AA: 2147 MW: 3517AF60F3012A61 CRC64;

Query Match 19.2%; Score 19; DB 1; Length 20;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 PVFVL 10


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Db      1 PMFV 5

RESULT 14
SUBC_CANFA STANDARD; PRT; 20 AA.
AC P99507;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PUTATIVE SUCCINYL-COA LIGASE (GDP-FORMING) BETA-CHAIN (EC 6.2.1.4)
DE (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA) (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.
RC TISSUE=HEART;
RX MEDLINE=9816340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
  dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: SUCCINATE + COA + GTP -> SUCCINYL-COA + GDP +
  ORTHOPHOSPHATE.
CC -1- PATHWAY: SUBSTRATE LEVEL PHOSPHORYLATION STEP OF THE TRICARBOXYLIC
  ACID CYCLE.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER BETA SUBUNITS OF SUCCINYL-COA SYNTHETASE,
  OF MALATE-COA LIGASE AND TO ATP CITRATE-LYASE.
DR HSC-2DPAGE; P99507; DOG.
DR INTERPRO: IPR000303; -.
DR PROSITE: PS01217; SUCCINYL-COA LIG 3: PARTIAL.
KM Ligase: Glycolysis; Tricarboxylic acid cycle; Mitochondrion.
FT NON_TER 20
SQ SEQUENCE 20 AA: 2248 MW: 8846FD54BDC2E CRC64;

Query Match 19.2%; Score 19; DB 1; Length 20;
Best Local Similarity 27.3%; Pred. No. 3.2e+03;
Matches 3; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 10 LLEVYTKMR 20
Db 3 LHEYMSMLQ 13

RESULT 15
NUOT_SOLTV STANDARD; PRT; 22 AA.
AC P80730;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE 16 KDA SUBUNIT (EC 1.6.5.3)
DE (EC 1.6.99.3) (COMPLEX I-16KD) (CI-16KD) (FRAGMENT).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
RN [1]
RP SEQUENCE.
RC STRAIN=CV. BINTJE; TISSUE=TUBER;
RA Herz U., Grohmann L.;
RT Submitted (DEC-1996) to the SWISS-PROT data bank.
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
  CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
  TO BE UBIQUINONE.
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
CC -1- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER

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CC MEMBRANE.
KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
FT NON_TER 22
SQ SEQUENCE 22 AA: 2435 MW: D4D64C57673C2613 CRC64;

Query Match 19.2%; Score 19; DB 1; Length 22;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 VTIKRM 19
Db 16 VYIKRM 21

RESULT 16
VGLG_RABVA STANDARD; PRT; 22 AA.
ID VGLG_RABVA
AC P15199;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE SPIKE GLYCOPROTEIN PRECURSOR (FRAGMENT).
GN GN
OS Rabies virus (strain AV01).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89150295; PubMed=147698;
RA Poch O., Torzo N., Keith G.;
RT "Sequence of the 3386 3' nucleotides of the genome of the AV01 strain
  rabies virus: structural similarities in the protein regions involved
  in transcription."
RL Biochimie 70:1019-1029(1988).
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CC -----
DR EMBL: X13357; CA31737.1; -.
DR PIR: S07817; S07817.
KM Transmembrane; Envelope protein; Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 20
FT NON_TER 22
SQ SEQUENCE 22 AA: 2469 MW: BBA59CE12F3EE85 CRC64;

Query Match 19.2%; Score 19; DB 1; Length 22;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEVLL 11
Db 7 LEVLL 11

RESULT 17
ATPY_SOLTV STANDARD; PRT; 25 AA.
ID ATRY_SOLTV
AC P80497;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ATP SYNTHASE 6 KDA SUBUNIT, MITOCHONDRIAL (EC 3.6.1.34) (FRAGMENT).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;

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OC Solanales; Solanaceae; Solanum.
RN [1]
RP SEQUENCE.
RC TISSUE=TUBER;
RX MEDLINE=97077345; PubMed=8919912;
RA Jansch L., Krull V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
of the protein complexes of plant mitochondria.";
RL Plant J. 9:357-368(1996).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC
COMPONENT (CF10) SUBUNIT OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
KW CF(0); Hydrogen ion transport; Mitochondrion.
FT NON_TER 25
SQ SEQUENCE 25 AA; 3297 MW; 7D5BD65935C917A4 CRC64;

Query Match 19.2%; Score 19; DB 1; Length 25;
Best Local Similarity 50.0%; Pred. No. 4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 PVFVLEY 13
   ||| |
DB 8 PVFVREW 15

RESULT 18
PSAJ_PEA STANDARD; PRT; 13 AA.
ID PSAJ_PEA P17229;
AC 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-J) (FRAGMENT).
GN PSAJ.
OS Pisum sativum (Garden pea).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
RN [1]
RP SEQUENCE.
RX MEDLINE=90242987; PubMed=2185953;
RA Ikeuchi M., Hirano A., Hiyama T., Inoue Y.;
RT "Polypeptide composition of higher plant photosystem I complex.
Identification of psal, psaj and psak gene products.";
RL FEBS Lett. 263:274-278(1990).
CC -1- FUNCTION: MAY HELP IN THE ORGANIZATION OF THE PSAE AND PSAF
SUBUNITS.
CC -1- SIMILARITY: BELONGS TO THE PSAJ FAMILY.
DR PIR: S09733; S09733.
KW Chloroplast; Photosystem I; Photosynthesis; Transmembrane.
FT TRANSMEM 6 >13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1516 MW; 9E2E45D11FDE3B41 CRC64;

Query Match 18.7%; Score 18.5; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 TY-ETAPV 7
   ||| |
DB 6 TYLXVAV 13

RESULT 19
CH10_CLOPA STANDARD; PRT; 19 AA.
ID CH10_CLOPA P81338;
AC 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)

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DE 10 KDA CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (CP 31) (FRAGMENT).
GN GROES.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flegstrand R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-AMP AND SUPPRESSES
THE ATPASE ACTIVITY OF THE LATTER (BY SIMILARITY).
CC -1- SUBUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING
(BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
DR INTERPRO: IPR001476; -.
DR PFAM: PF00166; cpn10; 1.
DR PROSITE: PS00681; CHAPERONINS_CPN10; PARTIAL.
KW Chaperone.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2026 MW; 7D699BD414E60A60 CRC64;

Query Match 18.7%; Score 18.5; DB 1; Length 19;
Best Local Similarity 35.3%; Pred. No. 3.7e+03;
Matches 6; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY 3 ETAPVLEYTYTKM 19
   ||| |
DB 2 KTFP--LGDNVVTKKL 15

RESULT 20
NIFS_BRAJA STANDARD; PRT; 11 AA.
ID NIFS_BRAJA P37030;
AC 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE NIFS PROTEIN (FRAGMENT).
GN NIFS.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
RN [1]
RP SEQUENCE FROM N.A.
RA Ebeling S.;
RT Submitted (DEC-1988) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: NOT KNOWN YET.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X13691; CAA31982.1; -.
CC PIR: S04875; S04875.
CC INTERPRO: IPR000192; -.
CC PROSITE: PS00595; AA_TRANSFERR_CLASS_5; PARTIAL.
KW Nitrogen fixation; Pyridoxal phosphate.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1308 MW; 09F0BB69476DCA04 CRC64;

```

Query Match 18.2%; Score 18; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 5 APFV 9
11111
DB 6 APFVL 10

RESULT 21

MILT_ONCKE STANDARD; PRT; 15 AA.

AC P81037;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MILTPAIN (EC 3.4.22.-) (FRAGMENT).
OS Oncorhynchus keta (Chum salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN [1]
RP SEQUENCE AND CHARACTERIZATION.
RX MEDLINE-97397031; PubMed-9253183;
RA Kawabata C., Ichishima E.;
RT Miltpain, new cysteine proteinase from the milt of chum salmon,
RT Oncorhynchus keta."
RL Comp. Biochem. Physiol. 117B:445-452(1997).
CC -1- FUNCTION: CYSTEINE PROTEINASE THAT HYDROLYSES BASIC PROTEINS.
CC HYDROLYZE BASIC PROTEINS SUCH AS HISTONE, SALMINE AND CLUPAINE BUT
CC NOT MILK CASEIN.
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE WITH BASIC RESIDUES AT
CC P2 AND P1.
KM MEROPS: C01.093; .
DM Hydrolyase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1730 MW; 766B7771C0F888E7 CRC64;

Query Match 18.2%; Score 18; DB 1; Length 15;
Best Local Similarity 44.4%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 6 PVFVLETV 14
1111111
DB 2 PSFLYAEV 10

RESULT 22

UC17_MAIZE STANDARD; PRT; 15 AA.

AC P80623;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLOGATED COLEOPTILE (SPOT 32)
DE (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE.
RC TISSUE-COLEOPTILE;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huot J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 42.7 KDA.
DR MAIZE-2DPAGE; P80623; COLEOPTILE.
DR MAIZEDB; 123949; .
FT NON_TER 1 1

FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1554 MW; COAFF15FECEBEC8 CRC64;

Query Match 18.2%; Score 18; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 PVFVL 10
11111
DB 5 PVFAV 9

RESULT 23

ALL2_CYPDPO STANDARD; PRT; 18 AA.

AC P82153;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYDIASTATIN 2.
OS Cydia pomonella (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
RN [1]
RP SEQUENCE.
RC TISSUE-LARVA;
RX MEDLINE-98054539; PubMed-9392829;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily."
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide: Amidation.
FT MOD_RES 18 18
SQ SEQUENCE 18 AA; 2169 MW; 8E66679CC0CDF175C CRC64;

Query Match 18.2%; Score 18; DB 1; Length 18;
Best Local Similarity 42.9%; Pred. No. 4.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 YE1APVF 8
111111
DB 8 YKRLPVY 14

RESULT 24

AROQ_AMTME STANDARD; PRT; 20 AA.

AC P46380;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-DEHYDROQUINASE).
DE (TYPE II DHOASE) (FRAGMENT).
GN AROQ.
OS Amycolatopsis methanolica.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardiales; Pseudonocardaceae;
OC Amycolatopsis.
RN [1]
RP SEQUENCE.
RC STRAIN-NCIB 11946;
RX MEDLINE-93123995; PubMed-1479361;
RA Euvlerink G.J.W., Hessel G.I., Vrijbloed J.W., Cogging J.R.,
RA Dijkhuizen L.;
RT "Purification and characterization of a dual function
RT 3-dehydroquinate dehydratase from Amycolatopsis methanolica."
RL J. Gen. Microbiol. 138:2449-2457(1992).
CC -1- FUNCTION: CATALYZE A TRANS-DEHYDRATION VIA AN ENOLATE
CC INTERMEDIATE. IS INVOLVED IN BOTH THE CATABOLISM OF QUINATE AND

CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS. HAS A TEMPERATURE
 CC OPTIMAL OF 76 DEGREES CELSIUS AND PH OPTIMAL OF 9.0. TYPE II
 CC ENZYMES ARE THERMOSTABLE.
 CC -1- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE - 3-DEHYDROSHIKIMATE + H(2)O.
 CC -1- PATHWAY: THIRD STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
 CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -1- SUBUNIT: HOMODECAMER.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-II 3-DEHYDROQUINASE FAMILY.
 CC INTERPRO: IPR001874; -
 DR PROSITE: PS01029; DEHYDROQUINASE II; PARTIAL.
 KW Quinate metabolism; Aromatic acid biosynthesis; lyase.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2197 MW; C2AA183B5CFD0A CRC64;

Query Match 18.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 VFVL 10
 ||||
 DB 3 VFVL 6

RESULT 25
 CPXX_RHQRH
 ID CPXX_RHQRH STANDARD; PRT; 20 AA.
 AC P31718;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYTOCHROME P450-RRI (EC 1.14.-.-) (P450-RRI) (FRAGMENT).
 OS Rhodococcus rhodochrous.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-116;
 RX MEDLINE-93238689; PubMed-8477696;
 RA Ellis L.D.; Karlson U.; Timmis K.N.;
 RT "Purification and characterization of cytochrome P450RRI from
 RT Rhodococcus rhodochrous";
 RL Eur. J. Biochem. 213:211-216(1993)
 CC -1- FUNCTION: P450-RRI CATALYZES THE O-DEALKYLATION OF 2-ETHOXYPHENOL
 CC AND 2-METHOXYPHENOL TO PRODUCE CATECHOL. THE CYTOCHROME BINDS
 CC OTHER ORTHO-SUBSTITUTED PHENOLS, INCLUDING 2-ETHOXYPHENOL,
 CC 2-METHYLPHENOL AND 2-CHLOROPHENOL.
 CC -1- INDUCTION: BY 2-ETHOXYPHENOL.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC INTERPRO: IPR001128; -
 DR PROSITE: PS00086; CYTOCHROME_P450; PARTIAL.
 KW Oxidoreductase; Monooxygenase; Electron transport; Heme.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2428 MW; BCA81586D8DD1496 CRC64;

Query Match 18.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 22.2%; Pred. No. 4.7e+03;
 Matches 2; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 11 LEVYTLKKM 19
 |:|:|:|:
 DB 7 LDETMEEL 15

Search completed: February 5, 2001, 10:56:03
 Job time: 503 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:49:31 ; Search time 58.67 Seconds
(without alignments)
23.147 Million cell updates/sec

Title: US-08-981-824-6

Sequence: 1 TYEIAFVFLVLEVTLLKMR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 5001

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR_66.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28.3	24	2	S30373	glutathione transf
2	26.3	20	2	A57106	hull allergen Gly
3	25.3	23	2	H24735	glutathione transf
4	24.2	16	2	I57530	gene c-fms protein
5	24.2	21	2	S09517	prolamin - sorghum
6	24.2	24	2	S33237	glutathione transf
7	23.2	14	2	PH1615	Ig H chain V-D-J r
8	23.2	24	2	A35187	glutathione transf
9	23.2	24	2	A20554	hemocyanin subunit
10	23.2	25	2	S18400	carboxylic acid re
11	22.2	6	2	B27696	contraction-inhibi
12	22.2	18	2	A43826	dark type molecula
13	22.2	19	2	S74114	3-hydroxyacyl-CoA
14	22.2	19	2	T22228	hypothetical prote
15	22.2	20	2	A48367	glutaryl-CoA dehyd
16	22.2	20	2	A46644	temperature-labile
17	22.2	22	2	S13899	glycoprotein, 11.7
18	22.2	23	2	JP0058	ribosomal protein
19	22.2	6	2	A60966	N-formyl oligopept
20	21.2	12	4	JK0315	amino transferase c
21	21.2	15	2	PQ0750	self-incompatibili
22	21.2	21	2	B48367	glutaryl-CoA dehyd
23	21.2	21	2	T07683	protease inhibitor
24	21.2	21	2	A32902	GMP reductase / g1
25	21.2	22	2	S09021	carboxylesterase (
26	21.2	23	2	S60564	homodomain protei
27	21.2	23	2	S37491	hypothetical prote
28	21.2	23	2	A56272	conjugation induc
29	21.2	24	2	H20554	hemocyanin subunit

30	21	21.2	24	2	PH1336	Ig heavy chain DJ
31	21	21.2	24	2	I67553	monocyte chemoat
32	21	21.2	25	2	E37520	glutathione transf
33	21	21.2	25	2	B20596	venom kallikrein (
34	21	21.2	25	2	F41606	homeotic protein S
35	21	21.2	25	2	S78343	hypothetical prote
36	20.5	20.7	22	2	S00189	molitin - dog (ten
37	20.5	20.7	25	2	H64710	hypothetical prote
38	20	20.2	13	2	PH1599	Ig H chain V-D-J r
39	20	20.2	13	2	I77387	AMP deaminase - ra
40	20	20.2	16	2	S24667	protein-tyrosine k
41	20	20.2	20	2	JP0060	ribosomal protein
42	20	20.2	20	2	JP0061	ribosomal protein
43	20	20.2	21	2	B49200	cystatin-related p
44	20	20.2	21	2	I53263	CRP-1 delta - rat
45	20	20.2	22	2	PM0048	estrogen receptor

ALIGNMENTS

```

RESULT 1
S30373
glutathione transferase (EC 2.5.1.18) mu (isoform PI 8.5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 03-May-1996
C:Accession: S30373; S30371
R:Awasthi, S.; Singhal, S.S.; Srivastava, S.K.; Awasthi, Y.C.
Arch. Biochem. Biophys. 301, 143-150, 1993
A:Title: Purification and characterization of glutathione S-transferase of murine ova
A:Reference number: S30369; M01D:93185007
A:Accession: S30373
A:Molecule type: protein
A:Residues: 1-24 <AW1>
A>Note: this form was identified by pi 8.5
A:Accession: S30371
A:Molecule type: protein
A:Residues: 1-24 <AW2>
A>Note: this form was identified by pi 7.9
C:Superfamily: glutathione transferase
C:Keywords: transferase

Query Match      28.3%  Score 28;  DB 2;  Length 24;
Best Local Similarity 62.5%  Pred. No. 2.8e+02;
Matches 5;  Conservative 2;  Mismatches 1;  Indels 0;  Gaps 0;

QY 6 PFEVILEY 13
   |::|
DB 15 PIRMLLEY 22

RESULT 2
A57106
hull allergen Gly m 2 - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 25-Oct-1996
R:Codina, R.; Swanson, M.C.; Fernandez-Caldas, E.; Lockey, R.F.; Trudeau, W.L.; Rama,
submitted to the Protein Sequence Database, October 1995
A:Description: Partial sequence of the Gly m 2 allergen from soybean hull.
A:Reference number: A57106
A:Accession: A57106
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <COD>
A:Experimental source: seed episperma
C:Keywords: seed

Query Match      26.3%  Score 26;  DB 2;  Length 20;
Best Local Similarity 50.0%  Pred. No. 5.1e+02;
Matches 4;  Conservative 1;  Mismatches 3;  Indels 0;  Gaps 0;

```

QY	1	TYEIA	8
		:	
Db	11	TYRLGP	18

RESULT 3
H24735
glutathione transferase (EC 2.5.1.18) MITT - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 25-Oct-1997 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C:Accession: H24735
R:Mannevik, B.; Alln, P.; Guttenberg, C.; Jansson, H.; Tahr, M.K.; Warholm, M.; Jorntun, P.; Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
A:Title: Identification of three classes of cytosolic glutathione transferase common to A:Reference number: A24735; MUID:86042634
A:Accession: H24735
A:Molecule type: protein
A:Residues: 1-23 <MAN>
C:Superfamily: glutathione transferase
C:Keywords: transferase

Query Match	25.3%	Score 25;	DB 2;	Length 23;
Best Local Similarity	50.0%	Pred. No. 8.6e+02;		
Matches	4;	Conservative	3;	Mismatches 1;
				Indels 0;
				Gaps 0;

```
QY      6 PVFVLEY 13
          | : : | | : |
Db     15 PIRMLLOY 22
```

RESULT 4
157530
gene c-fms protein - mouse (fragment)
C.Species: Mus.sp. (mouse)
C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-May-1997
C.Accession: 157530
R.Yue, X.; Favot, P.; Dunn, T.L.; Cassidy, A.I.; Hume, D.A.
Mol. Cell. Biol. 13, 3191-3201, 1993
A.Title: Expression of mRNA encoding the macrophage colony-stimulating factor receptor
A.Reference number: 157530; MUID:93268269
A.Accession: 157530
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-16 <RES>
A.Cross-references: GB:S62219; NID:g386001
C.Genetics:
A:Gene: c-fms
C:Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology

Query Match	24.28;	Score 24;	DB 2;	Length 16;
Best Local Similarity	55.68;	Pred. No. 8.8e+02;		
Matches	5;	Conservative	1;	Mismatches 3;
			Indels	0;
			Gaps	0;

```
QY      3 EIAPVFVL 11
        | : | 111
Db      2 ELGPPVLV 10
```

RESULT 5
S09517
Prolamin - sorghum (fragment)
C:Species: Sorghum bicolor (sorghum)
A:Variety: P721 lines
C:Date: 21-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 09-May-1997
C:Accession: S09517
R:Bietsz, J.A.
Biochem. Genet. 20, 1039-1053, 1982
A:Title: Cereal prolamin evolution and homology revealed by sequence analysis
Reference number: S09165; MIMD:83153005
Accession: S09517

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-21 <BIE>
C;Superfamily: zein

Query Match	24.2%	Score 24;	DB 2;	Length 21;
Best Local Similarity	18.2%	Pred. No. 1.2e+03;		
Matches	2;	Conservative	7;	Mismatches 2;
			Indels	0;
			Gaps	0;

```
QY      4 IAPVEVLEEV 14
        :||: : ::::
Db      8 LAPIAIAIQEL 18
```

```

RESULT      6
S33237
glutathione transferase (EC 2.5.1.18) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 07-May-1999
C:Accession: S33237
R:Ben-Arie, N.; Khen, M.; Lancet, D.
Biochem. J. 292, 379-384, 1993
A:Title: Glutathione S-transferases in rat olfactory epithelium: purification, molecu
A:Reference number: S33237; MUID:93277499
A:Accession: S33237
A:Molecule type: protein
A:Residues: 1-24 <BEN>
A:Note: 18-Ile, 21-Glu, 23-Thr and 23-Glu were also found
C:Superfamily: glutathione transferase
C:Keywords: transferase

```

Query Match	24.28;	Score 24;	DB 2;	Length 24;
Best Local Similarity	50.08;	Pred. No. 1.3e+03;		
Matches	5;	Conservative	2;	Mismatches 3; Indels 0; Gaps 0

```
QY      6 PVFVLLLEYVT 15
          | : : | | |
Db     15 PIRLLLLYYT 24
```

RESULT 7
PH1615
Ig H chain V-D-J region (clone B-less 22) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1615
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A/Reference number: PH1580; MUID:93301609
A/Accession: PH1615
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
;Keywords: immunoglobulin

Query Match	23.28;	Score 23;	DB 2;	Length 14;
Best Local Similarity	27.38;	Pred. No. 1.1e+03;		
Matches	3;	Conservative	4;	Mismatches 4;
				Indels 0;
				Gaps 0

```
QY      3 EIAPVEVILEY 13
        | |:::|
Db      4 ESNPIYYAMDY 14
```

```

RESULT      8
A35187
glutathione transferase (EC 2.5.1.18) Mu 8.3 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 23-Jun-1992

```

C:Accession: A35187
 R:Tsushima, S.; Maki, T.; Sato, K.
 J. Biol. Chem. 265, 7150-7157, 1990
 A:Title: Purification and characterization of glutathione transferases with an activity
 A:Reference number: A35187; MWID:90237002
 C:Accession: A35187
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-24 <TSU>
 C:Superfamily: glutathione transferase
 C:Keywords: transferase

Query Match 23.2%; Score 23; DB 2; Length 24;
 Best Local Similarity 57.1%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VFVLEY 13
 : : |||||
 DB 16 IXLLLEY 22

RESULT 9
 A20554
 hemocyanin subunit I - Atlantic horseshoe crab (fragment)
 C:Species: Limulus polyphemus (Atlantic horseshoe crab)
 C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 12-Apr-1995
 C:Accession: A20554
 R:Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiard, P.; Jolles, P.; Jolles, J.; Feldmann, R.
 Biochemistry 22, 5573-5583, 1983
 A:Title: Quaternary structure of Limulus polyphemus hemocyanin.
 A:Reference number: A90478
 A:Accession: A20554
 A:Molecule type: protein
 A:Residues: 1-24 <LAM>
 C:Comment: Limulus polyphemus hemocyanin is an association of eight different subunits
 C:Superfamily: hemocyanin

Query Match 23.2%; Score 23; DB 2; Length 24;
 Best Local Similarity 36.4%; Pred. No. 2e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 APVLEVY 15
 : : |||||
 DB 7 ASIALFEHLT 17

RESULT 10
 S18400
 carboxylic acid reductase - Clostridium formicoaceticum
 C:Species: Clostridium formicoaceticum
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
 C:Accession: S18400
 R:White, H.; Felcht, R.; Huber, C.; Lotspeich, F.; Simon, H.
 Biol. Chem. Hoppe-Seyler 372, 999-1005, 1991
 A:Title: Purification and some properties of the tungsten-containing carboxylic acid red
 A:Reference number: S18400; MWID:92172285
 A:Accession: S18400
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-25 <WHI>

Query Match 23.2%; Score 23; DB 2; Length 25;
 Best Local Similarity 40.0%; Pred. No. 2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 FVLEVYTLK 17
 : : |||||
 DB 4 FIRVDMTTLK 13

RESULT 11
 B27696
 contraction-inhibiting peptide II - blue mussel
 C:Species: Mytilus edulis (blue mussel)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-1995
 C:Accession: B27696
 R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
 Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988
 A:Title: Structures and actions of Mytilus inhibitory peptides.
 A:Reference number: A90142; MWID:88240357
 A:Accession: B27696
 A:Molecule type: protein
 A:Residues: 1-6 <HIR>
 C:Keywords: amidated carboxyl end
 F:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 22.2%; Score 22; DB 2; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 APVEV 9
 : : |||||
 DB 2 APMEV 6

RESULT 12
 A43826
 dnaK-type molecular chaperone - Mytilus edulis capsulatum (fragment)
 N:Alternate names: 80K heat shock protein 70 homolog
 C:Species: Mytilus edulis capsulatum, Histoplasma capsulatum
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 17-Mar-1999
 C:Accession: A43826
 R:Gomez, F.J.; Gomez, A.M.; Deepe Jr., G.S.
 Infect. Immun. 60, 2565-2571, 1992
 A:Title: An 80-kilodalton antigen from Histoplasma capsulatum that has homology to he
 A:Reference number: A43826; MWID:92307875
 A:Accession: A43826
 A:Molecule type: protein
 A:Residues: 1-18 <COM>
 C:Experimental source: extract of cell wall and cell membrane
 C:Function: involved in protein folding and assembling/disassembling of protein co
 A:Description: involved in protein folding and assembling/disassembling of protein co
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 22.2%; Score 22; DB 2; Length 18;
 Best Local Similarity 37.5%; Pred. No. 2.2e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TYELAPVF 8
 : : |||||
 DB 11 TYSVGIF 18

RESULT 13
 S74114
 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C:Accession: S74114
 R:Dieulaide-Noubhani, M.; Novikov, D.; Baumgart, E.; Vanhooren, J.C.T.; Fransen, M.; G
 Eur. J. Biochem. 240, 660-666, 1996
 A:Title: Further characterization of the peroxisomal 3-hydroxyacyl-CoA dehydrogenase
 e acids di- and tri-hydroxypropanoic acids are metabolized by separate multifunctio
 A:Reference number: S74113; MWID:97008958
 A:Accession: S74114
 A:Molecule type: protein
 A:Residues: 1-19 <DIE>
 A:Experimental source: liver
 C:Superfamily: 3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA dehydrogenase homol
 C:Keywords: fatty acid beta-oxidation; mitochondrion; NAD; oxidoreductase

Query Match 22.2% Score 22; DB 2; Length 19;
 Best Local Similarity 37.5%; Pred. No. 2.3e+03;
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 9 VLEEVYTL 16
 :|::|:
 Db 4 ILIKHVT 11

RESULT 14

122228
 hypochetrical protein F456.5 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22228
 R:McMurray, A.
 submitted to the EMBL Data Library, November 1995

A:Accession: T22228
 A:Reference number: Z19534
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-19 <M11>

A:Cross-references: EMBL:Z68117; PIDN:CA92179.1; GSPDB:GN00028; CESP:F456.5
 A:Experimental source: clone F4566
 C:Genetics:
 A:Gene: CESP:F456.5
 A:Map position: X

Query Match 22.2% Score 22; DB 2; Length 19;
 Best Local Similarity 44.4%; Pred. No. 2.3e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 IAPVVLLE 12
 :|::|:
 Db 11 ICPVYAVE 19

RESULT 15

A48367
 glutaryl-CoA dehydrogenase (EC 1.3.99.7) - Pseudomonas sp. (fragment)

C:Species: Pseudomonas sp.
 C:Date: 01-Dec-1993 #sequence_revision 29-Sep-1999 #text_change 29-Sep-1999

C:Accession: A48367
 R:Hartel, U.; Eckel, E.; Koch, J.; Fuchs, G.; Linder, D.; Buckel, W.
 Arch. Microbiol. 159, 174-181, 1993

A:Title: Purification of glutaryl-CoA dehydrogenase from Pseudomonas sp., an enzyme invc
 A:Reference number: A48367; MUID:9317588

A:Accession: A48367
 A:Molecule type: protein
 A:Residues: 1-20 <HAR>

A:Cross-references: PIDN:AA825430.1; PID:9265706
 A:Experimental source: strain KB 740

A>Note: sequence extracted from NCBI backbone (NCBIP:125304)
 C:Keywords: oxidoreductase

Query Match 22.2% Score 22; DB 2; Length 20;
 Best Local Similarity 26.7%; Pred. No. 2.4e+03;
 Matches 4; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 TYEIAPVVLEVT 15
 :|::|:
 Db 6 TFDADPYLXDQLT 20

RESULT 16

A46644
 temperature-labile cholesteryl ester hydrolase - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995

C:Accession: A46644
 R:Wee, S.; Grogan, W.M.
 J. Biol. Chem. 268, 8158-8163, 1993
 A:Title: Reticular temperature-labile cholesteryl ester hydrolase. Relationship to 1
 divalent cations.
 A:Reference number: A46644; MUID:93216794

A:Accession: A46644
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <ME5>
 A:Experimental source: testis
 A>Note: sequence extracted from NCBI backbone (NCBIP:129155)

Query Match 22.2% Score 22; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 PVFVTLER 13
 :|::|:
 Db 9 PAAVTLER 16

RESULT 17

S13899
 glycoprotein, 11.7S - frog (Lepidobatrachus laevis)

C:Species: Lepidobatrachus laevis
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S13899
 R:Carroll Jr., E.J.; Wei, S.H.; Nagel, G.M.
 Arch. Biochem. Biophys. 284, 346-351, 1991

A:Title: Purification, physicochemical characterization, and immunohistochemical loca
 A:Reference number: S13899; MUID:91112831

A:Accession: S13899
 A:Status: preliminary

A:Molecule type: protein
 A:Residues: 1-22 <ARC>

Query Match 22.2% Score 22; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 EYVTLK 17
 :|::|:
 Db 17 DYVTLK 22

RESULT 18

JP0058
 ribosomal protein L30 - Bacillus cycloheptanicus (fragment)

C:Species: Bacillus cycloheptanicus
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994

C:Accession: JP0058
 R:ochl, K.

submitted to JIPID, February 1994
 A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal

A:Reference number: JP0042
 A:Accession: JP0058

A:Molecule type: protein
 A:Residues: 1-23 <OCH>

C:Keywords: protein biosynthesis; ribosome

Query Match 22.2% Score 22; DB 2; Length 23;
 Best Local Similarity 80.0%; Pred. No. 2.8e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 14 VTLLK 18
 :|::|:
 Db 6 ITLLK 10

RESULT 19

A:Accession: A60986
 N-formyl oligopeptide - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
 C:Accession: A60986
 R:Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
 Experientia 45, 1097-1099, 1989
 A:Title: Purification and amino acid sequencing of naturally occurring N-formyl-methionyl
 A:Reference number: A60986; MWID:90092408
 A:Accession: A60986
 A:Molecule type: protein
 A:Residues: 1-6

 C:Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.
 F:1/Modified site: N-formylmethionine #status experimental

Query Match 21.2%; Score 21; DB 2; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VFVLL 11
 DB 2 VFLL 6

RESULT 20

amino transferase chimera DY18 - synthetic (fragment)
 C:Species: Synthetic
 C:Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
 C:Accession: JX0315
 R: Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
 J. Biochem. 115, 568-577, 1994
 A:Title: Construction of amino transferase chimeras and analysis of their substrate spec
 A:Reference number: JX0315; MWID:94334304
 A:Accession: JX0315
 A:Molecule type: DNA
 A:Residues: 1-12 <MY>
 C:Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransfer
 C:Keywords: amino transferase

Query Match 21.2%; Score 21; DB 4; Length 12;
 Best Local Similarity 42.9%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 PFEVLE 12
 DB 5 PILLME 11

RESULT 21

self-incompatibility protein S3 - potato (fragment)
 C:Species: Solanum tuberosum (potato)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 23-Mar-1995
 C:Accession: P00750
 R: Kirch, H.H.; Uhlid, H.; Lottspeich, F.; Salamini, F.; Thompson, R.D.
 Theor. Appl. Genet. 78, 581-588, 1989
 A:Title: Characterization of proteins associated with self-incompatibility in Solanum tu
 A:Reference number: P00749
 A:Accession: P00750
 A:Molecule type: protein
 A:Residues: 1-15 <KIR>
 A:Experimental source: style
 C:Keywords: glycoprotein

Query Match 21.2%; Score 21; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 2.7e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 FVLELYVT 15
 DB 2 FELLEYVS 9

RESULT 22

glutaryl-CoA dehydrogenase (EC 1.3.99.7) - Pseudomonas sp. (fragment)
 C:Species: Pseudomonas sp.
 C:Date: 29-Sep-1999 #sequence_revision 29-Sep-1999 #text_change 29-Sep-1999
 C:Accession: B48367
 R: Hartel, U.; Eckel, E.; Koch, J.; Fuchs, G.; Linder, D.; Buckel, W.
 Arch. Microbiol. 159, 174-181, 1993
 A:Title: Purification of glutaryl-CoA dehydrogenase from Pseudomonas sp., an enzyme 1
 A:Reference number: A48367; MWID:93175988
 A:Accession: B48367
 A:Molecule type: protein
 A:Residues: 1-21 <HAR>
 A:Cross-references: PIDN: AAB25431.1; PID: g265707
 A:Experimental source: strain K 172
 A:Note: sequence extracted from NCBI backbone (NCBIP.125302)
 C:Keywords: oxidoreductase

Query Match 21.2%; Score 21; DB 2; Length 21;
 Best Local Similarity 33.3%; Pred. No. 3.7e+03;
 Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 TYELAPVLELYVT 15
 DB 6 TFDWADPILLXOLT 20

RESULT 23

proteinnase inhibitor I homolog - potato (fragment)
 C:Species: Solanum tuberosum (potato)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: T07683
 R: Lee, J.S.
 submitted to the EMBL Data Library, June 1992
 A:Reference number: S24965
 A:Accession: T07683
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-21 <LEE>
 A:Cross-references: EMBL: D12819; NID: g21584; PID: g21585
 A:Experimental source: cv. Russet Burbank
 C:Keywords: proteinase inhibitor

Query Match 21.2%; Score 21; DB 2; Length 21;
 Best Local Similarity 45.5%; Pred. No. 3.7e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 VFVLELYVTLK 17
 DB 10 VFELKKYSFK 20

RESULT 24

GMP reductase / glucose-6-phosphate 1-dehydrogenase fusion protein - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1998 #sequence_revision 10-Sep-1998 #text_change 10-Sep-1998
 C:Accession: A32902
 R: Kanno, H.; Huang, I.Y.; Kan, Y.W.; Yoshida, A.
 Cell 58, 595-606, 1989
 A:Title: Two structural genes on different chromosomes are required for encoding the
 A:Reference number: A32902; MWID:89336791
 A:Accession: A32902
 A:Molecule type: protein

A:Residues: 1-21 <KAN>
R:Yoshida, A.; Kan, Y.W.
Cell 62, 11-12, 1990
A:Title: Origin of "fused" glucose-6-phosphate dehydrogenase.
A:Reference number: A55177
A:Contents: annotation
C:Comment: This peptide was sequenced from a fragment of a chimeric protein produced from a cDNA library. The peptide was later shown to be an artifact of purification and not a natural component of erythrin.
C:Keywords: fusion protein
F:1-13/Region: GMP reductase
F:14-21/Region: glucose-6-phosphate 1-dehydrogenase

Query Match 21.2%; Score 21; DB:4; Length 21;
Best Local Similarity 44.4%; Pred. No. 3.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 TYEIAPEV 9
|||:|
Db 2 TYSGIPIT 10

RESULT 25
S09021
carboxylesterase (EC 3.1.1.1) R11, microsomal - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C:Accession: S09021
R:Hosokawa, M.; Maki, T.; Satoh, T.
Arch. Biochem. Biophys. 277, 219-227, 1990
A:Title: Characterization of molecular species of liver microsomal carboxylesterases of rat.
A:Reference number: S09021; MUID:90179180
A:Accession: S09021
A:Molecule type: protein
A:Residues: 1-22 <HOS>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 21.2%; Score 21; DB:2; Length 22;
Best Local Similarity 62.5%; Pred. No. 3.9e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 9 VLEEVTL 16
|||:|
Db 15 VLGRYVSL 22

Search completed: February 5, 2001, 10:49:32
Job time: 745 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:47:34 ; Search time 68.99 seconds
(without alignments)
9.913 Million cell updates/sec

Title: US-08-981-824-6
Perfect score: 99
Sequence: 1 TYEIAPVLELVTLTKMR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 141170

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A-Geneseq_36:*

1: /SIDSL/gcgdata/geneseq/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/AA1983.DAT:*
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20: /SIDSL/gcgdata/geneseq/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	100.0	20	18	W18847
2	99	100.0	20	18	W01798
3	79	79.8	20	16	R72274
4	79	79.8	20	21	Y59574
5	66	66.7	14	16	R76651
6	66	66.7	14	18	W18859
7	63	63.6	15	18	W12408
8	50	50.5	15	18	W12407
9	49	49.5	14	16	R76652
10	49	49.5	14	18	W18860
11	45	45.5	20	16	R72375
12	45	45.5	20	21	Y59575

13	36	36.4	14	16	R76659	Peptide derived fr
14	36	36.4	14	18	W18867	65 kD Glutamic aci
15	31	31.3	10	18	W14898	Phakellistatin 9.
16	31	31.3	20	4	P30120	Sequence of peptid
17	31	31.3	20	4	P30121	Sequence of peptid
18	31	31.3	20	4	P30321	Sequence of peptid
19	30	30.3	10	18	W14897	Phakellistatin 8.
20	30	30.3	15	21	Y66492	Human Src peptide
21	30	30.3	15	21	Y66517	Human Src peptide
22	30	30.3	23	13	R22401	Modified pre seque
23	30	30.3	25	11	R06504	N-terminal seque
24	29	29.3	15	21	Y66490	Human PDGF recepto
25	29	29.3	15	21	Y66491	Human Lck peptide
26	29	29.3	15	21	Y66515	Human PDGF recepto
27	29	29.3	15	21	Y66516	Human Lck peptide
28	29	29.3	20	4	P30113	Sequence of peptid
29	29	29.3	20	4	P30118	Sequence of peptid
30	29	29.3	20	4	P30119	Sequence of peptid
31	29	29.3	20	4	P30320	Sequence of peptid
32	29	29.3	20	4	P30010	Sequence of fragme
33	28	28.3	16	17	W07285	Amphiphilic antilm
34	28	28.3	16	17	Y04725	Triabin/thrombin-b
35	28	28.3	25	20	W90171	Sindbis virus PE2
36	27	27.3	8	18	W43400	C-reactive protein
37	27	27.3	10	14	R39584	Diuretic hormone b
38	27	27.3	15	17	W07274	Amphiphilic antilm
39	27	27.3	15	19	W48362	Cyclic peptide 1 w
40	27	27.3	15	19	W48371	Cyclic peptide 10
41	27	27.3	15	21	Y66493	Human Abi peptide
42	27	27.3	15	21	Y66518	Human Abi peptide
43	27	27.3	18	12	R10600	Peptide with motil
44	27	27.3	20	14	R41484	Peptide cbl derive
45	27	27.3	20	17	R95382	Residues 141-160 o

ALIGNMENTS

RESULT 1	
ID W18847	W18847 standard; peptide; 20 AA.
AC W18847;	
DT 05-JAN-1998 (first entry)	
XX	
DE 65 kD Glutamic acid decarboxylase peptide fragment VI.	
XX	
KW GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;	
KW Insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;	
KW predilection; autoimmune; tumour; rheumatoid arthritis;	
KW multiple sclerosis.	
XX	
OS Synthetic.	
XX	
PN DE19526561-A1.	
XX	
PD 23-JAN-1997.	
XX	
PF 20-JUL-1995; 95DE-1026561.	
XX	
PR 20-JUL-1995; 95DE-1026561.	
XX	
PA (BOEF) BOEHRINGER MANNHEIM GMBH.	
XX	
PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;	
PI Porzilli P, Stahl P;	
XX	
DR WPI; 1997-088254/09.	
XX	
PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -	
PT Involving intradermal admn. of auto-reactive substances	

PS Claim 11; Page 10; 12pp; German.
 XX
 CC W18842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 XX
 SQ Sequence 20 AA:
 Query Match 100.0%; Score 99; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TYEIAPVFLLEYVTLKKMR 20
 ||||||||||||||||
 Db 1 tyeiapvflleyvtlkkmr 20
 RESULT 2
 W01798
 ID W01798 standard; peptide; 20 AA.
 XX
 AC W01798;
 XX
 DT 15-OCT-1997 (first entry)
 XX
 DE Human 65 kD glutamine decarboxylase peptide.
 XX
 KW Human: glutamine decarboxylase; GAD; diagnosis; predisposition;
 KW tumour; immunological; disease; autoimmune; diabetes; reagent;
 KW determination; T cell; subpopulation; medicament; treatment;
 KW prevention; production; antigen; immunogen; tolerogen; isolation;
 KW reinjection; inactivation.
 XX
 OS Homo sapiens.
 XX
 PN DE19525784-A1.
 XX
 PD 16-JAN-1997.
 XX
 PF 14-JUL-1995; /95DE-1025784.
 XX
 PR 14-JUL-1995; 95DE-1025784.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Albert W, Boltard C, Endl J, Jung G, Schendel D;
 PI Stahl P, Van Enderl P;
 XX
 DR WPI: 1997-078452/08.
 XX
 PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of
 PT diabetes, etc.
 XX
 PS Claim 1; Page 12; 15pp; German.
 XX
 CC The present peptide is a fragment of the human 65 kD glutamine
 CC decarboxylase (GAD), which can be used to diagnose, or diagnose a
 CC predisposition to, a tumour or immunological disease, preferably an
 CC autoimmune disease, especially diabetes. It can also be used as a
 CC reagent to determine specific T cell subpopulations, in medicaments
 CC to treat or prevent immunological diseases, preferably autoimmune
 CC diseases, especially diabetes, to produce antigens, especially
 CC immunogens or tolerogens and to isolate specific T cell
 CC subpopulations, which can be used to produce antigens or for
 CC reinjection, optionally after inactivation.

XX
 SQ Sequence 20 AA:
 Query Match 100.0%; Score 99; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TYEIAPVFLLEYVTLKKMR 20
 ||||||||||||||||
 Db 1 tyeiapvflleyvtlkkmr 20
 RESULT 3
 R72274
 ID R72274 standard; Peptide; 20 AA.
 XX
 AC R72274;
 XX
 DT 13-NOV-1995 (first entry)
 XX
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX
 KW Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KW insulin-dependant diabetes mellitus; stiff man disease.
 XX
 OS Homo sapiens.
 XX
 PN W09507992-A.
 XX
 PD 23-MAR-1995.
 XX
 PF 24-AUG-1994; 94WO-US09478.
 XX
 PR 17-SEP-1993; 93US-0123859.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Clare-Salier MJ, Erlander MG, Kaufman DL, Tobin AJ;
 XX
 DR WPI: 1995-131360/17.
 XX
 PT New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PT dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hybridoma(s) etc.
 XX
 PS Example 11; Page 76; 100pp; English.
 XX
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependant diabetes mellitus or stiff man disease.
 XX
 SQ Sequence 20 AA:
 Query Match 79.8%; Score 79; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TYEIAPVFLLEYVTL 16
 ||||||||||||
 Db 5 tyeiapvflleyvtl 20
 RESULT 4
 Y59574
 ID Y59574 standard; peptide; 20 AA.
 XX
 AC Y59574;

```

XX      03-APR-2000   (first entry)
DT
XX
DE      GAD65 fragment, peptide #14.
XX
KW      GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
        insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
        therapy.
OS
XX      Homo sapiens.
PN      US5998366-A.
PD      07-DEC-1999.
PF      09-APR-1997;    97US-0827618.
PX      07-JUN-1995;    95US-0485725.
PR      21-SEP-1990;    90US-0586536.
PP      18-JUN-1991;    91US-0716909.
PW      (REGC ) UNIV CALIFORNIA.
PI      Tobin AJ, Kaufman DL, Erlander MG;
PT      WPI: 2000-095930/08.
PT      Ameliorating glutamic acid decarboxylase associated autoimmune
PS      disorders such as insulin dependent diabetes mellitus and Stiff man
        disease -
        Example 11: Column 42; 61pp; English.
CC      This sequence represents a fragment of the glutamic acid decarboxylase 65
CC      (GAD65) protein. The invention relates to a method of ameliorating GAD
CC      associated autoimmune disorders by administering a GAD65 peptide to the
CC      patient. The method can be used for ameliorating GAD associated
CC      autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
CC      and Stiff man disease. GAD65 can also be useful for screening drugs that
CC      alter GAD function, for generating monoclonal antibodies and in
CC      immunossays. GAD65 is an effective diagnostic tool for predicting IDDM
CC      and the diagnosis is quite easy. It is also possible to obtain much
CC      larger quantities of polypeptide via recombinant techniques than are
        available from natural sources.
SQ      Sequence      20 AA:
        Query Match          79.8%; Score 79; DB 21; Length 20:
        Best Local Similarity 100.0%; Pred. No. 7.le-08;
        Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY      1 TVEIAPFEVLELYVL 16
        |||||
Db      5 tyeiapfvllleyvcl 20
RESULT      5
R76651
ID      R76651 standard; peptide; 14 AA.
AC      R76651;
DT      05-MAR-1996 (first entry)
DE      Peptide derived from human glutamic acid decarboxylase 10.
DX      diabetes; T-cell subpopulation; detection; antigen production;
        diagnosis; autoimmune disease.
OS      Homo sapiens.
PN      DE4418091-A1.

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XX PD 27-JUL-1995.
XX XX
XX PF 24-MAY-1994; 94DE-4418091.
XX XX
XX PR 04-FEB-1994; 94DE-4403522.
PR 20-JAN-1994; 94DE-4401629.
XX XX
PA (ENDL/) ENDL J.
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX PI Albert W., Dormair K., Endl J., Jung G., Wehl E.;
PI Stahl P., Schendel D.;
XX DR WPT: 1995-264505/35.
XX PT Antigen-specific activated T-lymphocytes and their detection - by
PT interaction with inventive peptide(s) of peptide-MHC complexes;
XX useful in diagnosis of e.g. diabetes and autoimmune diseases
PS Claim 1, Fig 2, 21pp; German.
XX R76642-62 are derived from human glutamic acid decarboxylase and
CC specifically react with T-cell sub-populations isolated from recently
CC diagnosed Type-I diabetics. Pharmaceutical compns. contg. these
CC peptides and those shown in R7571-72, are useful for the diagnosis of
CC a disease or predispositions of immune system diseases, tumours, and
CC autoimmune diseases, including diabetes. The peptides are able to detect
CC specific T-cell subpopulations that are then used for antigen produ..
CX e.g. by reinjection.
XX Sequence 14 AA;
SQ
Query Match 66.7%; Score 66; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYEIAPFVLLLEY 13
Db |||||||||
2 tyetaprvllley 14
RESULT 6
W18859 ID W18859 standard; peptide; 14 AA.
XX AC W18859;
DT 05-JAN-1998 (first entry)
XX DE 65 kD Glutamic acid decarboxylase peptide fragment 10.
XX KW GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
KW Insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
KM predilection; autoimmune; tumour; rheumatoid arthritis;
KM multiple sclerosis.
OS Synthetic.
XX OS
XX PN DE19526561-A1.
XX PD 23-JAN-1997.
XX PE 20-JUL-1995; 95DE-1026561.
XX PR 20-JUL-1995; 95DE-1026561.
XX PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX PI Donle F., Endl J., Ganz M., Jung G., Kiementsch-engel R;
PI Pozzilli P., Stahl P.;
XX
```

DR WPI: 1997-088254/09.
 XX Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
 PR involving intradermal admin. of auto-reactive substances
 XX
 PS Claim 11: Fig 2; 12pp; German.
 CC W18942-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 XX
 SQ Sequence 14 AA:

Query Match 66.7%; Score 66; DB 18; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTEIAPVFLLEY 13
 |||||
 DB 2 tyeIapvfvlley 14

RESULT 7
 W12408 standard; peptide: 15 AA.

AC W12408;
 XX
 DT 08-OCT-1997 (first entry)
 XX
 DE GAD65 residues 213-227.
 XX
 KW 65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;
 KW neuron; central nervous system; type I diabetes; autoimmune response;
 KW T cell; therapy.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH Misc-difference 1..15
 FT /note= "optionally substituted, providing at least 7
 FT residues remain wild type"
 FT

W09700891-A1.

09-JAN-1997.

24-JUN-1996; 96WO-US10790.

23-JUN-1995; 95US-0494624.

(KENN-) KENNEDY INST RHEUMATOLOGY.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.

Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;
 WPI: 1997-087322/08.

New human glutamic acid decarboxylase peptide(s) - used for
 treatment, diagnosis and determining predisposition to diabetes and
 for ameliorating auto-immune responses.

Claim 26; Page -: 28pp; English.

CC W12403-W12413 represent fragments and analogues of the 65 kD isoform
 CC of human glutamic acid decarboxylase (GAD65) (see W12402 for full length
 CC wild type protein). GAD is an enzyme expressed in the beta cells of the
 CC pancreas, and in neurons of the central nervous system. There are two
 CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of
 CC GAD65 have been identified in Type I diabetic patients. These GAD65
 CC fragments, and analogues, are used in the methods of the invention. The
 CC methods are for detecting or treating diabetes or a predisposition to
 CC diabetes. The peptides can also be used for ameliorating an autoimmune
 CC response in a patient. Alteration of the native peptides with selective
 CC changes of crucial residues can induce unresponsiveness or change the
 CC responsiveness of antigen-specific autoreactive T cells. The peptide
 CC analogues compete for binding to MHC and do not cause proliferation of
 CC the corresponding native peptide-specific T cells.
 XX
 SQ Sequence 15 AA:

Query Match 63.6%; Score 63; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 FYLLEYVTLKKMR 20
 |||||
 DB 1 fyleyvtlkkmr 13

RESULT 8
 W12407 standard; peptide: 15 AA.

AC W12407;
 XX
 DT 08-OCT-1997 (first entry)
 XX
 DE GAD65 residues 201-215.

KW 65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;
 KW neuron; central nervous system; type I diabetes; autoimmune response;
 KW T cell; therapy.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH Misc-difference 1..15
 FT /note= "optionally substituted, providing at least 7
 FT residues remain wild type"
 FT

W09700891-A1.

09-JAN-1997.

24-JUN-1996; 96WO-US10790.

23-JUN-1995; 95US-0494624.

(KENN-) KENNEDY INST RHEUMATOLOGY.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.

Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;
 WPI: 1997-087322/08.

New human glutamic acid decarboxylase peptide(s) - used for
 treatment, diagnosis and determining predisposition to diabetes and
 for ameliorating auto-immune responses.

Claim 25; Page -: 28pp; English.

CC W12403-W12413 represent fragments and analogues of the 65 kD isoform
 CC of human glutamic acid decarboxylase (GAD65) (see W12402 for full length
 CC wild type protein). GAD is an enzyme expressed in the beta cells of the

CC pancreas, and in neurons of the central nervous system. There are two
 CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of
 CC GAD65 have been identified in Type I diabetic patients. These GAD65
 CC fragments, and analogues, are used in the methods of the invention. The
 CC methods are for detecting or treating diabetes or a predisposition to
 CC diabetes. The peptides can also be used for ameliorating an autoimmune
 CC response in a patient. Alteration of the native peptides with selective
 CC changes of crucial residues can induce unresponsiveness or change the
 CC responsiveness of antigen-specific autoreactive T cells. The peptide
 CC analogues compete for binding to MHC and do not cause proliferation of
 CC the corresponding native peptide-specific T cells.

XX Sequence 15 AA;

Query Match 50.5%; Score 50; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0084;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVEIAPFVL 10
 |||||
 Db 6 tyeIapfvI 15

RESULT 9

R76652 ID R76652 standard; peptide; 14 AA.

XX AC R76652;

XX DT 05-MAR-1996 (first entry)

XX DE Peptide derived from human glutamic acid decarboxylase 11.

XX KW diabetes; T-cell subpopulation; detection; antigen production;

XX KW diagnosis; autoimmune disease.

XX OS Homo sapiens.

XX PN DE4418091-A1.

XX PD 27-JUL-1995.

XX PF 24-MAY-1994; 94DE-4418091.

XX PR 04-FEB-1994; 94DE-4403522.

XX PR 20-JAN-1994; 94DE-4401629.

XX PA (EMBL/) ENDL J.

XX PA (BOF) BOEHRINGER MANNHEIM GMBH.

XX PI Albert W, Dormair K, Endl J, Jung G, Meinel E;

XX PI Stahl P, Schendel D;

XX DR WPI; 1995-264505/35.

XX PT Antigen-specific activated T-lymphocytes and their detection - by
 PT interaction with inventive peptide(s) of peptide-MHC complexes;
 PT useful in diagnosis of e.g. diabetes and autoimmune diseases

XX PS Claim 1; Fig 2; 21pp; German.

XX R76642-62 are derived from human glutamic acid decarboxylase and
 CC specifically react with T-cell sub-populations isolated from recently
 CC diagnosed Type-I diabetics. Pharmaceutical compns. contg. these
 CC peptides and those shown in R7571-72, are useful for the diagnosis of
 CC a disease or predispositions of immune system diseases, tumours, and
 CC autoimmune diseases, including diabetes. The peptides are able to detect
 CC specific T-cell subpopulations that are then used for antigen prodn.,
 CC e.g. by reinjection.

XX Sequence 14 AA;

Query Match 49.5%; Score 49; DB 16; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LEVYTLKKMR 20
 |||||
 Db 1 levytlkkmr 10

RESULT 10

W18860 ID W18860 standard; peptide; 14 AA.

XX AC W18860;

XX DT 05-JAN-1998 (first entry)

XX DE 65 kD Glutamic acid decarboxylase peptide fragment 11.

XX KW GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;

XX KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;

XX KW predisposition; autoimmune; tumour; rheumatoid arthritis;

XX KW multiple sclerosis.

XX OS Synthetic.

XX PN DE19526561-A1.

XX PD 23-JAN-1997.

XX PF 20-JUL-1995; 95DE-1026561.

XX PR 20-JUL-1995; 95DE-1026561.

XX PA (BOF) BOEHRINGER MANNHEIM GMBH.

XX PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;

XX PI Pozzilli P, Stahl P;

XX DR WPI; 1997-088254/09.

XX PS Skin test for diagnosis of cell-mediated diseases, esp. diabetes -

XX PT involving intradermal admin. of auto-reactive substances

XX PT Claim 11; Fig 2; 12pp; German.

XX W18842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases
 CC such as Rheumatoid arthritis, multiple sclerosis and especially IDDM.

XX Sequence 14 AA;

Query Match 49.5%; Score 49; DB 18; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LEVYTLKKMR 20
 |||||
 Db 1 levytlkkmr 10

RESULT 11

R72275 ID R72275 standard; peptide; 20 AA.

XX R72275;
 XX 13-NOV-1995 (first entry)
 DE Glutamic acid decarboxylase (GAD65) fragment.
 XX Glutamic acid decarboxylase; GAD65; autoimmune disorders;
 KW insulin-dependent diabetes mellitus; stiff man disease.
 XX Homo sapiens.
 OS WO9507992-A.
 PN 23-MAR-1995.
 PD 24-AUG-1994; 94WO-US09478.
 PF 17-SEP-1993; 93US-0123859.
 PR (REGC) UNIV CALIFORNIA.
 PA Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
 PI WPI; 1995-131360/17.
 DR New polypeptide fragments of glutamic acid decarboxylase - for
 PT diagnosis and treatment of autoimmune disease, esp. insulin
 PI dependent diabetes, also related nucleic acid, vectors,
 PT antibodies, hydridoma(s) etc.
 PS Example 11: Page 76; 100pp; English.
 XX Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
 CC acid decarboxylase (GAD65) respectively, from which the GAD65
 CC fragments described in R72261-R72298 were derived. These fragments
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose
 CC and treat GAD-related autoimmune disorders, such as insulin
 CC dependant diabetes mellitus or stiff man disease.
 CC
 SQ Sequence 20 AA;

Query Match 45.5%; Score 45; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 EYVTLKKMR 20
 DB 1 eyvtlkkmr 9

RESULT 12
 ID Y59575 standard; peptide: 20 AA.
 XX Y59575;
 AC Y59575;
 XX 03-APR-2000 (first entry)
 DE GAD65 fragment, peptide #15.
 KW GAD65; glutamic acid decarboxylase 65; autoimmune disorder; IDDM;
 KW insulin dependent diabetes mellitus; Stiff man disease; diagnosis;
 KW therapy.
 XX Homo sapiens.
 OS US5998366-A.
 PN 07-DEC-1999.
 PD 09-APR-1997; 97US-0827618.
 PF

XX 07-JUN-1995; 95US-0485725.
 PR 21-SEP-1990; 90US-0586536.
 PR 18-JUN-1991; 91US-0716909.
 XX (REGC) UNIV CALIFORNIA.
 PA Tobin AJ, Kaufman DL, Erlander MG;
 PI WPI; 2000-095930/08.
 DR Ameliorating glutamic acid decarboxylase associated autoimmune
 PT disorders such as insulin dependent diabetes mellitus and Stiff man
 PI disease -
 PS Example 11: Column 42; 61pp; English.
 XX This sequence represents a fragment of the glutamic acid decarboxylase 65
 CC (GAD65) protein. The invention relates to a method of ameliorating GAD
 CC associated autoimmune disorders by administering a GAD65 peptide to the
 CC patient. The method can be used for ameliorating GAD associated
 CC autoimmune disorders such as IDDM (insulin dependent diabetes mellitus)
 CC and Stiff man disease. GAD65 can also be useful for screening drugs that
 CC alter GAD function, for generating monoclonal antibodies and in
 CC immunosays. GAD65 is an effective diagnostic tool for predicting IDDM
 CC and the diagnosis is quite easy. It is also possible to obtain much
 CC larger quantities of polypeptide via recombinant techniques than are
 CC available from natural sources.
 SQ Sequence 20 AA;

Query Match 45.5%; Score 45; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 EYVTLKKMR 20
 DB 1 eyvtlkkmr 9

RESULT 13
 ID R76659 standard; peptide; 14 AA.
 XX R76659;
 AC R76659;
 XX 05-MAR-1996 (first entry)
 DE Peptide derived from human glutamic acid decarboxylase 18.
 KW diabetes; T-cell subpopulation; detection; antigen production;
 KW diagnosis; autoimmune disease.
 XX Homo sapiens.
 OS DE4418091-A1.
 PN 27-JUL-1995.
 PD 24-MAY-1994; 94DE-4418091.
 PF 04-FEB-1994; 94DE-4403522.
 PR 20-JAN-1994; 94DE-4401629.
 XX (ENDL/) ENDL J.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX Albert W, Dormair K, Endl J, Jung G, Meinel E;
 PI Stahl P, Schendel D;
 DR WPI; 1995-264505/35.
 XX

PT Antigen-specific activated T-lymphocytes and their detection - by
 PT interaction with inventive peptide(s) of peptide-MHC complexes;
 PT useful in diagnosis of e.g. diabetes and auto-immune diseases
 XX
 PS Claim 1; Fig 2; 21pp; German.
 CC R76642-62 are derived from human glutamic acid decarboxylase and
 CC specifically react with T-cell sub-populations isolated from recently
 CC diagnosed Type-1 diabetics. Pharmaceutical compns. contg. these
 CC peptides and those shown in R7571-72, are useful for the diagnosis of
 CC a disease or predispositions of immune system diseases, tumours, and
 CC autoimmune diseases, including diabetes. The peptides are able to detect
 CC specific T-cell subpopulations that are then used for antigen prodn.,
 CC e.g. by reinfection.
 CC
 XX
 SQ Sequence 14 AA;
 DB
 OY 1 TYETAPV 7
 DB 8 lyeiapv 14
 RESULT 14
 ID W18867 standard; peptide; 14 AA.
 AC W18867;
 DT 05-JAN-1998 (first entry)
 XX
 DE 65 kD Glutamic acid decarboxylase peptide fragment 18.
 KW GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;
 KM Insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;
 KM predisposition; autoimmune; tumour; rheumatoid arthritis;
 KM Multiple sclerosis.
 OS Synthetic.
 PN DE19526561-A1.
 PD 23-JAN-1997.
 PF 20-JUL-1995; 95DE-1026561.
 PR 20-JUL-1995; 95DE-1026561.
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 PI Donle F, Endl J, Ganz M, Jung G, Klentsch-engel R;
 PI Pozzilli P, Stahl P;
 PI
 DR WPI; 1997-088254/09.
 PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -
 PT involving intradermal admin. of auto-reactive substances
 XX
 PS Claim 11; Fig 2; 12pp; German.
 CC W18842-70 are peptide fragments of the 65 kD human glutamic acid
 CC decarboxylase (GAD). The fragments are autoreactive substances used for
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is
 CC determined by using a claimed method for diagnosis of cell-mediated
 CC diseases or a predisposition to cell-mediated diseases, which is effected
 CC by administering an autoreactive substance intradermally and establishing
 CC the diagnosis on the basis of the occurrence or lack of a positive
 CC reaction at the site of administration. The method is used for diagnosis
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases

CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.
 XX
 SQ Sequence 14 AA;
 DB
 OY 1 TYETAPV 7
 DB 8 lyeiapv 14
 RESULT 15
 ID W14898 standard; peptide; 10 AA.
 AC W14898;
 DT 27-NOV-1997 (first entry)
 XX
 DE Phakellistatin 9.
 KW cyclic; decapeptide; phakellistatin; sponge; cytostatic;
 KW anticancer.
 OS Phakellia costata.
 FT Key Location/Qualifiers
 FT Modified-site 1 /note- "the imino group of this residue forms a
 FT peptide bond with the carboxy group of Val(10),
 FT i.e. the residue is a component of a cyclic
 FT peptide and is not an N-terminal"
 FT Modified-site 10 /note- "the carboxy group of this residue forms a
 FT peptide bond with the imino group of Pro(1),
 FT i.e. the residue is a component of a cyclic
 FT peptide and is not a C-terminal"
 PN US5646246-A.
 PD 08-JUL-1997.
 PF 14-NOV-1994; 94US-0338383.
 PR 14-NOV-1994; 94US-0338383.
 PA (UYAR-) UNIV ARIZONA STATE.
 PI Pettit GR, Xu J;
 PI
 DR WPI; 1997-362994/33.
 PT New cyclic peptide(s) designated phakellistatin -4, -5, -6, -7, -8
 PT and -9 - are isolated from the sponge Phakellia costata and may be
 PT used in treatment of cancer
 XX
 PS Claim 7; Column 55; 29pp; English.
 CC The patent discloses six new cyclic peptides which have been isolated
 CC from the Western Pacific Ocean sponge Phakellia costata. They are:
 CC cyclo-(Pro-Thr-Pro-Phe-Ile-Phe-Ser) (designated phakellistatin 4),
 CC cyclo-(Pro-Phe-Asn-Ala-Met-Ala-Ile) (designated phakellistatin 5),
 CC cyclo-(Pro-Trp-Leu-Pro-Ile-Pro-Phe) (designated phakellistatin 6),
 CC cyclo-(Pro-Pro-Ile-Phe-Ala-Leu-Pro-Pro-Tyr-Ile) (designated
 CC phakellistatin 7), cyclo-(Pro-Pro-Ile-Phe-Val-Leu-Pro-Tyr-Ile)
 CC (designated phakellistatin 8) and cyclo-(Pro-Pro-Ile-Phe-Val-Leu-Pro-
 CC Pro-Tyr-Val) (designated phakellistatin 9). The cyclic peptides all
 CC demonstrate in vitro p38 ED50 values of between 0.18 and 4.1 mcg/ml.
 CC They also demonstrate in vitro growth inhibitory activity against
 CC human cancer cell lines. They may thus be used in treatment of cancer.

CC The present sequence is that of phakellistatin 9 which demonstrates an
 CC in vitro ED50 value against P388 cells of 4.1 mcg/ml.
 XX
 SO Sequence 10 AA:

Query Match 31.3%; Score 31; DB 18; Length 10;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 6 PVPVLELY 14
 DB 2 PIVLPYPV 10

RESULT 16
 P30120
 ID P30120 standard; peptide: 20 AA.
 XX
 AC P30120;
 XX
 DT 03-APR-1992 (first entry)
 XX
 DE Sequence of peptide PP2c which corresp. to AAs 61-80 of VP1 capsid
 DE protein.
 XX
 KW Antigen; Picornavirus; capsid protein; antibody; detection; vaccine;
 KW diagnosis.
 XX
 OS Polio virus types 1 and 3.
 XX
 PN WO8303547-A.
 XX
 PD 27-OCT-1983.
 XX
 PF 14-APR-1983; 83WO-0002644.
 XX
 PR 25-MAR-1983; 83US-0478847.
 PR 14-APR-1982; 82US-0368308.
 PR 20-SEP-1984; 84US-0653475.
 PR 18-DEC-1984; 84US-0682819.
 XX
 PA (BITT/) BITTLE J L.
 PA (SCRI-) SCRIPPS CLINIC & RE.
 XX
 PI Bittle JL, Lerner RA;
 XX
 DR WPI: 1983-807942/44.
 XX
 WPI: 1983-807942/44.
 XX
 PT Antigenic peptide(s) corresp. to picornavirus capsid protein -
 PT useful in prodn. of vaccines and in diagnostic tests
 XX
 PS Example: Page 53; 90pp; English.
 XX
 CC The peptides of the invention corresp. to a region on the antigenic
 CC Picornavirus capsid protein. The capsid protein FMDV VP1 or Polio
 CC virus VP1. When linked to carriers the peptides are immunogenic.
 CC Dose is 20 ug-2 mg peptide for inoculations.
 XX
 SO Sequence 20 AA:

Query Match 31.3%; Score 31; DB 4; Length 20;
 Best Local Similarity 43.8%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TYEIAVPVLELYVTL 16
 DB 5 CYGTAPARISVPYVGL 20

RESULT 17
 P30121

ID P30121 standard; peptide: 20 AA.

AC P30121;
 XX
 DT 03-APR-1992 (first entry)
 XX
 DE Sequence of peptide PP2d which corresp. to AAs 61-80 of VP1 capsid
 DE protein.
 XX
 KW Antigen; Picornavirus; capsid protein; antibody; detection; vaccine;
 KW diagnosis.
 XX
 OS Polio virus types 1 and 3.
 XX
 PN WO8303547-A.
 XX
 PD 27-OCT-1983.
 XX
 PF 14-APR-1983; 83WO-0002644.
 XX
 PR 25-MAR-1983; 83US-0478847.
 PR 14-APR-1982; 82US-0368308.
 PR 20-SEP-1984; 84US-0653475.
 PR 18-DEC-1984; 84US-0682819.
 XX
 PA (BITT/) BITTLE J L.
 PA (SCRI-) SCRIPPS CLINIC & RE.
 XX
 PI Bittle JL, Lerner RA;
 XX
 DR WPI: 1983-807942/44.
 XX
 WPI: 1983-807942/44.
 XX
 PT Antigenic peptide(s) corresp. to picornavirus capsid protein -
 PT useful in prodn. of vaccines and in diagnostic tests
 XX
 PS Example: Page 53; 90pp; English.
 XX
 CC The peptides of the invention corresp. to a region on the antigenic
 CC Picornavirus capsid protein. The capsid protein FMDV VP1 or Polio
 CC virus VP1. When linked to carriers the peptides are immunogenic.
 CC Dose is 20 ug-2 mg peptide for inoculations.
 XX
 SO Sequence 20 AA:

Query Match 31.3%; Score 31; DB 4; Length 20;
 Best Local Similarity 43.8%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TYEIAVPVLELYVTL 16
 DB 5 CYGTAPARISVPYVGL 20

RESULT 18
 P30321
 ID P30321 standard; peptide: 20 AA.
 XX
 AC P30321;
 XX
 DT 03-APR-1992 (first entry)
 XX
 DE Sequence of polio virus VP1 capsid protein at position 182-201.
 DE
 KW Antigen; Picornavirus; capsid protein; antibody; detection; vaccine;
 KW diagnosis.
 XX
 OS Polio virus type 3 Leon strain.
 XX
 PN WO8303547-A.
 XX
 PD 27-OCT-1983.
 XX

XX The invention relates to inhibiting a protein kinase (I) that has Thr (or
 CC a residue less bulky than Thr) at the position equivalent to Thr 106 in
 CC SAPK2a/p38 by treatment with a pyridinyl-imidazole, or related inhibitor.
 CC The (I) is not SAPK2a/p38 or SAPK2b/p38beta2. The inhibitors are used
 CC therapeutically: (i) to treat extracellular matrix (ECM) deposition, to
 CC encourage tissue regeneration and/or repair, tissue remodelling and
 CC healing of wounds or injuries, also to reduce scar tissue formation
 CC following a brain injury; (ii) to treat patients with (or at risk of
 CC developing) end-stage organ failure, pathological ECM accumulation,
 CC (renal) fibrosis, immunosuppression, diabetic nephropathy, and kidney
 CC damage; (iii) to treat defects of bone growth or homeostasis (e.g.
 CC osteoporosis), arthritis and atherosclerosis in which transforming growth
 CC factorbeta (but not proinflammatory cytokines) are implicated, and (iv)
 CC to treat epithelial, mesenchymal or glial cancers, solid tumors,
 CC melanomas, small cell lung cancer, chronic myelogenous leukemia
 CC (including purging bone marrow of affected cells) and T cell lymphoma.
 CC Transgenic animals (or transfected cells) that include a protein kinase
 CC in which the position equivalent to 106 is mutated are used to determine
 CC the physiological role of the kinase and to identify its substrates, and
 CC the protein kinase can be used to screen for drugs (or lead compounds).
 CC The inhibitors are specific for the (i), i.e. they do not inhibit similar
 CC protein kinases in which the position equivalent to Thr 106 is occupied
 CC by Met or some other bulky residue.
 CC
 XX
 SQ Sequence 15 AA;

Query Match 30.3%; Score 30; DB 21; Length 15;
 Best Local Similarity 30.0%; Pred. No. 34;
 Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 6 PVEVLELYVT 15
 I::: I:::
 Db 3 pIyIvIeyms 12

RESULT 21
 Y66517
 ID Y66517 standard; peptide: 15 AA.

AC Y66517;
 DT 07-MAR-2000 (first entry)
 DE Human Src peptide fragment.
 DE
 KW Protein kinase; inhibitor; extracellular matrix deposition; ECM; cancer;
 KW tissue regeneration; tissue remodelling; wound healing; injury; fibrosis;
 KW immunosuppression; diabetic nephropathy; and kidney damage; bone growth;
 KW MAP kinase; osteoporosis; arthritis; atherosclerosis; cytokine; tumor.
 XX
 XX Homo sapiens.
 XX OS
 XX PN WO958128-A1.
 XX PD 18-NOV-1999.
 XX PF 04-MAY-1999; 99WO-GB01385.
 XX PR 09-MAY-1998; 98GB-0009869.
 XX PA (MED-) MEDICAL RES COUNCIL.
 XX PI Cohen P, Goedert M, Eyers PA;
 XX WPI: 2000-038954/03.
 XX Inhibiting particular protein kinases that have non-bulky residue in
 XX the ATP binding site using pyridinyl-imidazole derivative, e.g. for
 XX reducing deposition of extracellular matrix -
 XX Example 1; Fig 1; 93pp; English.

XX The invention relates to inhibiting a protein kinase (I) that has Thr (or
 CC a residue less bulky than Thr) at the position equivalent to Thr 106 in
 CC SAPK2a/p38 by treatment with a pyridinyl-imidazole, or related inhibitor.
 CC The (I) is not SAPK2a/p38 or SAPK2b/p38beta2. The inhibitors are used
 CC therapeutically: (i) to treat extracellular matrix (ECM) deposition, to
 CC encourage tissue regeneration and/or repair, tissue remodelling and
 CC healing of wounds or injuries, also to reduce scar tissue formation
 CC following a brain injury; (ii) to treat patients with (or at risk of
 CC developing) end-stage organ failure, pathological ECM accumulation,
 CC (renal) fibrosis, immunosuppression, diabetic nephropathy, and kidney
 CC damage; (iii) to treat defects of bone growth or homeostasis (e.g.
 CC osteoporosis), arthritis and atherosclerosis in which transforming growth
 CC factorbeta (but not proinflammatory cytokines) are implicated, and (iv)
 CC to treat epithelial, mesenchymal or glial cancers, solid tumors,
 CC melanomas, small cell lung cancer, chronic myelogenous leukemia
 CC (including purging bone marrow of affected cells) and T cell lymphoma.
 CC Transgenic animals (or transfected cells) that include a protein kinase
 CC in which the position equivalent to 106 is mutated are used to determine
 CC the physiological role of the kinase and to identify its substrates, and
 CC the protein kinase can be used to screen for drugs (or lead compounds).
 CC The inhibitors are specific for the (i), i.e. they do not inhibit similar
 CC protein kinases in which the position equivalent to Thr 106 is occupied
 CC by Met or some other bulky residue.
 CC
 XX
 SQ Sequence 15 AA;

Query Match 30.3%; Score 30; DB 21; Length 15;
 Best Local Similarity 30.0%; Pred. No. 34;
 Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 6 PVEVLELYVT 15
 I::: I:::
 Db 3 pIyIvIeyms 12

RESULT 22
 R22401
 ID R22401 standard; Protein: 23 AA.

AC R22401;
 DT 29-JUL-1992 (first entry)
 DE Modified pre sequence for AOA.
 DE
 KW Acylglycyl hydrolase; septicemia; LPS; vaccine; human.
 KW Synthetic.
 XX OS
 XX PN WO9204444-A.
 XX PD 19-MAR-1992.
 XX PF 11-SEP-1991; 91WO-US06569.
 XX PR 12-SEP-1990; 90GS-0581342.
 XX PA (ZYMO-) ZYMOGENETICS INC.
 XX PA (TEXA) UNIV OF TEXAS SYSTEM.
 XX PI Ohara FJ, Hagen FS, Grant FJ, Munford RS;
 XX WPI: 1992-114352/14.
 XX Prodn: of acylglycyl-hydrolase in eukaryotes - using DNA
 XX constructed encoding whole protein or its sub-units, and used to
 XX treat gram negative sepsis.
 XX Claim 18; Page 67; 97pp; English.
 XX DNA encoding the sequence was ligated to the AOA gene in an

expression vector. The vector was used to express the recombinant enzyme, which can be used prophylactically and therapeutically against Gram-negative septicemia in mammals. For treatment, 1 ug-10 mg AOA is given per 70 kg body wt. The recombinant enzyme is produced in higher levels than found naturally in neutrophils and is more easily purified. See also R22395-400.

Sequence 23 AA;

Query Match 30.3%; Score 30; DB 13; Length 23;

Best Local Similarity 62.5%; Pred. No. 56; Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 IAPVFLV 11
: : : : :
Db 10 vapflll 17

RESULT 23

R06504 R06504 standard; protein; 25 AA.

XX R06504;

DT 07-JAN-1991 (first entry)

XX N-terminal sequence of Mr.26000 of F.hepatoca GST (Fh26b).

XX Glutathione-S-transferase (GST); liver fluke infection vaccine; Fh26b.

XX Fasciola hepatica.

PN WO9008819-A.

PD 09-AUG-1990.

XX 31-JAN-1990; 90WO-AU00027.

PR 31-JAN-1989; 89AU-0002481.

PA (DARA-) DARATECH PTY LTD.

PI Camerli SL, Panaccio M, Wilson R, Wiffels GL, Spithill TW; Campbell NJ, Thompson C, Sexton JL;

DR WPI; 1990-260928/34.

PT Vaccine against liver fluke infection in ruminants. esp. sheep - comprises glutathione-S-transferase extracted from adult fasciola hepatica worms.

PS Disclosure; Fig 19; 44pp; English.

XX Fh26b is a GST isolated from the liver fluke F.hepatoca. Its

XX N-terminal sequence shows very high levels of homology with the

XX corresponding region of Schistosoma and mammalian GSTs.

CC Conservation of several key regions of sequence resulted in

CC identities of 55-77% for Fh26b.

CC See also Q05732-Q05736, R06503 and R06505-R06506.

XX Sequence 25 AA;

Query Match 30.3%; Score 30; DB 11; Length 25;

Best Local Similarity 66.7%; Pred. No. 62; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVFVLETV 14
: : : : :
Db 15 pvrllleyl 23

RESULT 24

ID Y66490 standard; peptide; 15 AA.

XX Y66490;

DT 07-MAR-2000 (first entry)

XX Human PDGF receptor peptide fragment.

XX Protein kinase; inhibitor; extracellular matrix deposition; ECM; cancer;

XX tissue regeneration; tissue remodeling; wound healing; injury; fibrosis;

XX immunosuppression; diabetic nephropathy; and kidney damage; bone growth;

XX MAP kinase; osteoporosis; arthritis; atherosclerosis; cytokine; tumor.

OS Homo sapiens.

XX WO958128-A1.

PD 18-NOV-1999.

XX 04-MAY-1999; 99WO-GH01385.

PR 09-MAY-1998; 98GB-0009869.

XX (MEDI-) MEDICAL RES COUNCIL.

PI Cohen P, Goedert M, Meyers PA;

DR WPI; 2000-038954/03.

XX Inhibiting particular protein kinases that have non-bulky residue in

XX the ATP binding site using pyridinyl-imidazole derivative, e.g. for

XX reducing deposition of extracellular matrix

PS Example 1; Fig 1; 93pp; English.

XX The invention relates to inhibiting a protein kinase (I) that has Thr (or

XX a residue less bulky than Thr) at the position equivalent to Thr 106 in

XX SAPK2a/p38 by treatment with a pyridinyl-imidazole, or related inhibitor.

XX The (I) is not SAPK2a/p38 or SAPK2b/p38beta2. The inhibitors are used

XX therapeutically: (i) to treat extracellular matrix (ECM) deposition, to

XX encourage tissue regeneration and/or repair, tissue remodeling and

XX healing of wounds or injuries, also to reduce scar tissue formation

XX following a brain injury; (ii) to treat patients with (or at risk of

XX developing) end-stage organ failure, pathological ECM accumulation,

XX (renal) fibrosis, immunosuppression, diabetic nephropathy, and kidney

XX damage; (iii) to treat defects of bone growth or homeostasis (e.g.

XX osteoporosis), arthritis and atherosclerosis in which transforming growth

XX factorbeta (but not proinflammatory cytokines) are implicated, and (iv)

XX to treat epithelial, mesenchymal or glial cancers, solid tumors,

XX melanomas, small cell lung cancer, chronic myelogenous leukemia

XX (including purging bone marrow of affected cells) and T cell lymphoma.

XX Transgenic animals (or transfected cells) that include a protein kinase

XX in which the position equivalent to 106 is mutated are used to determine

XX the physiological role of the kinase and to identify its substrates, and

XX the protein kinase can be used to screen for drugs (or lead compounds).

XX The inhibitors are specific for the (I), i.e. they do not inhibit similar

XX protein kinases in which the position equivalent to Thr 106 is occupied

XX by Met or some other bulky residue.

XX Sequence 15 AA;

Query Match 29.3%; Score 29; DB 21; Length 15;

Best Local Similarity 37.5%; Pred. No. 51; Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVFVLETV 13
: : : : :
Db 3 pylvlley 10

RESULT 25

ID Y66491 standard; peptide: 15 AA.

AC Y66491:

DT 07-MAR-2000 (first entry)

DE Human Lck peptide fragment.

Protein kinase; inhibitor; extracellular matrix deposition; ECM; cancer;
 tissue regeneration; tissue remodeling; wound healing; injury; fibrosis;
 immunosuppression; diabetic nephropathy; and kidney damage; bone growth;
 MAP kinase; osteoporosis; arthritis; atherosclerosis; cytokine; tumor.

OS Homo sapiens.

PN WO9958128-A1.

PD 18-NOV-1999.

PF 04-MAY-1999; 99WO-GB01385.

PR 09-MAY-1998; 98GB-0009869.

PA (MED1-) MEDICAL RES COUNCIL.

PI Cohen P, Goedert M, Eyers PA:

DR WPL: 2000-038954/03.

Inhibiting particular protein kinases that have non-bulky residue in
 the ATP binding site using pyridinyl-imidazole derivative, e.g. for
 reducing deposition of extracellular matrix -

PS Example 1; Fig 1; 93pp; English.

CC The invention relates to inhibiting a protein kinase (I) that has Thr (or
 CC a residue less bulky than Thr) at the position equivalent to Thr 106 in
 CC SAPK2a/p38 by treatment with a pyridinyl-imidazole, or related inhibitor.
 CC The (I) is not SAPK2a/p38 or SAPK2b/p38beta2. The inhibitors are used
 CC therapeutically: (i) to treat extracellular matrix (ECM) deposition, to
 CC encourage tissue regeneration and/or repair, tissue remodelling and
 CC healing of wounds or injuries, also to reduce scar tissue formation
 CC following a brain injury; (ii) to treat patients with (or at risk of
 CC developing) end-stage organ failure, pathological ECM accumulation,
 CC (renal) fibrosis, immunosuppression, diabetic nephropathy, and kidney
 CC damage; (iii) to treat defects of bone growth or homeostasis (e.g.
 CC osteoporosis), arthritis and atherosclerosis in which transforming growth
 CC factorbeta (but not proinflammatory cytokines) are implicated, and (iv)
 CC to treat epithelial, mesenchymal or glial cancers, solid tumors,
 CC melanomas, small cell lung cancer, chronic myelogenous leukemia
 CC (including purging bone marrow of affected cells) and T cell lymphoma.
 CC Transgenic animals (or transfected cells) that include a protein kinase
 CC in which the position equivalent to 106 is mutated are used to determine
 CC the physiological role of the kinase and to identify its substrates, and
 CC the protein kinase can be used to screen for drugs (or lead compounds).
 CC The inhibitors are specific for the (I); i.e. they do not inhibit similar
 CC protein kinases in which the position equivalent to Thr 106 is occupied
 CC by Met or some other bulky residue.

SQ Sequence 15 AA;

Query Match 29.3%; Score 29; DB 21; Length 15;

Best Local Similarity 37.5%; Pred. No. 51;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 PVEVLLEY 13

DB 3 pylvlley 10

Search completed: February 5, 2001, 10:47:34
 Job time: 628 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:55:28 ; Search time 93.77 Seconds
(without alignments)
24.999 Million cell updates/sec

Title: US-08-981-824-7

Sequence: 1 FFRWYISNPATRHODIFLI 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_prodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	26.2	14	2	09KEL4
2	27	26.2	15	5	09WT4
3	26	25.2	17	6	062645
4	26	25.2	18	6	046665
5	26	25.2	19	11	09JIC5
6	26	25.2	24	12	084272
7	25	24.3	18	10	010722
8	25	24.3	19	10	040183
9	25	24.3	21	10	040181
10	24	23.3	8	11	062527
11	24	23.3	20	2	09R4A6
12	24	23.3	20	12	069381
13	24	23.3	21	12	093G25
14	24	23.3	22	12	068988
15	24	23.3	22	12	090G68
16	24	23.3	22	12	090G62
17	24	23.3	22	12	090G60
18	24	23.3	22	12	090G66
19	24	23.3	22	12	090G62

20	24	23.3	22	12	090GFO	09qgfo human immun
21	24	23.3	22	12	090G68	09qg68 human immun
22	24	23.3	22	12	090G66	09qg66 human immun
23	24	23.3	25	3	09P857	09p857 saccharomyc
24	24	23.3	15	10	P93516	P93516 arabidopsi
25	23	22.3	15	10	09S8W9	09s8w9 nicotiana a
26	23	22.3	20	1	09UW8	09uw8 halobacteri
27	23	22.3	20	8	095947	095947 saccharomyc
28	23	22.3	23	8	P92627	P92627 dinodon sem
29	23	22.3	25	2	09X607	09x607 actinobacti
30	23	22.3	25	8	032966	032966 pinus thunb
31	22	21.4	10	12	P90391	P90391 tomato yell
32	22	21.4	11	9	038415	038415 bacterioph
33	22	21.4	12	2	052112	052112 acinetobact
34	22	21.4	18	13	073605	073605 human immun
35	22	21.4	18	13	09PRS6	09prs6 struthio ca
36	22	21.4	19	4	09UC21	09uc21 homo sapien
37	22	21.4	19	5	09TMR9	09tmr9 pyura stolo
38	22	21.4	19	8	092Y73	092y73 microplitis
39	22	21.4	20	6	09TR77	09tr77 ovis aries
40	22	21.4	21	8	092YB7	092yb7 spinaria sp
41	22	21.4	21	8	09T2R4	09t2r4 solanum tub
42	22	21.4	22	3	09URC3	09urc3 phanerocha
43	22	21.4	22	3	09URC2	09urc2 phanerocha
44	22	21.4	22	4	09UCH8	09uch8 homo sapien
45	22	21.4	22	4	045524	045524 bacillus su

ALIGNMENTS

RESULT 1	
09KEL4	PRELIMINARY; PRT; 14 AA.
ID	09KEL4
AC	09KEL4
DT	01-OCT-2000 (TRENBLREL. 15, Created)
DT	01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT	01-OCT-2000 (TRENBLREL. 15, Last annotation update)
DE	BH0838 PROTEIN.
GN	BH0838.
OS	Bacillus halodurans.
OC	Bacteria: Firmicutes: Bacillus/Clostridium group;
CC	Bacillus/Staphylococcus group; Bacillus.
OX	NCBI_TaxID=86665;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-C-125 / JCM 9153;
RA	Takami H., Nakasone K., Takaki Y.;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF001510; BAB04557.1;
SQ	SEQUENCE 14 AA: 1564 MW; C0359E12C13F5D4D CRC64;
Query Match	26.28; Score 27; DB 2; Length 14;
Best Local Similarity	40.0%; Pred. NO. 3.9e+02;
Matches	4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY	5 VISNPATRHQ 14
DB	5 VLNPATVIVE 14
RESULT 2	
09WT4	PRELIMINARY; PRT; 15 AA.
ID	09WT4
AC	09WT4
DT	01-MAY-2000 (TRENBLREL. 13, Created)
DT	01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT	01-JUN-2000 (TRENBLREL. 14, Last annotation update)
DE	HEMOGLOBIN (FRAGMENT).
OS	Lumbriculus terrestris (Common earthworm).
OC	Eukaryota: Metazoa: Annelida: Clitellata; Oligochaeta; Haplotaxidae;
CC	Lumbricina; Lumbricidae; Lumbricus.

OX NCB1_TaxID=6398;
 RN (1)
 RX MEDLINE=93293879; PubMed=8514787;
 RT SEQUENCE.
 RA Oenby D.W., Zhu H., Schneider K., Beavis R.C., Chat B.T., Riggs A.F.;
 "The extracellular hemoglobin of the earthworm, Lumbricus terrestris.
 RT Determination of subunit stoichiometry."
 RL J. Biol. Chem. 268:13539-13547(1993).
 SQ SEQUENCE 15 AA; 1665 MW; F9B83FE0050D91F5 CRC64;

Query Match 26.28; Score 27; DB 5; Length 15;
 Best Local Similarity 50.08; Pred. No. 4.2e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 7 SNPAATHODI 16
 DB 2 SPRAQSHDEI 11

RESULT 3
 ID 062645 PRELIMINARY; PRT; 17 AA.
 AC 062645;
 DT 01-AUG-1998 (TRENBLREL. 07, Created)
 DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
 DE MEMBRANE COFACTOR PROTEIN CD46 (FRAGMENT).
 OS Saguinus oedipus (Cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCB1_TaxID=9490;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=B95-8;
 RX MEDLINE=98161817; PubMed=9494106;
 RA Murekaml Y., Seta T., Kurita M., Fukui A., Ueda S., Nagasawa S.;
 "Molecular cloning of membrane cofactor protein (MCP; CD46) on B95a
 RT cell, an Epstein-Barr virus-transformed marmoset B cell line: B95a-MCP
 RT is susceptible to infection by the CAM, but not the Nagahata strain of
 RT the measles virus."
 RL Biochem. J. 330:1351-1359(1998).
 DR EMBL; AB001991; BAA25631.1; -.
 KW Membrane.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 1983 MW; 1301A0ECD008F939 CRC64;

Query Match 25.28; Score 26; DB 6; Length 17;
 Best Local Similarity 42.98; Pred. No. 7.2e+02;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 12 THODIDF 18
 DB 8 THREVN 14

RESULT 4
 ID 046665 PRELIMINARY; PRT; 18 AA.
 AC 046665;
 DT 01-JUN-1998 (TRENBLREL. 06, Created)
 DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
 DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
 DE GLUCOSE-6-PHOSPHATE DEHYDROGENASE (FRAGMENT).
 GN G6PD.
 OS Macropus robustus robustus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCB1_TaxID=35350;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224585; PubMed=9060417;

RA Loebel D.A.F., Johnston P.G.;
 RT "Analysis of the intron-exon structure of the G6PD gene of the
 RT wallaroo (Macropus robustus) by polymerase chain reaction."
 RL Mamm. Genome 8:146-147(1997).
 DR EMBL; U53775; AAC48790.1; -.
 DR INTERPRO; IPR001282; -.
 DR PFAM; PF00479; G6PD; 1.
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1992 MW; C6D5981B528258FB CRC64;

Query Match 25.28; Score 26; DB 6; Length 18;
 Best Local Similarity 33.38; Pred. No. 7.7e+02;
 Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 OY 4 MVISNPATHD 15
 DB 1 VAMEKPASTNSD 12

RESULT 5
 ID 09JIC5 PRELIMINARY; PRT; 19 AA.
 AC 09JIC5;
 DT 01-OCT-2000 (TRENBLREL. 15, Created)
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
 DE NAIP1 PROTEIN (FRAGMENT).
 GN NAIP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCB1_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Gromey J.D., Dietrich W.F.;
 RT "High Resolution Genetic and Physical Map of the Lgnl Interval in
 RT C57BL/6J Implicates Naip2 or Naip3 in Legionella pneumophila
 RT Pathogenesis."
 RL Genome Res. 0:0-0(2000).
 DR EMBL; AF240512; AAF81200.1; -.
 FT NON_TER 1
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 1996 MW; 086C67103542478A CRC64;

Query Match 25.28; Score 26; DB 11; Length 19;
 Best Local Similarity 44.48; Pred. No. 8.2e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 8 NPATHDQI 16
 DB 10 DPAAVHSTV 18

RESULT 6
 ID 084272 PRELIMINARY; PRT; 24 AA.
 AC 084272;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
 DE E6 PROTEIN (FRAGMENT).
 GN Human papillomavirus type 19.
 OS Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
 OC NCB1_TaxID=10608;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88089511; PubMed=2826651;
 RA Krubke J., Kraus J., Dellus H., Chow L., Broker T.R., Ifner T.,
 Pfister H.;

RT "Genetic relationship among human papillomaviruses associated with
RT benign and malignant tumours of patients with epidermodysplasia
RT verruciformis."
RL J. Gen. Virol. 68:3091-3103(1987).
DR EMBL: D00204; BAA0143.1; -.
FT NON_TER 24 24
SQ SEQUENCE 24 AA; 2562 MW; E0DD44BEA2811235 CRC64;

Query Match 25.2%; Score 26; DB 12; Length 24;
Best Local Similarity 28.6%; Pred. NO. 1.1e+03;
Matches 4; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 6 ISNPAATHODIDFL 19
Db 1 MANQATEEEIEIV 14

RESULT 7
Q10722 PRELIMINARY; PRT; 18 AA.

AC 010722;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 30 KDA ANTIFUNGAL PROTEIN (FRAGMENT).
OS Engelmannia pinnatifida.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asterales;
OC euasterids II; Asterales; Asteraceae; Asteroideae; Heliantheae;
OC Engelmannia.
OX NCBI_TaxID=53580;
RN [1]
RP TISSUE=LEAF;
RC MEDLINE=96265034; PubMed=8670144;
RX Hyun Q.K., Borgmeyer J.R., Smith C.E., Bell L.D., Shah D.M.;
RA "Isolation and characterization of a 30 kDa protein with antifungal
RT activity from leaves of Engelmannia pinnatifida."
RL Biochem. J. 316:723-727(1996).
CC "- FUNCTION: EXHIBITS BROAD-SPECTRUM ANTIFUNGAL ACTIVITY."
KM Fungicide.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2086 MW; AIF38FCFFOF45ICA CRC64;

Query Match 24.3%; Score 25; DB 10; Length 18;
Best Local Similarity 40.0%; Pred. NO. 1.1e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 FFRVVISNPA 10
Db 7 FETLALQXPA 16

RESULT 8
Q40183 PRELIMINARY; PRT; 19 AA.

AC 040183;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE NEGATIVELY LIGHT-REGULATED PROTEIN (LG106) (FRAGMENT).
OS Lemna gibba (Swollen duckweed).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Araceae; Lemna.
OX NCBI_TaxID=4470;

RN SEQUENCE FROM N.A.
RP Okubara P.A., Flores S., Tobin E.M.;
RA Plant Mol. Biol. 11:673-681(1988).
DR EMBL: M35866; AAA33395.1; -.
FT NON_TER 1 1

SQ SEQUENCE 19 AA; 2153 MW; 975F6176AAB87387 CRC64;

Query Match 24.3%; Score 25; DB 10; Length 19;
Best Local Similarity 36.4%; Pred. NO. 1.2e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 RMVISNPAATH 13
Db 1 RRIITOKASSH 11

RESULT 9
Q40181 PRELIMINARY; PRT; 21 AA.

AC 040181;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE SHORTEST ORF (FRAGMENT).
OS Lemna gibba (Swollen duckweed).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Araceae; Lemna.
OX NCBI_TaxID=4470;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L.;
RA Okubara P.A., Flores S., Tobin E.M.;
RL Plant Mol. Biol. 11:673-681(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=L.;
RA Okubara P.A., Flores S., Tobin E.M.;
RL Plant Mol. Biol. 15:955-956(1990).
DR EMBL: X14075; CAA32238.1; -.
FT NON_TER 1 1
SQ SEQUENCE 21 AA; 2324 MW; B8C75F610576DB73 CRC64;

Query Match 24.3%; Score 25; DB 10; Length 21;
Best Local Similarity 36.4%; Pred. NO. 1.4e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 RMVISNPAATH 13
Db 2 RRIITOKASSH 12

RESULT 10
Q62527 PRELIMINARY; PRT; 8 AA.

AC 062527;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TRANSTHYRETIN (PREALBUMIN) (FRAGMENT).
GN TTR.

OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;

RN SEQUENCE FROM N.A.
RP STRAIN=SPRET/ET;
RX MEDLINE=94319082; PubMed=8043949;

RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,
Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR."
RL Mamm. Genome 5:349-355(1994).
CC "- FUNCTION: THYROID HORMONE-BINDING PROTEIN. PROBABLY TRANSPORTS
CC THYROXINE FROM THE BLOODSTREAM TO THE BRAIN."
CC "- SUBUNIT: HOMOTETRAMER.
DR EMBL: U05689; AAB60461.1; -.

DR MGD; MGI:98865; Ttr.
 KM Albumin; Transport; Retinol-binding; Vitamin A; Thyroid hormone.
 FT NON_TER
 SQ SEQUENCE 8 AA; 828 MW; 9156C76455A2D2CD CRC64;

Query Match 23.3%; Score 24; DB 11; Length 8;
 Best Local Similarity 80.0%; Pred. No. 3.7e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 VISNP 9
 DB 2 VVSNP 6

RESULT 11
 O9RA46 PRELIMINARY; PRT; 20 AA.
 AC O9RA46;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE 2-OXOGUTARATE:FERREDOXIN OXIDOREDUCTASE BETA SUBUNIT
 (EC 1.2.7.3) (FRAGMENT).
 OS Hydrogenobacter thermophilus.
 OC Bacteria; Aquificales; Aquificaceae; Hydrogenobacter.
 OX NCBI_Taxid=940;
 RN [1]
 RX MEDLINE=96236061; PubMed=8655524;
 RA Yoon K.S., Ishii M., Tigarashi T., Kodama T.;
 RT "Purification and characterization of 2-oxoglutarate:ferredoxin
 oxidoreductase from a thermophilic, obligately chemolithoautotrophic
 bacterium, Hydrogenobacter thermophilus TK-6.";
 RL J. Bacteriol. 178:3365-3368(1996).
 SQ SEQUENCE 20 AA; 2284 MW; BA040417DA7A3392 CRC64;

Query Match 23.3%; Score 24; DB 2; Length 20;
 Best Local Similarity 44.4%; Pred. No. 1.9e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 9 PATHODID 17
 DB 8 PADTKSDVE 16

RESULT 12
 O69381 PRELIMINARY; PRT; 20 AA.
 AC O69381;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
 DE (HSV) DNA FOR IE MRNA-2 5' TERMINUS (FRAGMENT).
 OS Herpes simplex virus (type 2).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_Taxid=10310;
 RN [1]
 RX MEDLINE=84015370; PubMed=6312416;
 RA Whilton J.L., Rixon F.J., Easton A.J., Clements J.B.;
 RT "Immediate-early mRNA-2 of herpes simplex viruses types 1 and 2 is
 to transcription regulatory signals.";
 RL Nucleic Acids Res. 11:6271-6287(1983).
 DR EMBL, X01624; CA825766.1; -.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2180 MW; 11C39C0D07A447A9 CRC64;

Query Match 23.3%; Score 24; DB 12; Length 20;

Best Local Similarity 83.3%; Pred. No. 1.9e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 15 DIDFLI 20
 DB 4 DIDMLI 9

RESULT 13
 O9JG25 PRELIMINARY; PRT; 21 AA.
 AC O9JG25;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ORF2 (FRAGMENT).
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_Taxid=68887;
 RN [1]
 RX SEQUENCE FROM N.A.
 RC STRAIN-PATIENT 2;
 RA Okamoto H., Ukita M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,
 RA Tanaka T., Miyakawa Y., Mayumi M.;
 RT "Circular double-stranded forms of TT virus DNA in the liver.";
 RL J. Virol. 74:5161-5167(2000).
 DR EMBL, AB040782; BA094203.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 21 AA; 1949 MW; 39AD537BFACABEC CRC64;

Query Match 23.3%; Score 24; DB 12; Length 21;
 Best Local Similarity 45.5%; Pred. No. 2e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 9 PATHODIDFL 19
 DB 5 PAGGEDADFL 15

RESULT 14
 O68988 PRELIMINARY; PRT; 22 AA.
 AC O68988;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
 DE (HSV) DNA FOR IE MRNA-2 5' TERMINUS (FRAGMENT).
 OS human herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_Taxid=10298;
 RN [1]
 RX SEQUENCE FROM N.A.
 RA MEDLINE=84015370; PubMed=6312416;
 RA Whilton J.L., Rixon F.J., Easton A.J., Clements J.B.;
 RT "Immediate-early mRNA-2 of herpes simplex viruses types 1 and 2 is
 to transcription regulatory signals.";
 RL Nucleic Acids Res. 11:6271-6287(1983).
 DR EMBL, X01625; CA825767.1; -.
 FT NON_TER 22
 FT NON_TER 22
 SQ SEQUENCE 22 AA; 2411 MW; 03EBE1C22C0D07A4 CRC64;

Query Match 23.3%; Score 24; DB 12; Length 22;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 15 DIDFLI 20
 DB 4 DIDMLI 9

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RESULT 15
OY 090G8      PRELIMINARY;      PRT;      22 AA.
AC 090G8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RP;
RX MEDLINE=99412391; PubMed=10482626;
RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,
RA Bell J.E., Simmonds P.;
RT "Mosaic structure of the human immunodeficiency virus type 1 genome
RT infecting lymphoid cells and the brain: evidence for frequent in vivo
RT recombination events in the evolution of regional populations.";
RL J. Virol. 73:8720-8731(1999).
DR EMBL: AF174692; AAF00716.1; -.
DR INTERPRO: IPR000328; -.
DR PFAM: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 22 AA; 2704 MW; 86D008C65CAB43B4 CRC64;

Query Match      23.3%; Score 24; DB 12; Length 22;
Best Local Similarity 37.5%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 2 FRVYISNPATHDID 17
Db 3 FRAVHPRIRROGFE 18

RESULT 16
OY 090G2      PRELIMINARY;      PRT;      22 AA.
AC 090G2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RP;
RX MEDLINE=99412391; PubMed=10482626;
RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,
RA Bell J.E., Simmonds P.;
RT "Mosaic structure of the human immunodeficiency virus type 1 genome
RT infecting lymphoid cells and the brain: evidence for frequent in vivo
RT recombination events in the evolution of regional populations.";
RL J. Virol. 73:8720-8731(1999).
DR EMBL: AF174695; AAF00723.1; -.
DR INTERPRO: IPR000328; -.
DR PFAM: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 22 AA; 2704 MW; 86D008C65CAB43B4 CRC64;

Query Match      23.3%; Score 24; DB 12; Length 22;
Best Local Similarity 37.5%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Query Match      23.3%; Score 24; DB 12; Length 22;
Best Local Similarity 37.5%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
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Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 2 FRVYISNPATHDID 17
Db 3 FRAVHPRIRROGFE 18

RESULT 17
OY 090G0      PRELIMINARY;      PRT;      22 AA.
AC 090G0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LF;
RX MEDLINE=99412391; PubMed=10482626;
RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,
RA Bell J.E., Simmonds P.;
RT "Mosaic structure of the human immunodeficiency virus type 1 genome
RT infecting lymphoid cells and the brain: evidence for frequent in vivo
RT recombination events in the evolution of regional populations.";
RL J. Virol. 73:8720-8731(1999).
DR EMBL: AF174696; AAF00725.1; -.
DR INTERPRO: IPR000328; -.
DR PFAM: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 22 AA; 2704 MW; 86D008C65CAB43B4 CRC64;

Query Match      23.3%; Score 24; DB 12; Length 22;
Best Local Similarity 37.5%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 2 FRVYISNPATHDID 17
Db 3 FRAVHPRIRROGFE 18

RESULT 18
OY 090G6      PRELIMINARY;      PRT;      22 AA.
AC 090G6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LF;
RX MEDLINE=99412391; PubMed=10482626;
RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettle R.P.,
RA Bell J.E., Simmonds P.;
RT "Mosaic structure of the human immunodeficiency virus type 1 genome
RT infecting lymphoid cells and the brain: evidence for frequent in vivo
RT recombination events in the evolution of regional populations.";
RL J. Virol. 73:8720-8731(1999).
DR EMBL: AF174698; AAF00729.1; -.
DR INTERPRO: IPR000328; -.
DR PFAM: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
```

SQ SEQUENCE 22 AA; 2704 MW; 86D008C6CAB43B4 CRC64;

Query Match 23.3%; Score 24; DB 12; Length 22;

Best Local Similarity 37.5%; Pred. No. 2.1e+03;

Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 2 FRVVISNPAATHODID 17
DB 3 FRAVHIIPRRIRGGE 18

RESULT 19

O90GF2 PRELIMINARY; PRT; 22 AA.

AC O90GF2; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCB1_TaxID-11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LN1;

RX MEDLINE-99412391; PubMed-10482626;

RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettie R.P.,

RA Bell J.E., Simmonds P.;

RT "Mosaic structure of the human immunodeficiency virus type 1 genome

infected lymphoid cells and the brain: evidence for frequent in vivo

recombination events in the evolution of regional populations.";

RL J. Virol. 73:8720-8731(1999).

DR EMBL; AF174700; AAF00733.1;

DR INTERPRO: IPR000328;

DR PFAM: PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1

FT SEQUENCE 22 AA; 2676 MW; 86D008C6441C13B4 CRC64;

SQ SEQUENCE 22 AA; 2676 MW; 86D008C6441C13B4 CRC64;

Query Match 23.3%; Score 24; DB 12; Length 22;

Best Local Similarity 37.5%; Pred. No. 2.1e+03;

Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 2 FRVVISNPAATHODID 17

DB 3 FRAVHIIPRRIRGGE 18

RESULT 20

O90GF0 PRELIMINARY; PRT; 22 AA.

AC O90GF0; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCB1_TaxID-11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LN2;

RX MEDLINE-99412391; PubMed-10482626;

RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettie R.P.,

RA Bell J.E., Simmonds P.;

RT "Mosaic structure of the human immunodeficiency virus type 1 genome

infected lymphoid cells and the brain: evidence for frequent in vivo

recombination events in the evolution of regional populations.";

RL J. Virol. 73:8720-8731(1999).

DR EMBL; AF174701; AAF00735.1;

DR INTERPRO: IPR000328;

DR PFAM: PF00517; GP41; 1.

KT Envelope protein.

FT NON_TER 1

FT SEQUENCE 22 AA; 2676 MW; 86D008C6441C13B4 CRC64;

DR EMBL; AF174701; AAF00735.1;

DR INTERPRO: IPR000328;

DR PFAM: PF00517; GP41; 1.

KT Envelope protein.

FT NON_TER 1

FT SEQUENCE 22 AA; 2676 MW; 86D008C6441C13B4 CRC64;

Query Match 23.3%; Score 24; DB 12; Length 22;

Best Local Similarity 37.5%; Pred. No. 2.1e+03;

Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 2 FRVVISNPAATHODID 17

DB 3 FRAVHIIPRRIRGGE 18

RESULT 21

O90GE8 PRELIMINARY; PRT; 22 AA.

AC O90GE8; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCB1_TaxID-11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Cp-1;

RX MEDLINE-99412391; PubMed-10482626;

RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettie R.P.,

RA Bell J.E., Simmonds P.;

RT "Mosaic structure of the human immunodeficiency virus type 1 genome

infected lymphoid cells and the brain: evidence for frequent in vivo

recombination events in the evolution of regional populations.";

RL J. Virol. 73:8720-8731(1999).

DR EMBL; AF174702; AAF00737.1;

DR INTERPRO: IPR000328;

DR PFAM: PF00517; GP41; 1.

KW Envelope protein.

FT NON_TER 1

FT SEQUENCE 22 AA; 2676 MW; 86D008C6441C13B4 CRC64;

Query Match 23.3%; Score 24; DB 12; Length 22;

Best Local Similarity 37.5%; Pred. No. 2.1e+03;

Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 2 FRVVISNPAATHODID 17

DB 3 FRAVHIIPRRIRGGE 18

RESULT 22

O90GE6 PRELIMINARY; PRT; 22 AA.

AC O90GE6; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCB1_TaxID-11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Cp-2;

RX MEDLINE-99412391; PubMed-10482626;

RA Morris A., Marsden M., Halcrow K., Hughes E.S., Brettie R.P.,

RA Bell J.E., Simmonds P.;
 RT "Mosaic structure of the human immunodeficiency virus type 1 genome
 RT infecting lymphoid cells and the brain: evidence for frequent in vivo
 RT recombination events in the evolution of regional populations.";
 RL J. Virol. 73:8720-8731(1999).
 DR EMBL: AF174703; AAF00739.1;
 DR INTERPRO: IPR000328;
 DR PFM: PFO0517; GP41; 1.
 KW Envelope protein.
 FT NON_TER 1
 SQ SEQUENCE 22 AA; 2662 MW; 86D008C640C733B4 CRC64;

Query Match 23.3%; Score 24; DB 12; Length 22;
 Best Local Similarity 37.5%; Pred. No. 2.1e+03;
 Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 QY 2 FRWVSNPATHQDID 17
 DB 3 FRAVHIFRRIKQCFE 18

RESULT 23
 ID 09P8S7 PRELIMINARY; PRT; 25 AA.
 AC 09P8S7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE ALCOHOL DEHYDROGENASE ISOLYME 2 (FRAGMENT).
 OS Saccharomyces douglasi (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RX [1]
 RN NCBI_TaxID=46617;
 RP SEQUENCE FROM N.A.
 RA Young E.T., Sloan J., Miller B., Li N., van Riper K., Dombeck K.M.;
 RT "Evolution of a glucose-regulated ADH gene in the genus
 RT Saccharomyces.";
 RL Gene 245:299-309(2000).
 DR EMBL: AF218307; AAF43643.1;
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2860 MW; 219627E5620191F9 CRC64;

Query Match 23.3%; Score 24; DB 3; Length 25;
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 7 SNPAATHQDI 16
 DB 15 SNGKLEHKDI 24

RESULT 24
 ID 093516 PRELIMINARY; PRT; 15 AA.
 AC 093516;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE COPPER AMINE OXIDASE (FRAGMENT).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 RX [1]
 RN NCBI_TaxID=3702;
 RP SEQUENCE FROM N.A.
 RA Moller S.G., McPherson M.J.;
 RL Biochem. Soc. Trans. 23:0-0(1995).
 DR EMBL: S82298; AAB37691.1;
 DR INTERPRO: IPR000269;

DR PFM: PFO1179; Cu_amine_oxid; 1.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1765 MW; 1A836E041E00C5CE CRC64;

Query Match 22.3%; Score 23; DB 10; Length 15;
 Best Local Similarity 45.5%; Pred. No. 2.1e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 10 AATHQDIDFLI 20
 DB 3 AATVGNVDYII 13

RESULT 25
 ID 09S8W9 PRELIMINARY; PRT; 15 AA.
 AC 09S8W9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE SELF-INCOMPATIBILITY S3 GLYCOPROTEIN (FRAGMENT).
 OS Nicotiana glauca (Winged tobacco) (Persian tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
 OC Solanales; Solanaceae; Nicotiana.
 RX [1]
 RN NCBI_TaxID=4087;
 RP SEQUENCE.
 RA MEDLIN:92404717; PubMed=2535548;
 RA Jahnke W., Batterham M.P., Clarke A.E., Moritz R.L., Simpson R.J.;
 RT "Identification, isolation, and N-terminal sequencing of style
 RT glycoproteins associated with self-incompatibility in Nicotiana
 RT glauca.";
 RL Plant Cell 1:493-499(1989).
 SQ SEQUENCE 15 AA; 1814 MW; D9F5D7B05B215937 CRC64;

Query Match 22.3%; Score 23; DB 10; Length 15;
 Best Local Similarity 36.4%; Pred. No. 2.1e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 FFRWVSNPAA 11
 DB 4 YMQVLQWPPAA 14

Search completed: February 5, 2001, 10:55:30
 Job time: 919 sec

Tue Feb 6 08:48:27 2001

us-08-981-824-7.rspt

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:56:03 Search time 32.57 seconds
(without alignments)

19.831 Million cell updates/sec

Title: US-08-981-824-7

Sequence: 103
1 FFRVVISNPATHDIDELI 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 1436

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	24.3	15	UN01_PINPS	P81106 pinus pinas
2	25	24.3	24	HEMU_LINRE	P23544 linula ree
3	25	24.3	25	PK12_SOLTU	P24744 solanum tub
4	24	23.3	24	PQQA_PSEFL	P55171 pseudomonas
5	23	22.3	9	BUK_CLOPA	P81337 clostridium
6	23	22.3	15	UC29_MAIZE	P80635 zea mays (m
7	23	22.3	21	SRTD_ATREN	P13211 atractaspis
8	22	21.4	17	ARGD_SALTY	P40732 salmonella
9	22	21.4	18	RLZ3_HALCU	P05975 halobacteri
10	22	21.4	19	FIBA_CEREL	P14446 cervus elap
11	22	21.4	19	MIFR_TRISP	P81529 trichinella
12	22	21.4	21	BTX_ATRBI	P80163 attractaspis
13	21	20.4	21	AROE_BUCAT	O44607 buchnera ap
14	21	20.4	21	ECDI_LYMDI	P80896 lymphotria d
15	21	20.4	22	IF26_PIG	P20461 sus scrofa
16	21	20.4	22	MOT1_CANFA	P19833 canis fami
17	21	20.4	25	LMCP_YEAST	P08521 saccharomyc
18	21	20.4	10	SMRP_RAT	P80968 rattus norv
19	20	19.4	10	LCMS_LEUMA	P21144 leucophaea
20	20	19.4	15	ALIS_MANSE	P42559 manduca sex
21	20	19.4	17	UPJ7_UPBMJ	P82044 uperoleia m
22	20	19.4	19	PSAE_CUCSA	P42047 cucumis sat
23	20	19.4	20	COXM_THUOB	P80981 thunnus obe
24	20	19.4	20	COXM_THUOB	P80980 thunnus obe
25	20	19.4	20	PGK_CLOPA	P81346 clostridium
26	20	19.4	20	STVA_STYCL	P81469 styela clav
27	20	19.4	20	STVA_STYCL	P81470 styela clav
28	20	19.4	21	FAT1_TREHY	P81424 tetrahymena
29	20	19.4	25	FLB1_TREHY	P80158 treponema h
30	19	18.4	16	CXAB_CONPE	P50985 conus penna
31	19	18.4	18	AGI_EUPMA	P33889 euphorbia m
32	19	18.4	19	FIBA_BISBO	P14441 blison bonas
33	19	18.4	20	CONO_ONCMY	P80335 oncorhynchus

34	19	18.4	20	1	HEIT_HELHO	P46693 heloderma h
35	19	18.4	20	1	RECC_AZOVI	P37863 azotobacter
36	19	18.4	23	1	MDH_TREHAL	P33163 thermoleoph
37	19	18.4	23	1	UH44_HUMAN	P49289 homo sapien
38	19	18.4	24	1	PQQA_ACICA	P27532 acinetobact
39	19	18.4	24	1	RIPA_SAMNI	P33183 sanbucus nl
40	19	18.4	25	1	CHLY_CARPA	P81241 carica papa
41	19	18.4	25	1	FLB3_TREHY	P80161 treponema h
42	19	18.4	25	1	OM53_PORGI	P81363 porphyromon
43	19	18.4	25	1	RS11_TRETH	P80376 thermus aqu
44	18.5	18.0	17	1	JHBP_PLAVG	P56675 platyrepia
45	18	17.5	6	1	TMOF_SARBU	P41495 sarcophaga

ALIGNMENTS

RESULT 1	UN01_PINPS	STANDARD:	PRT:	15 AA.
ID	UN01_PINPS			
AC	P81106;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (S1247/S1248) (N150/N151) (FRAGMENT).			
OS	Pinus pinaster (Maritime pine).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=NEEDLE;			
RA	Plomion C., Costa P., Bahman N., Frigerio J.M.;			
RT	"Genetic analysis of needle proteins in maritime pine. 1. Mapping dominant and codominant protein markers assayed on diploid tissue, in a haploid-based genetic map."			
RL	Silvae Genetica 46:161-165(1997).			
RN	[2]			
RP	SEQUENCE.			
RC	TISSUE=NEEDLE;			
RX	MEDLINE-99274088; PubMed-10344291;			
RA	Coste P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A., Frigerio J.-M., Plomion C.;			
RT	"Separation and characterization of needle and xylem maritime pine proteins."			
RL	Electrophoresis 20:1098-1108(1999).			
CC	-1- MICROPHORESIS ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.5, ITS MW IS: 62 KDA.			
CC	PROTEIN IS: 5.5, ITS MW IS: 62 KDA.			
FT	NON_TER			
FT	1			
FT	15			
SO	SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;			
Query Match	24.3%;	Score 25;	DB 1;	Length 15;
Best Local Similarity	40.0%;	Pred. No. 2.1e+02;		
Matches	4;	Conservative	4;	Mismatches 2;
			Indels	0;
			Gaps	0;
OY	6 ISNPATHD 15			
DB	5 ITOPSATND 14			
RESULT 2	HEMU_LINRE	STANDARD:	PRT:	24 AA.
ID	HEMU_LINRE			
AC	P23544;			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	HEMERYTHRIN BETA CHAIN (FRAGMENT).			
OS	Lingula reeii.			
OC	Eukaryota; Metazoa; Brachiopoda; Linguliformea; Lingulata; Lingulida; Lingulidae; Lingulidae; Lingula.			

RN [1]
 RP SEQUENCE.
 RX MEDLINE-91369922; PubMed-1892823;
 RA Zhang J.-H., Kurtz D.M. Jr.:
 RT "Two distinct subunits of hemerythrin from the brachiopod Lingula
 RL reveal: an apparent requirement for cooperatively in O₂ binding."
 CC Biochemistry 30:9121-9124(1991).
 CC -1- FUNCTION: HEMERYTHRIN IS A RESPIRATORY PROTEIN IN BLOOD CELLS OF
 CC CERTAIN MARINE WORMS. THE OXYGEN-BINDING SITE IN EACH CHAIN
 CC CONTAINS TWO IRON ATOMS.
 CC -1- SUBUNIT: OCTAMER COMPOSED OF TWO TYPES OF CHAINS: ALPHA AND BETA.
 CC -1- SIMILARITY: BELONGS TO THE HEMERYTHRIN FAMILY.
 DR INTERPRO: IPR002063; -
 DR PROSITE: PS00550; HEMERYTHRINS; PARTIAL.
 KW Oxygen transport; Metal-binding; Iron.
 FT METAL.
 FT NON_TER 24 24 IRON 1 (BY SIMILARITY).
 SO SEQUENCE 24 AA: 2787 MW: 2F0121054632028A CRC64;

Query Match 24.3%; Score 25; DB 1; Length 24;
 Best Local Similarity 45.5%; Pred. No. 3.5e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 7 SNPATTMODID 17
 Db 11 SDFATTYENID 21

RESULT 3
 PK12_SOLUTU STANDARD; PRT: 25 AA.
 AC P24744;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE KUNITZ-TYPE INHIBITOR-2 (PK1-2) (FRAGMENT).
 OS Solanum tuberosum (Potato).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Asteridae I;
 CC Solanales; Solanaceae; Solanum.
 RN [1]
 RP SEQUENCE.
 RP STRAIN-CV. RUSSET BURBANK; TISSUE-TUBER;
 RA Walsh T.A., Twilchell W.P.:
 RT "Two Kunitz-type proteinase inhibitors from potato tubers."
 RL Plant Physiol. 97:15-18(1991).
 CC -1- FUNCTION: POTENT INHIBITOR OF SUBTILISIN. MODERATE INHIBITOR
 CC OF TRYPSIN AND CHYMOTRYPSIN.
 CC -1- TISSUE SPECIFICITY: CONTEXT OF POTATO TUBER.
 CC -1- SIMILARITY: TO SOYBEAN TRYPSIN INHIBITOR (KUNITZ) FAMILY OF
 CC PROTEASE INHIBITOR.
 DR INTERPRO: IPR002160; -
 DR PFAM: PF00197; Kunitz legume; 1.
 DR PROSITE: PS00283; SOYBEAN_KUNITZ; 1.
 KW Serine protease inhibitor.
 FT NON_TER 25 25
 SO SEQUENCE 25 AA: 2920 MW: 1F5607405921DFDC CRC64;

Query Match 24.3%; Score 25; DB 1; Length 25;
 Best Local Similarity 57.1%; Pred. No. 3.7e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 RMVSNP 9
 Db 19 RYINNP 25

RESULT 4
 POQA_PSEFL STANDARD; PRT: 24 AA.
 ID POQA_PSEFL
 AC P55171;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE COENZYME PQQ SYNTHESIS PROTEIN A.
 GN POQA.
 OS Pseudomonas fluorescens.
 CC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN-CHAO;
 RX MEDLINE-96064397; PubMed-8526497;
 RA Schneider U., Keel C., Defago G., Haas D.;
 RT "175-directed cloning of pqq genes from Pseudomonas fluorescens CHAO:
 RT mutational inactivation of the genes results in overproduction of the
 RT antibiotic pyoluteorin."
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).
 CC -1- FUNCTION: REQUIRED FOR COENZYME PYRROLO-QUINOLINE-QUINONE (PQQ)
 CC BIOSYNTHESIS. THIS PROTEIN COULD FUNCTION AS A TEMPLATE FOR PQQ
 CC SYNTHESIS AND PROVIDE THE GLUTAMATE AND TYROSINE RESIDUES WHICH
 CC ARE NECESSARY FOR THE SYNTHESIS.
 CC -1- SIMILARITY: TO OTHER BACTERIAL POQA.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@sib-sib.ch).
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 DR EMBL: X87299; CAA60732.1; -
 DR EMBL: X87299; CAA60731.1; ALT_INIT.
 KW PQQ.
 SO SEQUENCE 24 AA: 2871 MW: ED13A879B2EA3E8E CRC64;

Query Match 23.3%; Score 24; DB 1; Length 24;
 Best Local Similarity 46.7%; Pred. No. 5.2e+02;
 Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 4 MVSNPATMODID 18
 Db 1 MTWSKPATYDRIGF 15

RESULT 5
 BUR_CLOPA STANDARD; PRT: 9 AA.
 ID BUR_CLOPA
 AC P81337;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE BUTYRATE KINASE (EC 2.7.2.7) (BK) (CP 38) (FRAGMENT).
 GN BUR.
 OS Clostridium pasteurianum.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 CC Clostridium.
 RN [1]
 RP SEQUENCE.
 RP STRAIN-W5.
 RX MEDLINE-96291870; PubMed-9629918;
 RA Flengard R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5."
 RL Electrophoresis 19:802-806(1998).
 CC -1- FUNCTION: CATALYSES THE CONVERSION OF BUTYRYL-COA THROUGH BUTYRYL
 CC PHOSPHATE TO BUTYRATE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + 2-BUTANOATE -> ADP + BUTANOYL PHOSPHATE.
 CC -1- PATHWAY: INVOLVED IN THE ACIDOGENIC PHASE OF FERMENTATION.
 CC -1- SIMILARITY: BELONGS TO THE ACETOKINASE FAMILY.
 DR INTERPRO: IPR000890; -
 DR PROSITE: PS01075; ACETATE_KINASE_1; PARTIAL.


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DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
KW TRANSFERASE; KINASE.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match
Best Local Similarity 22.3%; Score 23; DB 1; Length 9;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 FRWISNP 9
Db 2 YKLLINP 9

RESULT 6
UC29_MAIZE STANDARD; PRT; 15 AA.
AC P80635;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 45)
DE (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
RN [1]
RP SEQUENCE.
RA TISSUE-COLEOPTILE;
RA Touzet P., Niccardi F., Morin C., Damerwal C., Huet J.-C.,
RA Percollet J.-C., Zivy M., de Vienne D.;
RT The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 37.6 KDA.
DR MAIZE-2DPAGE; P80635; COLEOPTILE.
DR MAIZE-2DPAGE; P80635; COLEOPTILE.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1679 MW; 3D53086B1601B8C1 CRC64;

Query Match
Best Local Similarity 22.3%; Score 23; DB 1; Length 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 DIDFL 19
Db 11 DIDYL 15

RESULT 7
SRD_ATREN STANDARD; PRT; 21 AA.
AC P13211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE SARAFOTOXIN-D (S6D) (SRFX-D).
OS Atractaspis engaddensis (Israeli burrowing asp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Atractaspididae; Atractaspis.
RN [1]
RP SEQUENCE.
RC TISSUE-VENOM;
RX MEDLINE-90033283; Pubmed-2509240;
RA Bolah A., Wollberg Z., Flemlinger G.;
RT "SRFX-d, a new native peptide of the endothelin/sarafotoxin family.";
RL FEBS Lett. 256:1-3(1989)
CC -1- FUNCTION: VASOCONSTRICTOR ACTIVITY. THESE TOXINS CAUSE CARDIAC

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CC ARREST PROBABLY AS A RESULT OF CORONARY VASOPLASM.
CC -1- MISCELLANEOUS: LD(50) IS 0.35 MG/KG BY INTRAVENOUS INJECTION.
CC -1- SIMILARITY: BELONGS TO THE ENDOTHELIN/SARAFOTOXIN FAMILY.
KW PIR; S06145; S06145.
DR HSSP; P13208; 1SRB.
DR INTERPRO; IPR001928; -.
DR PRAM; PF00332; endothelin; 1.
DR PRINTS; PR00365; ENDOTHELIN.
DR PROSITE; PS00270; ENDOTHELIN; 1.
KW Venom; Vasoconstrictor; Toxin.
FT DISULFID 1 15
FT DISULFID 3 11
FT DISULFID 11 15
SQ SEQUENCE 21 AA; 2596 MW; 83A8A04D1D536AE2 CRC64;

Query Match
Best Local Similarity 22.3%; Score 23; DB 1; Length 21;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 HODI 16
Db 16 HODI 19

RESULT 8
ARGD_SALTY STANDARD; PRT; 17 AA.
AC P40732;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE ACETYLORNITHINE AMINOTRANSFERASE (EC 2.6.1.11) (ACOAT) (FRAGMENT).
GN ARGD OR DTU.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90094246; Pubmed-2403545;
RA Tran P.V., Bannor T.A., Doktor S.Z., Nichols B.P.;
RT "Chromosomal organization and expression of Escherichia coli paba.";
RL J. Bacteriol. 172:397-410(1990).
CC -1- CATALYTIC ACTIVITY: N2-ACETYL-L-ORNITHINE + 2-OXOGlutamate -
CC N-ACETYL-L-GLUTAMATE 5-SEMIALDEHYDE + L-GLUTAMATE.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FOURTH STEP IN ARGinine BIOSYNTHESIS.
CC -1- MISCELLANEOUS: THE REACTION CATALYZED BY ACOAT IS HIGHLY
CC REVERSIBLE. MOREOVER THIS ENZYME MAY TRANSMUTATE ORNITHINE.
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M32354; AAA24265.1; -.
DR EMBL; M32355; AAA27178.1; -.
DR STYGENE; SG10488; ARGD.
DR INTERPRO; IPR000954; -.
DR PROSITE; PS00600; AA TRANSFER CLASS_3; PARTIAL.
KW Transferase; Aminotransferase; Pyridoxal phosphate;
KW Arginine biosynthesis.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1909 MW; 03DD865FE9D1E6B9 CRC64;

Query Match
Best Local Similarity 21.4%; Score 22; DB 1; Length 17;
Matches 6; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

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QY 4 VVISNPAATHQDIDFLI 20
DB 1 MAIEQFAIRAFDEVI 17

RESULT 9

RL23_HALCU STANDARD: PRT; 18 AA.

AC P05975;

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 50S RIBOSOMAL PROTEIN L23P (HL31) (FRAGMENT).

GN RPL23P.

OS Halobacterium cutirubrum.

OC Archaea: Euryarchaeota; Halobacteriales; Halobacteriaceae;

CC Halobacterium.

RM [1]

RP SEQUENCE.

RX MEDLINE-84282108; PubMed-6467081;

RA Matheson A.T., Yaguchi M., Christensen P., Rollin C.F., Hasnain S.;

RT "Purification, properties, and N-terminal amino acid sequence of

RT certain 50S ribosomal subunit proteins from the archaeobacterium

RL Halobacterium cutirubrum."

Can. J. Biochem. Cell Biol. 62:426-433(1984).

CC -1- FUNCTION: BINDS TO A SPECIFIC REGION ON THE 23S RNA

(BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.

DR INTERPRO: IPR001014;

DR PROSITE: PS00050; RIBOSOMAL_L23; PARTIAL.

KW Ribosomal protein; rRNA-binding.

FT NON_TER

SQ SEQUENCE 18 AA; 2041 MW; 3E61DC53F8B4D4C CRC64;

Query Match 21.4%; Score 22; DB 1; Length 18;

Best Local Similarity 30.8%; Pred. No. 8.4e+02;

Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 VVISNPAATHQDIDFLI 17

DB 3 IIDYPLVTEKAMD 15

RESULT 10

FIBA_CEREL STANDARD: PRT; 19 AA.

AC P14446;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DE FIBRINOPEPTIDE A.

OS Ceruus elaphus (red deer), and Ceruus elaphus nelsoni (American elk).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;

OC Cervidae; Cervinae; Cervus.

RM [1]

RP SEQUENCE.

RC SPECIES-C. ELAPHUS;

RA Blomback B., Blomback M., Grondahl N.J.;

RT "Studies on fibrinopeptides from mammals."

RL Acta Chem. Scand. 19:1789-1791(1965).

RM [2]

RP SEQUENCE.

RC SPECIES-C. E. NELSONI;

RA Mross G.A., Doolittle R.F.;

RT "Amino acid sequence studies on artiodactyl fibrinopeptides."

Arch. Biochem. Biophys. 122:674-684(1967).

CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT

CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET

CC AGGREGATION.

CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR HSPD: P02671; 1BBR.

KW Blood coagulation; Plasma.

FT NON_TER

SQ SEQUENCE 19 AA; 1808 MW; 9BA54C26873B59C5 CRC64;

Query Match 21.4%; Score 22; DB 1; Length 19;

Best Local Similarity 46.2%; Pred. No. 8.9e+02;

Matches 6; Conservative 3; Mismatches 0; Indels 4; Gaps 1;

QY 7 SNPAATHQDIDFLI 19

DB 4 SDPASS----DFL 12

RESULT 11

MIFH_TRISP STANDARD: PRT; 19 AA.

AC P81529;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE L-DOPACHROME-METHYL ESTER TAUTOMERASE (MACROPHAGE MIGRATION INHIBITORY

DE FACTOR HOMOLOG) (FRAGMENT).

OS Trichinella spiralis.

OC Eukaryota; Metazoa; Nematoda; Enoplia; Trichocephalida;

OC Trichocephalina; Trichinelloidea; Trichinellidae; Trichinella.

RM [1]

RP SEQUENCE.

RX MEDLINE-99013685; PubMed-9794786;

RA Pennock J.L., Behnke J.M., Bickle O.D., Devaney E., Grencis R.K.,

RA Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;

RT "Rapid purification and characterization of L-dopamine-methyl ester

RT tautomerase (macrophage migration inhibitory factor) from Trichinella

RT spiralis, Trichuris muris and Brugia pahangi."

RL Biochem. J. 335:495-498(1998).

CC -1- FUNCTION: TAUTOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.

CC -1- INDUCTION: INHIBITED BY FREE FATTY ACIDS AND HAEMATIN.

CC -1- SIMILARITY: BELONGS TO THE MIF FAMILY.

DR INTERPRO: IPR001398;

DR PROSITE: PS01158; MIF; PARTIAL.

FT CYCLOKINE.

FT NON_TER

SQ SEQUENCE 19 AA; 2106 MW; F7CA05F112A628D CRC64;

Query Match 21.4%; Score 22; DB 1; Length 19;

Best Local Similarity 46.2%; Pred. No. 8.9e+02;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 7 SNPAATHQDIDFLI 19

DB 7 TIKATDVPSDFL 19

RESULT 12

BTX_ATRBI STANDARD: PRT; 21 AA.

AC P80163;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE BIROROXIN (BTX).

OS Attractaspis bibroni (Southern bibron's) (Stiletto snake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Attractaspididae; Attractaspis.

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RN [1]
RP SEQUENCE.
RX TISSUE-VENOM;
RA Becker A., Dowdle E.B., Hechler U., Kauser K., Donner P.,
RT Schleuning W.-D.;
RT "Bibrotaxin, a novel member of the endothelin/sarafotoxin peptide
family, from the venom of the burrowing asp Atractaspis bibroni.";
RL FEBS Lett. 315:100-103(1993).
CC -1- FUNCTION: VASOCONSTRICTOR ACTIVITY. THESE TOXINS CAUSE CARDIAC
ARRREST PROBABLY AS A RESULT OF CORONARY VASOPLASIA.
CC -1- SIMILARITY: BELONGS TO THE ENDOTHELIN/SARAFOTOXIN FAMILY.
DR HSP; S27039; S27039.
DR HSP; P13208; ISR.
DR INTERPRO; IPR001928;
DR PFAM; PF00322; endothelin; 1.
DR PRINTS; PR00365; ENDOTHELIN.
DR PROSITE; PS00270; ENDOTHELIN; 1.
KM Venom; Vasconstrictor; Toxin.
FT DISULFID 1 15 BY SIMILARITY.
FT DISULFID 3 11 BY SIMILARITY.
SQ SEQUENCE 21 AA; 2511 MW; 83A5DF81D036AE2 CRC64;

Query Match 21.4%; Score 22; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 HQDI 16
Db 16 HQDV 19

RESULT 13
AROE_BUCAI STANDARD; PRT; 21 AA.
ID 044607;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25) (FRAGMENT).
AROE OR BU493.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95212914; Pubmed-7535281;
RA Roubbaksh D., Baumann P.;
RT "Characterization of a putative 23S-5S rRNA operon of Buchnera
aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
gene.";
RL Gene 155:107-112(1995).
CC -1- CATALYTIC ACTIVITY: SHIKIMATE + NADP(+) -> 5-DEHYDROSHIKIMATE +
NADPH.
CC -1- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE
BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- SIMILARITY: BELONGS TO THE SHIKIMATE DEHYDROGENASE FAMILY.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 13.
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CC -----
DR EMBL; U10496; AAA79125.1; ALT.FRAME.
KW Aromatic amino acid biosynthesis; Oxidoreductase; NADP.
FT NON_TER 1 1
SQ SEQUENCE 21 AA; 2590 MW; -23AE77462AB812E6 CRC64;

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Query Match 20.4%; Score 21; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 15 DIDFLI 20
Db 11 EIDYII 16

RESULT 14
ECD1_LYMDI STANDARD; PRT; 21 AA.
ID ECD1_LYMDI
AC P80936; P55898;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TESTIS ECDYSTOTROPIN PEPTIDE 1 (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Lymantriidae; Lymantria.
RN [1]
RP SEQUENCE.
RC TISSUE-BRAIN;
RA Wagner R.M., Loeb M.J., Kochansky J.P., Gelman D.B., Lusby W.R.,
RA Bell R.A.;
RT "Identification and characterization of an ecdysiotropic peptide from
RT brain extracts of the gypsy moth, Lymantria dispar.";
RL Arch. Insect Biochem. Physiol. 34:175-189(1997).
CC -1- FUNCTION: START OR BOOST ECDYSTEROID SYNTHESIS IN TESTIS OF LARVAE
AND PUPAE.
SQ SEQUENCE 21 AA; 2474 MW; E6E819624D1DEB62 CRC64;

Query Match 20.4%; Score 21; DB 1; Length 21;
Best Local Similarity 36.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 NPAATHODIDF 18
Db 11 NDAONNEVLD 21

RESULT 15
IF2G_PIG STANDARD; PRT; 22 AA.
ID IF2G_PIG
AC P20461;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE EUKARYOTIC TRANSLATION INITIATION FACTOR 2 GAMMA SUBUNIT (EIF-2-
DE GAMMA) (FRAGMENT).
CN EIF2S3 OR EIF2G.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
RN [1]
RP SEQUENCE.
RC TISSUE-LIVER.
RA Suzuki R., Mukoyama E.B.;
RT "Pig liver translational initiation factor eif-2: N-terminal amino
RT acid sequences of alpha and gamma subunits and the phosphorylation
RT site structure.";
RL Agric. Biol. Chem. 52:1397-1408(1988).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR tRNA. THIS
CC COMPLEX BINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY RNA BINDING
CC TO FORM A 43S PREINITIATION COMPLEX. JUNCTION OF THE 60S RIBOSOMAL
CC SUBUNIT TO FORM THE 80S INITIATION COMPLEX IS PRECEDED BY
CC HYDROLYSIS OF THE GTP BOUND TO EIF-2 AND RELEASE OF AN EIF-2-GDP
CC BINARY COMPLEX. IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER

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CC ROUND OF INITIATION, THE GDP BOUND TO EIF-2 MUST EXCHANGE WITH GTP
CC BY WAY OF A REACTION CATALYZED BY EIF-2B.
CC -1- SUBUNIT: HETERODIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EIF2G SUBFAMILY.
CC PIR: P70052; P70052.
CC Initiation factor; Protein biosynthesis; GTP-binding.
CC NON_TER 22
CC SEQUENCE 22 AA; 2203 MW; 428BA7D77D18B03C CRC64;

OY Query Match 20.4%; Score 21; DB 1; Length 22;
    Best Local Similarity 25.0%; Pred. No. 1.6e+03;
    Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

DB 4 MVSINPATRHO 15
    1 1 1 1 1
    7 VTIGOPSIXKMD 18

RESULT 16
MOTI_CANFA STANDARD; PRT: 22 AA.
AC P19863:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MOTILIN.
GN MLN.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RM SEQUENCE.
RC TISSUE-INTERESTINE; PubMed-6844663;
RX MEDLINE-83195948;
RA Poltras P., Reeve J.R. Jr., Hunkapiller M.W., Hood L.E., Walsh J.H.;
RT "Purification and characterization of canine intestinal motilin.";
RL Regul. Pept. 5:197-208(1983).
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
CC INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
CC RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
CC PIR: S00189; S00189.
CC DR PIR: A60313; A60313.
CC KW Hormone.
CC FT UNSURE
CC SEQUENCE 1 1
    22 AA; 2685 MW; 4BECB840ABE0639F CRC64;

OY Query Match 20.4%; Score 21; DB 1; Length 22;
    Best Local Similarity 37.5%; Pred. No. 1.6e+03;
    Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 9 PATRHO 16
    1 1 1 1 1
    3 PIFTHSEL 10

RESULT 17
LPCP_YEAST STANDARD; PRT: 25 AA.
ID LPCP_YEAST
AC P08521;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CPA1 LEADER PEPTIDE.
GN YOR302W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87215944; PubMed-3555844;
RA Werner M., Feller A., Messenguy F., Pierard A.;
RT "The leader peptide of yeast gene CPA1 is essential for the
RT translational repression of its expression.";
RL Cell 49:805-813(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-85101411; PubMed-3881260;
RA Werner M., Feller A., Pierard A.;
RT "Nucleotide sequence of yeast gene CP A1 encoding the small subunit
RT of arginine-pyruvate carboxyl-phosphate synthetase. Homology of the
RT deduced amino acid sequence to other glutamine amidotransferases.";
RL Eur. J. Biochem. 146:371-381(1985).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / FY1679;
RX MEDLINE-97298310; PubMed-9153758;
RA Potrey R., Cziepluch C., Tobiasch E., Pujol A., Kordes E.,
RA Jauniaux J.-C.;
RT "Sequence and analysis of a 36.2 kb fragment from the right arm of
RT yeast chromosome XV reveals 19 open reading frames including SNF2 (5'
RT end), CPA1, SLX4, a putative transport ATPase, a putative ribosomal
RT protein and an SNF2 homologue.";
RL Yeast 13:479-482(1997).
CC -1- SIMILARITY: NO A HYPOTHETICAL PROTEIN IN ARG-2 5' REGION FROM
CC NEUROSPORA CRASSA.
CC CC
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CC CC
CC EMBL: M16590; AAA34526.1; -
CC DR EMBL: X01764; CAN25904.1; -
CC DR EMBL: Z75210; CAN95620.1; -
CC DR PIR: A26965; A26965.
CC DR PIR: S25434; S25434.
CC SGP: S0005828; YOR302W.
CC KW Leader peptide.
CC SEQUENCE 25 AA; 2979 MW; 01D494C8AFEA4AA CRC64;

OY Query Match 20.4%; Score 21; DB 1; Length 25;
    Best Local Similarity 50.0%; Pred. No. 1.8e+03;
    Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

DB 6 ISNPATRHO 15
    1 1 1 1 1
    4 LNSOYTCOD 13

RESULT 18
SMBP_RAT STANDARD; PRT: 25 AA.
ID SMBP_RAT
AC P80968;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SM-11044 BINDING PROTEIN (FRAGMENTS).
OS Rattus norvegicus (Rat).
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE.
RC STRAIN-WISTAR.
RX MEDLINE-97407910; PubMed-9261134;
RA Sugisawa T., Matsuzaki-Fujita M., Guillaume J.-L., Camoin L.,
RA Morooka S., Stroberg A.D.;

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RT "Characterization of a novel Iodocyanopindolol and SM-11044 binding
RT protein, which may mediate relaxation of depolarized rat colon
RT tons";
RL J. Biol. Chem. 272:21244-21252(1997).
CC -1- FUNCTION: MAY MEDIATE RELAXATION OF DEPOLARIZED COLON TONS.
CC IT BINDS IODOCYANOPINDOLOL AND SM-11044.
CC -1- MISCELLANEOUS: THE ORDER OF THE FRAGMENTS IS UNKNOWN.
FT NON_TER 1 1
FT UNSURE 6 6 OR Y.
FT NON_CONS 18 19
FT NON_TER 25 25
SQ SEQUENCE 25 AA: 3177 MW: D14FCB9B778C2CB CRC64;

Query Match 20.4%; Score 21; DB 1; Length 25;
Best Local Similarity 28.6%; Pred. No. 1.8e+03;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 1 FFRWVSNPATRQ 14
DB 2 FVFFILADPARFQ 15

RESULT 19
LCMS_LEDMA STANDARD; PRT; 10 AA.
AC P21144; P41497;
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LEUCOMYOSUPPRESSIN (LMS) (LEM-MS).
OC Leucophaea maderae (Madelira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidae; Blaberidae; Leucophaea.
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-HEAD;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucomyosuppressin,
RT an insect neuropeptide that inhibits spontaneous contractions of the
RT cockroach hindgut";
RL Comp. Biochem. Physiol. 85C:329-333(1986).
CC -1- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH
CC PROPODEUM (HINDGUT).
KM Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1275 MW: D3C45229D2C1EAB2 CRC64;

Query Match 19.4%; Score 20; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 9.5e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 14 QDID 17
DB 1 QDVD 4

RESULT 20
ALUS_MANSE STANDARD; PRT; 15 AA.
ID ALUS_MANSE
AC P42559;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE ALATOSTATIN (MAS-AS).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyyla;
OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
RN [1]

RP SEQUENCE.
RC TISSUE-HEAD;
RX MEDLINE-92052112; PubMed-1946359;
RA Kramer S.J., Toschi A., Miller C.A., Kataoka H., Quistad G.B.,
RL J.P., Carney R.L., Schooley D.A.;
RT "Identification of an allatostatin from the tobacco hornworm Manduca
RT sexta";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9458-9462(1991).
CC -1- FUNCTION: STRONGLY INHIBITS JUVENILE HORMONE BIOSYNTHESIS IN VITRO
CC BY THE CORPORA ALLATA FROM FIFTH-STADIUM LARVAE AND ADULT FEMALES.
CC -1- SIMILARITY: BELONGS TO THE ALATOSTATIN FAMILY.
KM Neuropeptide.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 15 AA: 1908 MW: 1605B77CDEBC838E CRC64;

Query Match 19.4%; Score 20; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 FFRVSNP 9
DB 4 FROCFNP 11

RESULT 21
UP37_UPEMJ STANDARD; PRT; 17 AA.
ID UP37_UPEMJ
AC P82044;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UPERIN 3.7.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
OC Uperoleia.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperolein peptides from the dorsal glands of the
RT Australian toadlet Uperoleia mjobergii";
RL Aust. J. Chem. 49:1325-1331(1996).
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW-1844; METHOD-MS-FAB.
KM Amphibian skin; Amidation.
FT MOD_RES 1 1 AMIDATION.
SQ SEQUENCE 17 AA: 1845 MW: 655B748FB438B67B CRC64;

Query Match 19.4%; Score 20; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 FFRVSNP 7
DB 6 FFRVSNP 11

RESULT 22
PSAE_CUCSA STANDARD; PRT; 19 AA.
ID PSAE_CUCSA
AC P42047;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV (PHOTOSYSTEM I 19.5 KDA
DE PROTEIN) (PSI-E) (PS I SUBUNIT 6) (FRAGMENT).
GN PSAE.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

```

OC Cucurbitales; Cucurbitaceae; Cucumis.
RN [1]
RP SEQUENCE.
RC TISSUE=COXYLEDON.
RX MEDLINE-91355209; PubMed-1883835;
RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT "Characterization of genes that encode subunits of cucumber PS I
RL complex by N-terminal sequencing."
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -1- FUNCTION: MAY FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-
CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE PSAE FAMILY.
KM Photosynthesis; Photosystem I; Chloroplast; Thylakoid membrane.
FT NON_TER 19
SQ SEQUENCE 19 AA; 1810 MW; A93E8BD089FB738 CRC64;

Query Match 19.4%; Score 20; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 PAAT 12
DB 8 PAAT 11

RESULT 23
COXM_THUOB STANDARD; PRT; 20 AA.
ID COXM_THUOB
AC P80981;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIB-LIVER (EC 1.9.3.1) (FRAGMENT).
OS Thunnus obesus (Bigeye tuna).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
CC Scombridae; Thunnus.
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER.
RX MEDLINE-97454291; PubMed-9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver."
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +
CC 4 FERRICYTOCHROME C.
KM Oxidoreductase; Mitochondrion.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2213 MW; 03B902A70F3E41A6 CRC64;

Query Match 19.4%; Score 20; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 12 THOD 15
DB 4 SHOD 7

RESULT 24
COXM_THUOB STANDARD; PRT; 20 AA.
ID COXM_THUOB
AC P80980;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE VIIB-HEART (EC 1.9.3.1) (FRAGMENT).
OS Thunnus obesus (Bigeye tuna).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
CC Scombridae; Thunnus.
RN [1]
RP SEQUENCE.
RC TISSUE=HEART.
RX MEDLINE-97454291; PubMed-9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver."
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O +
CC 4 FERRICYTOCHROME C.
KM Oxidoreductase; Mitochondrion.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2303 MW; 0A33BD340065A6 CRC64;

Query Match 19.4%; Score 20; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 12 THOD 15
DB 4 SHOD 7

RESULT 25
PGK_CLOPA STANDARD; PRT; 20 AA.
ID PGK_CLOPA
AC P81346;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE POTASSIUM PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) (CP 11) (FRAGMENT).
OS Clostridium pasteurianum.
CC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
CC Clostridium.
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE-98291870; PubMed-9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -1- CATALYTIC ACTIVITY: ATP + 3-PHOSPHO-D-GLYCERATE -> ADP +
CC 3-PHOSPHO-D-GLYCERYL PHOSPHATE.
CC -1- PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 5.6, ITS MW IS: 56.2 KDA.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
DR INTERPRO: IPR001576;
DR PROSITE: PS00111; PGLYCERATE_KINASE; PARTIAL.
KM Transferase; Kinase; Glycolysis.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2355 MW; 749E31E595C85529 CRC64;

Query Match 19.4%; Score 20; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;

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Tue Feb 6 08:48:26 2001

us-08-981-824-7.rsp

Page 9

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 THODID 17
|:|:|
Db 6 TIEDID 11

Search completed: February 5, 2001, 10:56:04
Job time: 504 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 10:49:32 ; Search time 58.67 seconds
(Without alignments)
23.147 Million cell updates/sec

Title: US-08-981-824-7

Sequence: 103
1 FFRWVSNPAATHODIDFLI 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 5001

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	30.1	16	2	S02473
2	30	29.1	20	2	S00494
3	27	26.2	22	2	S35200
4	25	24.3	14	2	S62374
5	25	24.3	15	2	A45096
6	25	24.3	18	2	S70611
7	25	24.3	21	2	A59325
8	25	24.3	24	2	S62890
9	25	24.3	25	2	B57001
10	24	23.3	8	2	I49404
11	24	23.3	15	2	PQ0194
12	24	23.3	17	2	PH1312
13	24	23.3	18	2	A54195
14	24	23.3	19	2	S00495
15	24	23.3	23	2	PH1364
16	24	23.3	24	1	S58242
17	24	23.3	24	2	I54329
18	24	23.3	25	2	JP0045
19	23	22.3	15	2	PQ0174
20	23	22.3	22	2	PH1325
21	23	22.3	22	2	H49410
22	23	22.3	23	2	B43958
23	23	22.3	24	2	PT0076
24	23	22.3	25	2	T07504
25	23	22.3	25	2	S35926
26	22	21.4	11	2	S42449
27	22	21.4	12	2	S43013
28	22	21.4	12	2	J02308
29	22	21.4	12	2	J02318

30	22	21.4	16	2	PH0763	T-cell receptor be
31	22	21.4	17	2	S58660	H+-transporting AT
32	22	21.4	17	2	B48943	phage antigenic de
33	22	21.4	18	2	I52851	brain-derived neur
34	22	21.4	19	2	PA0010	seed storage prote
35	22	21.4	19	2	S03519	T-cell receptor ga
36	22	21.4	20	2	S72501	protein kinase C 1
37	22	21.4	20	2	S59494	formate dehydrogen
38	22	21.4	21	2	B35417	30K serine protease
39	22	21.4	21	2	A47144	aquaporin-CHIP - h
40	22	21.4	21	2	S27039	blibrotaxin - Bbro
41	22	21.4	23	2	A60226	pyruvate dehydroge
42	22	21.4	24	2	I39289	ZF3 domain - human
43	22	21.4	24	2	PN0456	basic eosinophil p
44	21.5	20.9	20	2	B60365	chymotrypsin inhnb
45	21	20.4	13	2	A54326	glandular kallikre

ALIGNMENTS

RESULT 1
S02473
coat protein VP1 - human poliovirus 1 (fragment)
C:Species: human poliovirus 1
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C:Accession: S02473
R:Martin, A.; Wychowski, C.; Couderc, T.; Craignic, R.; Hogle, J.; Girard, M.
EMBO J. 7, 2839-2847, 1988
A:Title: Engineering a poliovirus type 2 antigenic site on a type 1 capsid results in
A:Reference number: S02473; PMID:89030650
A:Accession: S02473
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-16 <MAR>

Query Match 30.1% Score 31; DB 2; Length 16;
Best Local Similarity 55.6% Pred. No. 40;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 MYISNPAAT 12
DB 1 MYVDNPAST 9

RESULT 2
S00494
hemocyanin chain II - Japanese spiny lobster (fragment)
C:Species: Panulirus japonicus (Japanese spiny lobster)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Aug-1997
C:Accession: S00494
R:Makino, N.; Kimura, S.
Eur. J. Biochem. 173, 423-430, 1988
A:Title: Subunits of Panulirus japonicus hemocyanin. I. Isolation and properties.
A:Reference number: S00492; PMID:8196131
A:Accession: S00494
A:Molecule type: protein
A:Residues: 1-20 <MAK>
C:Superfamily: hemocyanin
C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match 29.1% Score 30; DB 2; Length 20;
Best Local Similarity 41.2% Pred. No. 78;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 MYISNPAATHODIDFLI 20
DB 2 VVASSTAHKODINHL 18

RESULT 3

S35200
 hypothetical protein 7 - Saccharopolyspora hirsuta
 C:Species: Saccharopolyspora hirsuta
 C>Date: 10-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 17-Mar-1999
 C:Accession: S35200
 R:Le Gouill, C.; Desmarais, D.; Dery, C.V.
 M61. Gen. Genet. 240, 146-150, 1993
 A:Title: Saccharopolyspora hirsuta 367 encodes clustered genes similar to ketoacyl synth
 A:Reference number: S35194; MUID:93344153
 C:Accession: S35200
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <GOU>

Query Match 26.2%; Score 27; DB 2; Length 22;
 Best Local Similarity 62.5%; Pred. No. 2.9e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 RMVSNPA 10
 DB 12 RLVVSAPA 19

RESULT 4
 S62374
 alpha-1-antichymotrypsin - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997
 C:Accession: S62374
 R:Tsuda, M.; Sei, T.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;
 Eur. J. Biochem. 235, 821-827, 1996
 A:Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin varia
 A:Reference number: S62374; MUID:96184564
 C:Accession: S62374
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-14 <TSU>

Query Match 24.3%; Score 25; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 3.7e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FFRWISNP 9
 DB 3 FPMKVTNP 11

RESULT 5
 A45096
 thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A45096
 R:de la Pena, P.; Delgado, L.M.; del Camino, D.; Barros, F.
 J. Biol. Chem. 267, 25703-25708, 1992
 A:Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alterna
 A:Reference number: A45096; MUID:93100278
 C:Accession: A45096
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-15 <DEI>
 A:Cross-references: GB:S51512; NID:9261982; PIDN:AAB24549.1; PID:9261983
 A:Experimental source: GH3 anterior pituitary cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:120927)

Query Match 24.3%; Score 25; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 4e+02;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 8 NPATRHDI 16

DB 6 DPLVHMDI 14

RESULT 6
 S70611
 30K protein - Engelmannia pinnatifida (fragment)
 C:Species: Engelmannia pinnatifida
 C>Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 07-May-1999
 C:Accession: S70611
 R:Huyh, O.K.; Borgmeyer, J.R.; Smith, C.E.; Bell, L.D.; Shah, D.M.
 Biochem. J. 316, 723-727, 1996
 A:Title: Isolation and characterization of a 30 kDa protein with antifungal activity
 A:Reference number: S70611; MUID:96265034
 C:Accession: S70611
 A:Molecule type: protein
 A:Residues: 1-18 <HUY>
 A:Experimental source: leaves
 C:Keywords: antifungal

Query Match 24.3%; Score 25; DB 2; Length 18;
 Best Local Similarity 40.0%; Pred. No. 5e+02;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 FFRWISNP 10
 DB 7 FFLALQXPA 16

RESULT 7
 A59325
 probable bacteriophage receptor Bacta [Imported] - Bacteroides fragilis (fragment)
 C:Species: Bacteroides fragilis
 C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
 C:Accession: A59325
 R:Frias-Lopez, J.
 submitted to the Protein Sequence Database, July 2000
 A:Description: Identification of cell wall proteins of Bacteroides fragilis to which
 A:Reference number: A59325
 A:Accession: A59325
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-21 <FRI>
 A:Experimental source: strain ATCC 51477
 A:Note: putative receptor for bacteriophage B40-8

Query Match 24.3%; Score 25; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 6e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 9 PATRHDI 16
 DB 9 PALHDEM 16

RESULT 8
 S62890
 non-histone protein 1 75K chain - human (fragments)
 C:Species: Homo sapiens (man)
 C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C:Accession: S62890
 R:Oderwald, H.; Hughes, M.J.; Jost, J.P.
 FEBS Lett. 382, 313-318, 1996
 A:Title: Non-histone protein 1 (NHP1) is a member of the Ku protein family which is u
 A:Reference number: S62890; MUID:96184511
 C:Accession: S62890
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14;15-24 <ODE>

Query Match 24.3%; Score 25; DB 2; Length 24;
Best Local Similarity 33.3%; Pred. No. 7e+02;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 6 ISNPAATHODID 17
: ||| :
Db 8 LDNPGAKSELD 19

RESULT 9

endo-1,4-beta-xylanase (EC 3.2.1.8) 2 - Streptomyces roseiscleroticius (fragment)
C:Species: Streptomyces roseiscleroticius
C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 06-Dec-1996
C:Accession: B57001
R:Grabski, A.C.; Forrester, I.T.; Patel, R.; Jeffries, T.W.
Protein Expr. Purif. 4, 120-129, 1993
A:Title: Characterization and N-terminal amino acid sequences of beta-(1,4)-endoxylnases
A:Reference number: A57001; M0ID:93229899
A:Accession: B57001
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-25 <GRA>
A:Experimental source: strain NRRL B-11019
A:Note: sequence extracted from NCBI backbone (NCBIP:130008)
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

Query Match 24.3%; Score 25; DB 2; Length 25;
Best Local Similarity 36.4%; Pred. No. 7.4e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 MVTISNPAATHQ 14
: | :
Db 3 VVTTNQTGTHE 13

RESULT 10

prealbumin - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49404
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maeraki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; M0ID:94319082
A:Accession: I49404
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: EMBL:U05669; NID:9497008; PIDN:AAB60461.1; PID:9642825

Query Match 23.3%; Score 24; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 VISNP 9
: ||| :
Db 2 VVSNP 6

RESULT 11

PQ0194
S2-glycoprotein - Persian tobacco (fragment)
C:Species: Nicotiana glauca (Persian tobacco)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 03-Mar-1995
C:Accession: PQ0194

R:Ma, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.;
Planta 169, 184-191, 1986
A:Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with ex
A:Reference number: PQ0192
A:Accession: PQ0194

A:Molecule type: protein
A:Residues: 1-15 <MAU>
A:Experimental source: style
C:Keywords: glycoprotein

Query Match 23.3%; Score 24; DB 2; Length 15;
Best Local Similarity 27.3%; Pred. No. 6e+02;
Matches 3; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 FPMVISNPAA 11
: ||| :
Db 4 YQVLVTPXPS 14

RESULT 12

PH1312
Ig heavy chain DJ region (clone C68-105) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1312
R:Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor B
A:Reference number: PH1302; M0ID:93094761
A:Accession: PH1312
A:Molecule type: DNA
A:Residues: 1-17 <NAS>
C:Keywords: heterotrimer; immunoglobulin

Query Match 23.3%; Score 24; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 FPMVISNPAT 12
: ||| :
Db 2 FGVVTPAT 12

RESULT 13

AS4195
Na+/K+-exchanging ATPase (EC 3.6.1.37) - spiny dogfish (fragment)
C:Species: Squalus acanthias (spiny dogfish)
C:Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: AS4195
R:Esman, M.; Karlish, S.J.; Sottrop-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994
A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K
A:Reference number: AS4195; M0ID:94297020
A:Accession: AS4195
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-18 <ESM>
A:Experimental source: rectal gland
A:Note: sequence extracted from NCBI backbone (NCBIP:149363)
C:Keywords: hydrolase

Query Match 23.3%; Score 24; DB 2; Length 18;
Best Local Similarity 38.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 6 ISNPAATHODIF 18
: ||| :
Db 6 LTPPTPYDIKF 18

RESULT 14

S00495

hemocyanin chain III - Japanese spiny lobster (fragment)

C:Species: Panulirus japonicus (Japanese spiny lobster)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 01-Aug-1997

C:Accession: S00495

R:Maikino, N.; Kimura, S.

Eur. J. Biochem. 173, 423-430, 1988

A:Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.

A:Reference number: S00495; MUID:88196131

A:Accession: S00495

A:Molecule type: protein

A:Residues: 1-19 <MAK>

C:Superfamily: hemocyanin

C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match

23.3%; Score 24; DB 2; Length 19;

Best Local Similarity 42.9%; Pred. No. 7.9e+02;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 7 SNPAATHODIFLI 20

| | | | |

DB 5 SCNAKQDINHIL 18

RESULT 15

PH1364

1g heavy chain DJ region (clone C178-136A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1364

R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761

A:Accession: PH1364

A:Molecule type: DNA

A:Residues: 1-23 <WAS>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match

23.3%; Score 24; DB 2; Length 23;

Best Local Similarity 55.6%; Pred. No. 9.9e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 SNPAATHOD 15

| | | | |

DB 1 STAAATNRD 9

RESULT 16

S58242

pyrroloquinoline quinone precursor pqqa - Pseudomonas fluorescens

N:Alternate names: pyrroloquinoline quinone biosynthesis A

C:Species: Pseudomonas fluorescens

C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C:Accession: S58242

R:Schneider, U.; Keel, C.; Defago, G.; Haas, D.

submitted to the EMBL Data Library, May 1995

A:Description: Tn5-directed cloning of pqg genes from Pseudomonas fluorescens CHAO: the1

A:Reference number: S58239;

A:Accession: S58242

A:Molecule type: DNA

A:Residues: 'MYROHSHPPORSNF', 1-24 <SCH>

A:Cross-references: EMBL:X87299; NID:9929799; PIDN:CA60731.1; PID:9929803; PIDN:CA6073

A>Note: In Genbank entry PF000ABC, release 116.0, the indicated alternative sequence (F

C:Genetics:

A:Gene: pqqa

C:Superfamily: pyrroloquinoline quinone precursor pqqa

C:Keywords: quinoprotein

F:16/20/Product: pyrroloquinoline quinone #status predicted <MAT>

F:16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match

23.3%; Score 24; DB 1; Length 24;

Best Local Similarity 46.7%; Pred. No. 1e+03;

Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 MWISNPATHDIDF 18

| | | | |

DB 1 MTWSKPAYTDLRIGF 15

RESULT 17

I54329

gene NF1 protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 05-Nov-1999

C:Accession: I54329

R:Upadhyaya, K.; Shen, M.; Cherryson, A.; Farnham, J.; Maynard, J.; Huson, S.M.; Harp

Hum. Mol. Genet. 1, 735-740, 1992

A:Title: Analysis of mutations at the neurofibromatosis 1 (NF1) locus.

A:Reference number: I54329; MUID:93258316

A:Accession: I54329

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-24 <RES>

A:Cross-references: GB:S61428; NID:9300449; PIDN:AAB26693.1; PID:9300450

C:Genetics:

A:Gene: GDB:NF1

A:Cross-references: GDB:120231; OMIM:162200

A:Map position: 17q11.2-17q11.2

Query Match

23.3%; Score 24; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 THQD 15

| | | | |

DB 6 THQD 9

RESULT 18

JP0045

ribosomal protein L30 - Staphylococcus aureus (fragment)

C:Species: Staphylococcus aureus

C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03-May-1996

C:Accession: JP0045

R:Ochi, K.

submitted to JRPID, February 1994

A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal

A:Reference number: JP0042

A:Accession: JP0045

A:Molecule type: protein

A:Residues: 1-25 <OCH>

C:Superfamily: Escherichia coli ribosomal protein L30

C:Keywords: protein biosynthesis; ribosome

Query Match

23.3%; Score 24; DB 2; Length 25;

Best Local Similarity 29.4%; Pred. No. 1.1e+03;

Matches 5; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 3 RNVISNPATHDIDFL 19

| | | | |

DB 9 RSVIGRPETQRKTVEAL 25

RESULT 19

PQ0174

stylar glycoprotein 3 - Persian tobacco (fragment)

N:Alternate names: glycoprotein S7

C:Species: Nicotiana glauca (Persian tobacco)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 13-Mar-1997
C:Accession: P00174
R:Jahnen, M.; Batterham, M.P.; Clarke, A.E.; Moritz, R.L.; Sampson, R.
Plant Cell 1, 493-499, 1989
A:Title: Identification, isolation, and N-terminal sequencing of style glycoproteins
A:Reference number: P00173; MUID:92404717
A:Accession: P00174
A:Molecule type: protein
A:Residues: 1-15 <JAH>
A:Experimental source: style
C:Comment: The protein is involved in self-incompatibility of flowering plants.
C:Superfamily: Enterobacter ribonuclease
C:Keywords: glycoprotein

Query Match 22.3% Score 23; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 8.9e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 FFRVVISNPA 11
: : : : :
Db 4 YMDLVLMWPA 14

RESULT 20
PH1325
Ig heavy chain DJ region (clone C199-121) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1325
R:Wasserman, R.; Gailit, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761
A:Accession: PH1325
A:Molecule type: DNA
A:Residues: 1-22 <WAS>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 22.3% Score 23; DB 2; Length 22;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 VISNPATN 13
: : : : :
Db 2 IVVVPAAIH 10

RESULT 21
H49410
t-complex polypeptide 1 homolog (peak 7 fraction) - rabbit (fragments)
N:Alternate names: chaperonin homolog (peak 7)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 23-Mar-1995
C:Accession: H49410
R:Rommelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; Art
Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993
A:Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven rela
A:Reference number: A49410; MUID:94085752
A:Accession: H49410
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-22 <ROM>
A:Experimental source: reticulocyte

Query Match 22.3% Score 23; DB 2; Length 22;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 WVISNPAT 12

Db 1 LEVTNDPAT 9
: : : : :
: : : : :

RESULT 22
B43958
GTP-binding protein, synaptic vesicle-specific - marbled electric ray (fragments)
C:Species: Torpedo marmorata (marbled electric ray)
C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 28-May-1999
C:Accession: B43958
R:Volkmann, W.; Bensner, J.; Elferink, L.A.; Schilling, J.; Scheller, R.H.
Brain Res. Mol. Brain Res. 11, 285-290, 1991
A:Title: A synaptic vesicle specific GTP-binding protein from ray electric organ.
A:Reference number: A43958; MUID:92099847
A:Accession: B43958
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23 <VOL>
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding

Query Match 22.3% Score 23; DB 2; Length 23;
Best Local Similarity 30.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 11 AFHODIDFLI 20
: : : : :
Db 2 AVDQNFDMV 11

RESULT 23
PT0076
leucine dehydrogenase (EC 1.4.1.9) - Corynebacterium diptheriae (fragment)
C:Species: Corynebacterium diptheriae
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C:Accession: PT0076
R:Misono, H.; Sugihara, K.; Kuwamoto, Y.; Nagata, S.; Nagasaki, S.
Agric. Biol. Chem. 54, 1491-1498, 1990
A:Title: Leucine dehydrogenase from Corynebacterium pseudodiptheriticum: Purificatio
A:Reference number: PT0076; MUID:91103959
A:Accession: PT0076
A:Molecule type: protein
A:Residues: 1-24 <MIS>
A:Experimental source: strain ICR2210
C:Comment: This enzyme catalyzes the reversible deamination of branched-chain and str
C:Keywords: oxidoreductase

Query Match 22.3% Score 23; DB 2; Length 24;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 THDID 17
: : : : :
Db 4 THVD 9

RESULT 24
T07504
hypothetical protein 25 - Japanese black pine chloroplast
C:Species: chloroplast plants thunbergiana (Japanese black pine)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
C:Accession: T07504
R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Suglura, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast gen
A:Reference number: Z16030; MUID:95024047
A:Accession: T07504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-25 <WAS>
A:Cross-references: EMBL:DJ7510; NID:9529643; PIDD:BA04382.1; PID:91262665

C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 22.3%; Score 23; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 MVTSP 9
DB 15 MVTSP 20

RESULT 25

S35926
T-cell receptor gamma chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 30-May-1997
C:Accession: S35926
R:Mathioudakis, G.; Platsoucas, C.D.
submitted to the EMBL Data Library, May 1993
A:Description: An alternative splicing between Vgamma2gamma2.3 and Cgamma2 gene segments
A:Reference number: S32764
A:Accession: S35926
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-25 <MAT>
A:Cross-references: EMBL:Z22688
C:Keywords: T-cell receptor

Query Match 22.3%; Score 23; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 FMVISPATQDI 16
DB 7 YLLIRNSLAEQHL 21

Search completed: February 5, 2001, 10:49:32
Job time: 745 sec